

25				30				35								
ggc	gca	cgc	cgt	tac	ctc	aaa	aat	ggc	gag	ctg	ctc	acc	gac	gag	gat	259
Gly	Ala	Arg	Arg	Tyr	Leu	Lys	Asn	Gly	Glu	Leu	Leu	Thr	Asp	Glu	Asp	
		40					45					50				
ctg	gca	tcc	ctg	cgc	gag	cat	gac	gcg	atc	ctt	ctt	ggc	gct	atc	ggt	307
Leu	Ala	Ser	Leu	Arg	Glu	His	Asp	Ala	Ile	Leu	Leu	Gly	Ala	Ile	Gly	
		55				60					65					
gca	cca	ggt	tcc	gtc	cct	cca	gga	att	ctc	gag	cgt	ggt	ttg	ctg	ctg	355
Ala	Pro	Gly	Ser	Val	Pro	Pro	Gly	Ile	Leu	Glu	Arg	Gly	Leu	Leu	Leu	
	70				75					80					85	
aag	atg	cga	ttc	gca	ctg	gat	cac	cac	gtg	aac	ctg	cgc	cca	tcc	aag	403
Lys	Met	Arg	Phe	Ala	Leu	Asp	His	His	Val	Asn	Leu	Arg	Pro	Ser	Lys	
				90					95					100		
ctg	tac	gac	ggc	gtg	gag	tcc	cca	ctg	cgt	aac	cca	ggc	aag	att	gat	451
Leu	Tyr	Asp	Gly	Val	Glu	Ser	Pro	Leu	Arg	Asn	Pro	Gly	Lys	Ile	Asp	
			105					110					115			
ttc	gtt	gtg	gtc	cgc	gaa	ggt	acc	gaa	ggc	gcc	tac	act	ggc	aac	ggt	499
Phe	Val	Val	Val	Arg	Glu	Gly	Thr	Glu	Gly	Ala	Tyr	Thr	Gly	Asn	Gly	
		120					125					130				
gga	gca	atc	cgc	gtg	gga	acc	cct	cac	gag	att	gcc	aac	gaa	acc	tcc	547
Gly	Ala	Ile	Arg	Val	Gly	Thr	Pro	His	Glu	Ile	Ala	Asn	Glu	Thr	Ser	
		135				140					145					
gtg	aac	act	cgc	tac	ggc	gct	gag	cgc	gtt	att	cgc	tac	gca	ttc	gag	595
Val	Asn	Thr	Arg	Tyr	Gly	Ala	Glu	Arg	Val	Ile	Arg	Tyr	Ala	Phe	Glu	
	150				155					160					165	
ctg	gca	cag	agc	cgc	cgc	aag	aag	ctc	acc	ctc	gtg	cac	aag	acc	aac	643
Leu	Ala	Gln	Ser	Arg	Arg	Lys	Lys	Leu	Thr	Leu	Val	His	Lys	Thr	Asn	
				170				175						180		
gtc	ctg	gtt	cac	ggt	ggt	ggc	ctg	tgg	cag	cgc	acc	gta	gat	gag	gtt	691
Val	Leu	Val	His	Gly	Gly	Gly	Leu	Trp	Gln	Arg	Thr	Val	Asp	Glu	Val	
			185					190					195			
gca	aag	gaa	tac	cca	gag	gta	gcc	gtc	gat	tac	aac	cac	atc	gat	gca	739
Ala	Lys	Glu	Tyr	Pro	Glu	Val	Ala	Val	Asp	Tyr	Asn	His	Ile	Asp	Ala	
		200					205					210				
gca	acc	atc	tat	ctg	gtc	act	gat	cct	tcc	cgc	ttc	gat	gtg	att	gtt	787
Ala	Thr	Ile	Tyr	Leu	Val	Thr	Asp	Pro	Ser	Arg	Phe	Asp	Val	Ile	Val	
		215				220					225					
acc	gat	aac	ctc	ttc	ggc	gac	atc	ctc	acc	gat	gag	gca	ggc	gca	gtc	835
Thr	Asp	Asn	Leu	Phe	Gly	Asp	Ile	Leu	Thr	Asp	Glu	Ala	Gly	Ala	Val	
	230				235					240					245	
tct	ggc	gga	att	ggc	ctc	gca	gca	tcc	ggc	aac	atc	gat	gcc	acg	ggc	883
Ser	Gly	Gly	Ile	Gly	Leu	Ala	Ala	Ser	Gly	Asn	Ile	Asp	Ala	Thr	Gly	
				250					255					260		
acc	aac	cct	tcc	atg	ttc	gag	cca	gtc	cac	ggc	tct	gca	cca	gat	atc	931
Thr	Asn	Pro	Ser	Met	Phe	Glu	Pro	Val	His	Gly	Ser	Ala	Pro	Asp	Ile	
			265					270					275			

gca ggc cag gga atc gca gac cca acg gca gca atc cta tcc gct gcg 979  
 Ala Gly Gln Gly Ile Ala Asp Pro Thr Ala Ala Ile Leu Ser Ala Ala  
           280                                  285                                  290

atg ctg ctg cgt cac tta ggt gat gaa gac aac gca gta cgt att gaa  
 1027  
 Met Leu Leu Arg His Leu Gly Asp Glu Asp Asn Ala Val Arg Ile Glu  
           295                                  300                                  305

aca gcc atc gca gct gat gtg gct ggc cga gat aac tct cag ccg att  
 1075  
 Thr Ala Ile Ala Ala Asp Val Ala Gly Arg Asp Asn Ser Gln Pro Ile  
 310                                  315                                  320                                  325

tct acc act gag gtg gga gac cgc atc gtc aag gcg ctg caa agc  
 1120  
 Ser Thr Thr Glu Val Gly Asp Arg Ile Val Lys Ala Leu Gln Ser  
                                   330                                  335                                  340

taaatttcaa cgccgacccc ctt  
 1143

<210> 270  
 <211> 340  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 270  
 Met Lys Leu Ala Val Ile Gly Gly Asp Gly Ile Gly Pro Glu Val Thr  
   1                                  5                                  10                                  15  
 Ala Glu Ala Leu Lys Val Leu Asn Ala Val Arg Asp Asp Ile Glu Thr  
                                   20                                  25                                  30  
 Thr Asp Tyr Asp Leu Gly Ala Arg Arg Tyr Leu Lys Asn Gly Glu Leu  
                                   35                                  40                                  45  
 Leu Thr Asp Glu Asp Leu Ala Ser Leu Arg Glu His Asp Ala Ile Leu  
   50                                  55                                  60  
 Leu Gly Ala Ile Gly Ala Pro Gly Ser Val Pro Pro Gly Ile Leu Glu  
   65                                  70                                  75                                  80  
 Arg Gly Leu Leu Leu Lys Met Arg Phe Ala Leu Asp His His Val Asn  
                                   85                                  90                                  95  
 Leu Arg Pro Ser Lys Leu Tyr Asp Gly Val Glu Ser Pro Leu Arg Asn  
                                   100                                  105                                  110  
 Pro Gly Lys Ile Asp Phe Val Val Val Arg Glu Gly Thr Glu Gly Ala  
                                   115                                  120                                  125  
 Tyr Thr Gly Asn Gly Gly Ala Ile Arg Val Gly Thr Pro His Glu Ile  
   130                                  135                                  140  
 Ala Asn Glu Thr Ser Val Asn Thr Arg Tyr Gly Ala Glu Arg Val Ile  
 145                                  150                                  155                                  160  
 Arg Tyr Ala Phe Glu Leu Ala Gln Ser Arg Arg Lys Lys Leu Thr Leu



					165						170						175
Val	His	Lys	Thr	Asn	Val	Leu	Val	His	Gly	Gly	Gly	Leu	Trp	Gln	Arg		
			180					185					190				
Thr	Val	Asp	Glu	Val	Ala	Lys	Glu	Tyr	Pro	Glu	Val	Ala	Val	Asp	Tyr		
		195					200					205					
Asn	His	Ile	Asp	Ala	Ala	Thr	Ile	Tyr	Leu	Val	Thr	Asp	Pro	Ser	Arg		
	210					215					220						
Phe	Asp	Val	Ile	Val	Thr	Asp	Asn	Leu	Phe	Gly	Asp	Ile	Leu	Thr	Asp		
225					230					235					240		
Glu	Ala	Gly	Ala	Val	Ser	Gly	Gly	Ile	Gly	Leu	Ala	Ala	Ser	Gly	Asn		
				245					250					255			
Ile	Asp	Ala	Thr	Gly	Thr	Asn	Pro	Ser	Met	Phe	Glu	Pro	Val	His	Gly		
			260					265					270				
Ser	Ala	Pro	Asp	Ile	Ala	Gly	Gln	Gly	Ile	Ala	Asp	Pro	Thr	Ala	Ala		
		275					280					285					
Ile	Leu	Ser	Ala	Ala	Met	Leu	Leu	Arg	His	Leu	Gly	Asp	Glu	Asp	Asn		
	290					295					300						
Ala	Val	Arg	Ile	Glu	Thr	Ala	Ile	Ala	Ala	Asp	Val	Ala	Gly	Arg	Asp		
305					310					315					320		
Asn	Ser	Gln	Pro	Ile	Ser	Thr	Thr	Glu	Val	Gly	Asp	Arg	Ile	Val	Lys		
				325					330					335			
Ala	Leu	Gln	Ser														
			340														

<210> 271  
 <211> 403  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(403)  
 <223> FRXA01132

<400> 271  
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 cactagtga gtcctatatag tgagaaggga atcccacaac atg aaa ctt gct gtt 115  
 Met Lys Leu Ala Val  
 1 5  
 att ggt gga gat ggt atc ggc cca gag gtt act gca gaa gcc ctc aag 163  
 Ile Gly Gly Asp Gly Ile Gly Pro Glu Val Thr Ala Glu Ala Leu Lys  
 10 15 20  
 gtt cta aac gct gtc cgc gac gac atc gag acc acc gat tat gac ctt 211  
 Val Leu Asn Ala Val Arg Asp Asp Ile Glu Thr Thr Asp Tyr Asp Leu  
 25 30 35

ggc gca cgc cgt tac ctc aaa aat ggc gag ctg ctc acc gac gag gat 259  
 Gly Ala Arg Arg Tyr Leu Lys Asn Gly Glu Leu Leu Thr Asp Glu Asp  
                   40                  45                  50  
 ctg gca tcc ctg cgc gag cat gac gcg atc ctt ctt ggc gct atc ggt 307  
 Leu Ala Ser Leu Arg Glu His Asp Ala Ile Leu Leu Gly Ala Ile Gly  
                   55                  60                  65  
 gca cca ggt tcc gtc cct cca gga att ctc gag cgt ggt ttg ctg ctg 355  
 Ala Pro Gly Ser Val Pro Pro Gly Ile Leu Glu Arg Gly Leu Leu Leu  
                   70                  75                  80                  85  
 aag atg cga ttc gca ctg gat cac cac gtg aac ctg cgc cca tcc aag 403  
 Lys Met Arg Phe Ala Leu Asp His His Val Asn Leu Arg Pro Ser Lys  
                   90                  95                  100

&lt;210&gt; 272

&lt;211&gt; 101

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 272

Met Lys Leu Ala Val Ile Gly Gly Asp Gly Ile Gly Pro Glu Val Thr  
   1                  5                  10                  15  
 Ala Glu Ala Leu Lys Val Leu Asn Ala Val Arg Asp Asp Ile Glu Thr  
                   20                  25                  30  
 Thr Asp Tyr Asp Leu Gly Ala Arg Arg Tyr Leu Lys Asn Gly Glu Leu  
                   35                  40                  45  
 Leu Thr Asp Glu Asp Leu Ala Ser Leu Arg Glu His Asp Ala Ile Leu  
                   50                  55                  60  
 Leu Gly Ala Ile Gly Ala Pro Gly Ser Val Pro Pro Gly Ile Leu Glu  
                   65                  70                  75                  80  
 Arg Gly Leu Leu Leu Lys Met Arg Phe Ala Leu Asp His His Val Asn  
                   85                  90                  95  
 Leu Arg Pro Ser Lys  
                   100

&lt;210&gt; 273

&lt;211&gt; 1494

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1471)

&lt;223&gt; RXN00536

&lt;400&gt; 273

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 tcgtggaccc acccaaaact ttttaagaag gttgaacaca atg tct cct aac gat 115  
   Met Ser Pro Asn Asp  
   1                  5

gca	ttc	atc	tcc	gca	cct	gcc	aag	atc	gaa	acc	cca	gtt	ggg	cct	cgc	163
Ala	Phe	Ile	Ser	Ala	Pro	Ala	Lys	Ile	Glu	Thr	Pro	Val	Gly	Pro	Arg	
				10					15					20		
aac	gaa	ggc	cag	cca	gca	tgg	aat	aag	cag	cgt	ggc	tcc	tca	atg	cca	211
Asn	Glu	Gly	Gln	Pro	Ala	Trp	Asn	Lys	Gln	Arg	Gly	Ser	Ser	Met	Pro	
			25					30					35			
gtt	aac	cgc	tac	atg	cct	ttc	gag	gtt	gag	gta	gaa	gat	att	tct	ctg	259
Val	Asn	Arg	Tyr	Met	Pro	Phe	Glu	Val	Glu	Val	Glu	Asp	Ile	Ser	Leu	
			40				45					50				
ccg	gac	cgc	act	tgg	cca	gat	aaa	aaa	atc	acc	gtt	gca	cct	cag	tgg	307
Pro	Asp	Arg	Thr	Trp	Pro	Asp	Lys	Lys	Ile	Thr	Val	Ala	Pro	Gln	Trp	
	55					60					65					
tgt	gct	gtt	gac	ctg	cgt	gac	ggc	aac	cag	gct	ctg	att	gat	ccg	atg	355
Cys	Ala	Val	Asp	Leu	Arg	Asp	Gly	Asn	Gln	Ala	Leu	Ile	Asp	Pro	Met	
	70				75				80						85	
tct	cct	gag	cgt	aag	cgc	cgc	atg	ttt	gag	ctg	ctg	gtt	cag	atg	ggc	403
Ser	Pro	Glu	Arg	Lys	Arg	Arg	Met	Phe	Glu	Leu	Leu	Val	Gln	Met	Gly	
				90					95					100		
ttc	aaa	gaa	atc	gag	gtc	ggc	ttc	cct	tca	gct	tcc	cag	act	gat	ttt	451
Phe	Lys	Glu	Ile	Glu	Val	Gly	Phe	Pro	Ser	Ala	Ser	Gln	Thr	Asp	Phe	
			105					110					115			
gat	ttc	gtt	cgt	gag	atc	atc	gaa	aag	ggc	atg	atc	cct	gac	gat	gtc	499
Asp	Phe	Val	Arg	Glu	Ile	Ile	Glu	Lys	Gly	Met	Ile	Pro	Asp	Asp	Val	
		120					125					130				
acc	att	cag	gtt	ctg	gtt	cag	gct	cgt	gag	cac	ctg	att	cgc	cgt	act	547
Thr	Ile	Gln	Val	Leu	Val	Gln	Ala	Arg	Glu	His	Leu	Ile	Arg	Arg	Thr	
		135				140					145					
ttt	gaa	gct	tgc	gaa	ggc	gca	aaa	aac	gtt	atc	gtg	cac	ttc	tac	aac	595
Phe	Glu	Ala	Cys	Glu	Gly	Ala	Lys	Asn	Val	Ile	Val	His	Phe	Tyr	Asn	
	150				155					160					165	
tcc	acc	tcc	atc	ctg	cag	cgc	aac	gtg	gtg	ttc	cgc	atg	gac	aag	gtg	643
Ser	Thr	Ser	Ile	Leu	Gln	Arg	Asn	Val	Val	Phe	Arg	Met	Asp	Lys	Val	
				170					175					180		
cag	gtg	aag	aag	ctg	gct	acc	gat	gcc	gct	gaa	cta	atc	aag	acc	atc	691
Gln	Val	Lys	Lys	Leu	Ala	Thr	Asp	Ala	Ala	Glu	Leu	Ile	Lys	Thr	Ile	
			185					190					195			
gct	cag	gat	tac	cca	gac	acc	aac	tgg	cgc	tgg	cag	tac	tcc	cct	gag	739
Ala	Gln	Asp	Tyr	Pro	Asp	Thr	Asn	Trp	Arg	Trp	Gln	Tyr	Ser	Pro	Glu	
		200					205					210				
tcc	ttc	acc	ggc	act	gag	gtt	gag	tac	gcc	aag	gaa	gtt	gtg	gac	gca	787
Ser	Phe	Thr	Gly	Thr	Glu	Val	Glu	Tyr	Ala	Lys	Glu	Val	Val	Asp	Ala	
	215					220					225					
gtt	gtt	gag	gtc	atg	gat	cca	act	cct	gag	aac	cca	atg	atc	atc	aac	835
Val	Val	Glu	Val	Met	Asp	Pro	Thr	Pro	Glu	Asn	Pro	Met	Ile	Ile	Asn	
	230				235					240					245	

ctg cct tcc acc gtt gag atg atc acc cct aac gtt tac gca gac tcc	883
Leu Pro Ser Thr Val Glu Met Ile Thr Pro Asn Val Tyr Ala Asp Ser	
250 255 260	
att gaa tgg atg cac cgc aat cta aac cgt cgt gat tcc att atc ctg	931
Ile Glu Trp Met His Arg Asn Leu Asn Arg Arg Asp Ser Ile Ile Leu	
265 270 275	
tcc ctg cac ccg cac aat gac cgt ggc acc ggc gtt ggc gca gct gag	979
Ser Leu His Pro His Asn Asp Arg Gly Thr Gly Val Gly Ala Ala Glu	
280 285 290	
ctg ggc tac atg gct ggc gct gac cgc atc gaa ggc tgc ctg ttc ggc	
1027 Leu Gly Tyr Met Ala Gly Ala Asp Arg Ile Glu Gly Cys Leu Phe Gly	
295 300 305	
aac ggc gag cgc acc ggc aac gtc tgc ctg gtc acc ctg gca ctg aac	
1075 Asn Gly Glu Arg Thr Gly Asn Val Cys Leu Val Thr Leu Ala Leu Asn	
310 315 320 325	
atg ctg acc cag ggc gtt gac cct cag ctg gac ttc acc gat ata cgc	
1123 Met Leu Thr Gln Gly Val Asp Pro Gln Leu Asp Phe Thr Asp Ile Arg	
330 335 340	
cag atc cgc agc acc gtt gaa tac tgc aac cag ctg cgc gtt cct gag	
1171 Gln Ile Arg Ser Thr Val Glu Tyr Cys Asn Gln Leu Arg Val Pro Glu	
345 350 355	
cgc cac cca tac ggc ggt gac ctg gtc ttc acc gct ttc tcc ggt tcc	
1219 Arg His Pro Tyr Gly Gly Asp Leu Val Phe Thr Ala Phe Ser Gly Ser	
360 365 370	
cac cag gac gct gtg aac aag ggt ctg gac gcc atg gct gcc aag gtt	
1267 His Gln Asp Ala Val Asn Lys Gly Leu Asp Ala Met Ala Ala Lys Val	
375 380 385	
cag cca ggt gct agc tcc act gaa gtt tct tgg gag cag ctg cgc gac	
1315 Gln Pro Gly Ala Ser Ser Thr Glu Val Ser Trp Glu Gln Leu Arg Asp	
390 395 400 405	
acc cga atg gga ggt tcc tta cct gcc tat cga tcc aaa gga tgt cgg	
1363 Thr Arg Met Gly Gly Ser Leu Pro Ala Tyr Arg Ser Lys Gly Cys Arg	
410 415 420	
tcg cga cta cga ggc tgt tat ccg cgt gaa ctc cca gtc cgg caa ggg	
1411 Ser Arg Leu Arg Gly Cys Tyr Pro Arg Glu Leu Pro Val Arg Gln Gly	
425 430 435	
cgg cgt tgc tta cat cat gaa gac cga tca cgg tct gca gat ccc tcg	
1459 Arg Arg Cys Leu His His Glu Asp Arg Ser Arg Ser Ala Asp Pro Ser	
440 445 450	

ctc cat gca ggt tgagttctcc accgttggtcc aga

1494

Leu His Ala Gly

455

<210> 274

<211> 457

<212> PRT

<213> Corynebacterium glutamicum

<400> 274

Met Ser Pro Asn Asp Ala Phe Ile Ser Ala Pro Ala Lys Ile Glu Thr  
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Pro Val Gly Pro Arg Asn Glu Gly Gln Pro Ala Trp Asn Lys Gln Arg  
20 25 30

Gly Ser Ser Met Pro Val Asn Arg Tyr Met Pro Phe Glu Val Glu Val  
35 40 45

Glu Asp Ile Ser Leu Pro Asp Arg Thr Trp Pro Asp Lys Lys Ile Thr  
50 55 60

Val Ala Pro Gln Trp Cys Ala Val Asp Leu Arg Asp Gly Asn Gln Ala  
65 70 75 80

Leu Ile Asp Pro Met Ser Pro Glu Arg Lys Arg Arg Met Phe Glu Leu  
85 90 95

Leu Val Gln Met Gly Phe Lys Glu Ile Glu Val Gly Phe Pro Ser Ala  
100 105 110

Ser Gln Thr Asp Phe Asp Phe Val Arg Glu Ile Ile Glu Lys Gly Met  
115 120 125

Ile Pro Asp Asp Val Thr Ile Gln Val Leu Val Gln Ala Arg Glu His  
130 135 140

Leu Ile Arg Arg Thr Phe Glu Ala Cys Glu Gly Ala Lys Asn Val Ile  
145 150 155 160

Val His Phe Tyr Asn Ser Thr Ser Ile Leu Gln Arg Asn Val Val Phe  
165 170 175

Arg Met Asp Lys Val Gln Val Lys Lys Leu Ala Thr Asp Ala Ala Glu  
180 185 190

Leu Ile Lys Thr Ile Ala Gln Asp Tyr Pro Asp Thr Asn Trp Arg Trp  
195 200 205

Gln Tyr Ser Pro Glu Ser Phe Thr Gly Thr Glu Val Glu Tyr Ala Lys  
210 215 220

Glu Val Val Asp Ala Val Val Glu Val Met Asp Pro Thr Pro Glu Asn  
225 230 235 240

Pro Met Ile Ile Asn Leu Pro Ser Thr Val Glu Met Ile Thr Pro Asn  
245 250 255

Val Tyr Ala Asp Ser Ile Glu Trp Met His Arg Asn Leu Asn Arg Arg  
 260 265 270

Asp Ser Ile Ile Leu Ser Leu His Pro His Asn Asp Arg Gly Thr Gly  
 275 280 285

Val Gly Ala Ala Glu Leu Gly Tyr Met Ala Gly Ala Asp Arg Ile Glu  
 290 295 300

Gly Cys Leu Phe Gly Asn Gly Glu Arg Thr Gly Asn Val Cys Leu Val  
 305 310 315 320

Thr Leu Ala Leu Asn Met Leu Thr Gln Gly Val Asp Pro Gln Leu Asp  
 325 330 335

Phe Thr Asp Ile Arg Gln Ile Arg Ser Thr Val Glu Tyr Cys Asn Gln  
 340 345 350

Leu Arg Val Pro Glu Arg His Pro Tyr Gly Gly Asp Leu Val Phe Thr  
 355 360 365

Ala Phe Ser Gly Ser His Gln Asp Ala Val Asn Lys Gly Leu Asp Ala  
 370 375 380

Met Ala Ala Lys Val Gln Pro Gly Ala Ser Ser Thr Glu Val Ser Trp  
 385 390 395 400

Glu Gln Leu Arg Asp Thr Arg Met Gly Gly Ser Leu Pro Ala Tyr Arg  
 405 410 415

Ser Lys Gly Cys Arg Ser Arg Leu Arg Gly Cys Tyr Pro Arg Glu Leu  
 420 425 430

Pro Val Arg Gln Gly Arg Arg Cys Leu His His Glu Asp Arg Ser Arg  
 435 440 445

Ser Ala Asp Pro Ser Leu His Ala Gly  
 450 455

&lt;210&gt; 275

&lt;211&gt; 1333

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1333)

&lt;223&gt; FRXA00536

&lt;400&gt; 275

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tcgtggaccc acccaaaact ttttaagaag gttgaacaca atg tct cct aac gat 115  
 Met Ser Pro Asn Asp  
 1 5

gca ttc atc tcc gca cct gcc aag atc gaa acc cca gtt ggg cct cgc 163  
 Ala Phe Ile Ser Ala Pro Ala Lys Ile Glu Thr Pro Val Gly Pro Arg  
 10 15 20

aac gaa ggc cag cca gca tgg aat aag cag cgt ggc tcc tca atg cca	211
Asn Glu Gly Gln Pro Ala Trp Asn Lys Gln Arg Gly Ser Ser Met Pro	
25 30 35	
gtt aac cgc tac atg cct ttc gag gtt gag gta gaa gat att tct ctg	259
Val Asn Arg Tyr Met Pro Phe Glu Val Glu Val Glu Asp Ile Ser Leu	
40 45 50	
ccg gac cgc act tgg cca gat aaa aaa atc acc gtt gca cct cag tgg	307
Pro Asp Arg Thr Trp Pro Asp Lys Lys Ile Thr Val Ala Pro Gln Trp	
55 60 65	
tgt gct gtt gac ctg cgt gac ggc aac cag gct ctg att gat ccg atg	355
Cys Ala Val Asp Leu Arg Asp Gly Asn Gln Ala Leu Ile Asp Pro Met	
70 75 80 85	
tct cct gag cgt aag cgc cgc atg ttt gag ctg ctg gtt cag atg ggc	403
Ser Pro Glu Arg Lys Arg Arg Met Phe Glu Leu Leu Val Gln Met Gly	
90 95 100	
ttc aaa gaa atc gag gtc ggt ttc cct tca gct tcc cag act gat ttt	451
Phe Lys Glu Ile Glu Val Gly Phe Pro Ser Ala Ser Gln Thr Asp Phe	
105 110 115	
gat ttc gtt cgt gag atc atc gaa aag ggc atg atc cct gac gat gtc	499
Asp Phe Val Arg Glu Ile Ile Glu Lys Gly Met Ile Pro Asp Asp Val	
120 125 130	
acc att cag gtt ctg gtt cag gct cgt gag cac ctg att cgc cgt act	547
Thr Ile Gln Val Leu Val Gln Ala Arg Glu His Leu Ile Arg Arg Thr	
135 140 145	
ttt gaa gct tgc gaa ggc gca aaa aac gtt atc gtg cac ttc tac aac	595
Phe Glu Ala Cys Glu Gly Ala Lys Asn Val Ile Val His Phe Tyr Asn	
150 155 160 165	
tcc acc tcc atc ctg cag cgc aac gtg gtg ttc cgc atg gac aag gtg	643
Ser Thr Ser Ile Leu Gln Arg Asn Val Val Phe Arg Met Asp Lys Val	
170 175 180	
cag gtg aag aag ctg gct acc gat gcc gct gaa cta atc aag acc atc	691
Gln Val Lys Lys Leu Ala Thr Asp Ala Ala Glu Leu Ile Lys Thr Ile	
185 190 195	
gct cag gat tac cca gac acc aac tgg cgc tgg cag tac tcc cct gag	739
Ala Gln Asp Tyr Pro Asp Thr Asn Trp Arg Trp Gln Tyr Ser Pro Glu	
200 205 210	
tcc ttc acc ggc act gag gtt gag tac gcc aag gaa gtt gtg gac gca	787
Ser Phe Thr Gly Thr Glu Val Glu Tyr Ala Lys Glu Val Val Asp Ala	
215 220 225	
gtt gtt gag gtc atg gat cca act cct gag aac cca atg atc atc aac	835
Val Val Glu Val Met Asp Pro Thr Pro Glu Asn Pro Met Ile Ile Asn	
230 235 240 245	
ctg cct tcc acc gtt gag atg atc acc cct aac gtt tac gca gac tcc	883
Leu Pro Ser Thr Val Glu Met Ile Thr Pro Asn Val Tyr Ala Asp Ser	
250 255 260	
att gaa tgg atg cac cgc aat cta aac cgt cgt gat tcc att atc ctg	931

Ile Glu Trp Met His Arg Asn Leu Asn Arg Arg Asp Ser Ile Ile Leu  
 265 270 275

tcc ctg cac ccg cac aat gac cgt ggc acc ggc gtt ggc gca gct gag 979  
 Ser Leu His Pro His Asn Asp Arg Gly Thr Gly Val Gly Ala Ala Glu  
 280 285 290

ctg ggc tac atg gct ggc gct gac cgc atc gaa ggc tgc ctg ttc ggc  
 1027  
 Leu Gly Tyr Met Ala Gly Ala Asp Arg Ile Glu Gly Cys Leu Phe Gly  
 295 300 305

aac ggc gag cgc acc ggc aac gtc tgc ctg gtc acc ctg gca ctg aac  
 1075  
 Asn Gly Glu Arg Thr Gly Asn Val Cys Leu Val Thr Leu Ala Leu Asn  
 310 315 320 325

atg ctg acc cag ggc gtt gac cct cag ctg gac ttc acc gat ata cgc  
 1123  
 Met Leu Thr Gln Gly Val Asp Pro Gln Leu Asp Phe Thr Asp Ile Arg  
 330 335 340

cag atc cgc agc acc gtt gaa tac tgc aac cag ctg cgc gtt cct gag  
 1171  
 Gln Ile Arg Ser Thr Val Glu Tyr Cys Asn Gln Leu Arg Val Pro Glu  
 345 350 355

cgc cac cca tac ggc ggt gac ctg gtc ttc acc gct ttc tcc ggt tcc  
 1219  
 Arg His Pro Tyr Gly Gly Asp Leu Val Phe Thr Ala Phe Ser Gly Ser  
 360 365 370

cac cag gac gct gtg aac aag ggt ctg gac gcc atg gct gcc aag gtt  
 1267  
 His Gln Asp Ala Val Asn Lys Gly Leu Asp Ala Met Ala Ala Lys Val  
 375 380 385

cag cca ggt gct agc tcc act gaa gtt tct tgg gag cag ctg cgc gac  
 1315  
 Gln Pro Gly Ala Ser Ser Thr Glu Val Ser Trp Glu Gln Leu Arg Asp  
 390 395 400 405

acc gaa tgg gag gtt cct  
 1333  
 Thr Glu Trp Glu Val Pro  
 410

<210> 276  
 <211> 411  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 276  
 Met Ser Pro Asn Asp Ala Phe Ile Ser Ala Pro Ala Lys Ile Glu Thr  
 1 5 10 15  
 Pro Val Gly Pro Arg Asn Glu Gly Gln Pro Ala Trp Asn Lys Gln Arg  
 20 25 30  
 Gly Ser Ser Met Pro Val Asn Arg Tyr Met Pro Phe Glu Val Glu Val



35					40					45						
Glu	Asp	Ile	Ser	Leu	Pro	Asp	Arg	Thr	Trp	Pro	Asp	Lys	Lys	Ile	Thr	
50					55					60						
Val	Ala	Pro	Gln	Trp	Cys	Ala	Val	Asp	Leu	Arg	Asp	Gly	Asn	Gln	Ala	
65					70					75					80	
Leu	Ile	Asp	Pro	Met	Ser	Pro	Glu	Arg	Lys	Arg	Arg	Met	Phe	Glu	Leu	
85					90					95						
Leu	Val	Gln	Met	Gly	Phe	Lys	Glu	Ile	Glu	Val	Gly	Phe	Pro	Ser	Ala	
100					105					110						
Ser	Gln	Thr	Asp	Phe	Asp	Phe	Val	Arg	Glu	Ile	Ile	Glu	Lys	Gly	Met	
115					120					125						
Ile	Pro	Asp	Asp	Val	Thr	Ile	Gln	Val	Leu	Val	Gln	Ala	Arg	Glu	His	
130					135					140						
Leu	Ile	Arg	Arg	Thr	Phe	Glu	Ala	Cys	Glu	Gly	Ala	Lys	Asn	Val	Ile	
145					150					155					160	
Val	His	Phe	Tyr	Asn	Ser	Thr	Ser	Ile	Leu	Gln	Arg	Asn	Val	Val	Phe	
165					170					175						
Arg	Met	Asp	Lys	Val	Gln	Val	Lys	Lys	Leu	Ala	Thr	Asp	Ala	Ala	Glu	
180					185					190						
Leu	Ile	Lys	Thr	Ile	Ala	Gln	Asp	Tyr	Pro	Asp	Thr	Asn	Trp	Arg	Trp	
195					200					205						
Gln	Tyr	Ser	Pro	Glu	Ser	Phe	Thr	Gly	Thr	Glu	Val	Glu	Tyr	Ala	Lys	
210					215					220						
Glu	Val	Val	Asp	Ala	Val	Val	Glu	Val	Met	Asp	Pro	Thr	Pro	Glu	Asn	
225					230					235					240	
Pro	Met	Ile	Ile	Asn	Leu	Pro	Ser	Thr	Val	Glu	Met	Ile	Thr	Pro	Asn	
245					250					255						
Val	Tyr	Ala	Asp	Ser	Ile	Glu	Trp	Met	His	Arg	Asn	Leu	Asn	Arg	Arg	
260					265					270						
Asp	Ser	Ile	Ile	Leu	Ser	Leu	His	Pro	His	Asn	Asp	Arg	Gly	Thr	Gly	
275					280					285						
Val	Gly	Ala	Ala	Glu	Leu	Gly	Tyr	Met	Ala	Gly	Ala	Asp	Arg	Ile	Glu	
290					295					300						
Gly	Cys	Leu	Phe	Gly	Asn	Gly	Glu	Arg	Thr	Gly	Asn	Val	Cys	Leu	Val	
305					310					315					320	
Thr	Leu	Ala	Leu	Asn	Met	Leu	Thr	Gln	Gly	Val	Asp	Pro	Gln	Leu	Asp	
325					330					335						
Phe	Thr	Asp	Ile	Arg	Gln	Ile	Arg	Ser	Thr	Val	Glu	Tyr	Cys	Asn	Gln	
340					345					350						
Leu	Arg	Val	Pro	Glu	Arg	His	Pro	Tyr	Gly	Gly	Asp	Leu	Val	Phe	Thr	
355					360					365						

Ala Phe Ser Gly Ser His Gln Asp Ala Val Asn Lys Gly Leu Asp Ala  
370 375 380

Met Ala Ala Lys Val Gln Pro Gly Ala Ser Ser Thr Glu Val Ser Trp  
385 390 395 400

Glu Gln Leu Arg Asp Thr Glu Trp Glu Val Pro  
405 410

<210> 277

<211> 714

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(691)

<223> RXN02965

<400> 277

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ctgtcctcac ctgcagatat ctaaggaagg ctagaaaaca atg gaa aaa ttt acc 115  
Met Glu Lys Phe Thr  
1 5

acc tac acc ggc gtt ggc gtt cca ctg cag cga tcc aac gtg gac acc 163  
Thr Tyr Thr Gly Val Gly Val Pro Leu Gln Arg Ser Asn Val Asp Thr  
10 15 20

gac cag atc atc cca gcc gtc tac ctc aag cgc gtc acc cgg acc ggc 211  
Asp Gln Ile Ile Pro Ala Val Tyr Leu Lys Arg Val Thr Arg Thr Gly  
25 30 35

ttc gaa gac gga ctg ttt tcc aac tgg cgc caa aac gac ccc aac ttt 259  
Phe Glu Asp Gly Leu Phe Ser Asn Trp Arg Gln Asn Asp Pro Asn Phe  
40 45 50

gtc ctc aac acc gac acc tac aag aac ggc tcc gtt ctc gta gca ggc 307  
Val Leu Asn Thr Asp Thr Tyr Lys Asn Gly Ser Val Leu Val Ala Gly  
55 60 65

cct gac ttt ggc acc ggc tcc tcc cgc gag cac gcc gtc tgg gca ctc 355  
Pro Asp Phe Gly Thr Gly Ser Ser Arg Glu His Ala Val Trp Ala Leu  
70 75 80 85

atg gac tac ggc ttc cgc gct gtc ttc tcc tca cga ttc gcc gac atc 403  
Met Asp Tyr Gly Phe Arg Ala Val Phe Ser Ser Arg Phe Ala Asp Ile  
90 95 100

ttc cgc ggc aac tcc gga aaa gcg ggc atg ctc acc ggc atc atg gaa 451  
Phe Arg Gly Asn Ser Gly Lys Ala Gly Met Leu Thr Gly Ile Met Glu  
105 110 115

cag tcc gac atc gaa ctt ctg tgg aag ctc atg gaa caa acc cca ggc 499  
Gln Ser Asp Ile Glu Leu Leu Trp Lys Leu Met Glu Gln Thr Pro Gly  
120 125 130

ctc gaa ctg acc gtg aac ctg gaa aag cag atc gtc acc gca ggc gac 547

Leu Glu Leu Thr Val Asn Leu Glu Lys Gln Ile Val Thr Ala Gly Asp  
 135 140 145  
 gta gtg atc agc ttc gaa gtt gac ccc tac atc cgc tgg cgt ttg atg 595  
 Val Val Ile Ser Phe Glu Val Asp Pro Tyr Ile Arg Trp Arg Leu Met  
 150 155 160 165  
 gaa ggc ctc gac gac gct ggc ctg acc ctg cgc aag ctc gat gaa att 643  
 Glu Gly Leu Asp Asp Ala Gly Leu Thr Leu Arg Lys Leu Asp Glu Ile  
 170 175 180  
 gaa gac tac gag gct aag cgc cct gcg ttt aag cca cgc act aac gct 691  
 Glu Asp Tyr Glu Ala Lys Arg Pro Ala Phe Lys Pro Arg Thr Asn Ala  
 185 190 195  
 taagtttcag tctgatagcg aaa 714

<210> 278  
 <211> 197  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 278  
 Met Glu Lys Phe Thr Thr Tyr Thr Gly Val Gly Val Pro Leu Gln Arg  
 1 5 10 15  
 Ser Asn Val Asp Thr Asp Gln Ile Ile Pro Ala Val Tyr Leu Lys Arg  
 20 25 30  
 Val Thr Arg Thr Gly Phe Glu Asp Gly Leu Phe Ser Asn Trp Arg Gln  
 35 40 45  
 Asn Asp Pro Asn Phe Val Leu Asn Thr Asp Thr Tyr Lys Asn Gly Ser  
 50 55 60  
 Val Leu Val Ala Gly Pro Asp Phe Gly Thr Gly Ser Ser Arg Glu His  
 65 70 75 80  
 Ala Val Trp Ala Leu Met Asp Tyr Gly Phe Arg Ala Val Phe Ser Ser  
 85 90 95  
 Arg Phe Ala Asp Ile Phe Arg Gly Asn Ser Gly Lys Ala Gly Met Leu  
 100 105 110  
 Thr Gly Ile Met Glu Gln Ser Asp Ile Glu Leu Leu Trp Lys Leu Met  
 115 120 125  
 Glu Gln Thr Pro Gly Leu Glu Leu Thr Val Asn Leu Glu Lys Gln Ile  
 130 135 140  
 Val Thr Ala Gly Asp Val Val Ile Ser Phe Glu Val Asp Pro Tyr Ile  
 145 150 155 160  
 Arg Trp Arg Leu Met Glu Gly Leu Asp Asp Ala Gly Leu Thr Leu Arg  
 165 170 175  
 Lys Leu Asp Glu Ile Glu Asp Tyr Glu Ala Lys Arg Pro Ala Phe Lys  
 180 185 190  
 Pro Arg Thr Asn Ala

195

<210> 279  
 <211> 936  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

<220>  
 <221> CDS  
 <222> (101)..(913)  
 <223> RXN01929

<400> 279  
 aaaatttgac tccataacga gaacttaate gagcaacacc cctgaacagt gaatcaaate 60

ggaatttatt tattctgagc tggatcatcac atctatactc atg ccc atg tca ggc 115  
 Met Pro Met Ser Gly  
 1 5

att gat gca aag aaa atc cgc acc cgt cat ttc cgc gaa gct aaa gta 163  
 Ile Asp Ala Lys Lys Ile Arg Thr Arg His Phe Arg Glu Ala Lys Val  
 10 15 20

aac ggc cag aaa gtt tcg gtt ctc acc agc tat gat gcg ctt tcg gcg 211  
 Asn Gly Gln Lys Val Ser Val Leu Thr Ser Tyr Asp Ala Leu Ser Ala  
 25 30 35

cgc att ttt gat gag gct ggc gtc gat atg ctc ctt gtt ggt gat tcc 259  
 Arg Ile Phe Asp Glu Ala Gly Val Asp Met Leu Leu Val Gly Asp Ser  
 40 45 50

gct gcc aac gtt gtg ctg ggt cgc gat acc acc ttg tcg atc acc ttg 307  
 Ala Ala Asn Val Val Leu Gly Arg Asp Thr Thr Leu Ser Ile Thr Leu  
 55 60 65

gat gag atg att gtg ctg gcc aag gcg gtg acg atc gct acg aag cgt 355  
 Asp Glu Met Ile Val Leu Ala Lys Ala Val Thr Ile Ala Thr Lys Arg  
 70 75 80 85

gcg ctt gtg gtg gtt gat ctg ccg ttt ggt acc tat gag gtg agc cca 403  
 Ala Leu Val Val Val Asp Leu Pro Phe Gly Thr Tyr Glu Val Ser Pro  
 90 95 100

aat cag gcg gtg gag tcc gcg atc cgg gtc atg cgt gaa acg ggt gcg 451  
 Asn Gln Ala Val Glu Ser Ala Ile Arg Val Met Arg Glu Thr Gly Ala  
 105 110 115

gct gcg gtg aag atc gag ggt ggc gtg gag atc gcg cag acg att cga 499  
 Ala Ala Val Lys Ile Glu Gly Gly Val Glu Ile Ala Gln Thr Ile Arg  
 120 125 130

cgc att gtt gat gct gga att ccg gtt gtc ggc cac atc ggg tac acc 547  
 Arg Ile Val Asp Ala Gly Ile Pro Val Val Gly His Ile Gly Tyr Thr  
 135 140 145

ccg cag tcc gag cat tcc ttg ggc ggc cac gtg gtt cag ggt cgt ggc 595  
 Pro Gln Ser Glu His Ser Leu Gly Gly His Val Val Gln Gly Arg Gly  
 150 155 160 165

gcg agt tct gga aag ctc atc gcc gat gcc cgc gcg ttg gag cag gcg 643

Ala Ser Ser Gly Lys Leu Ile Ala Asp Ala Arg Ala Leu Glu Gln Ala  
 170 175 180

ggt gcg ttt gcg gtt gtg ttg gag atg gtt cca gca gag gca gcg cgc 691  
 Gly Ala Phe Ala Val Val Leu Glu Met Val Pro Ala Glu Ala Ala Arg  
 185 190 195

gag gtt acc gag gat ctt tcc atc acc act atc gga atc ggt gcc ggc 739  
 Glu Val Thr Glu Asp Leu Ser Ile Thr Thr Ile Gly Ile Gly Ala Gly  
 200 205 210

aat ggc aca gat ggg cag gtt ttg gtg tgg cag gat gcc ttc ggc ctc 787  
 Asn Gly Thr Asp Gly Gln Val Leu Val Trp Gln Asp Ala Phe Gly Leu  
 215 220 225

aac cgc ggc aag aag cca cgc ttc gtc cgc gag tac gcc acc ttg ggc 835  
 Asn Arg Gly Lys Lys Pro Arg Phe Val Arg Glu Tyr Ala Thr Leu Gly  
 230 235 240 245

gat tcc ttg cac gac gcc gcg cag gcc tac atc gcc gat atc cac gcg 883  
 Asp Ser Leu His Asp Ala Ala Gln Ala Tyr Ile Ala Asp Ile His Ala  
 250 255 260

ggt acc ttc cca ggc gaa gcg gag tcc ttt taatgcaggt agcaaccaca 933  
 Gly Thr Phe Pro Gly Glu Ala Glu Ser Phe  
 265 270

aag 936

&lt;210&gt; 280

&lt;211&gt; 271

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 280

Met Pro Met Ser Gly Ile Asp Ala Lys Lys Ile Arg Thr Arg His Phe  
 1 5 10 15

Arg Glu Ala Lys Val Asn Gly Gln Lys Val Ser Val Leu Thr Ser Tyr  
 20 25 30

Asp Ala Leu Ser Ala Arg Ile Phe Asp Glu Ala Gly Val Asp Met Leu  
 35 40 45

Leu Val Gly Asp Ser Ala Ala Asn Val Val Leu Gly Arg Asp Thr Thr  
 50 55 60

Leu Ser Ile Thr Leu Asp Glu Met Ile Val Leu Ala Lys Ala Val Thr  
 65 70 75 80

Ile Ala Thr Lys Arg Ala Leu Val Val Val Asp Leu Pro Phe Gly Thr  
 85 90 95

Tyr Glu Val Ser Pro Asn Gln Ala Val Glu Ser Ala Ile Arg Val Met  
 100 105 110

Arg Glu Thr Gly Ala Ala Ala Val Lys Ile Glu Gly Gly Val Glu Ile  
 115 120 125

Ala Gln Thr Ile Arg Arg Ile Val Asp Ala Gly Ile Pro Val Val Gly

130	135	140
His Ile Gly Tyr Thr Pro Gln Ser Glu His Ser Leu Gly Gly His Val 145 150 155 160		
Val Gln Gly Arg Gly Ala Ser Ser Gly Lys Leu Ile Ala Asp Ala Arg 165 170 175		
Ala Leu Glu Gln Ala Gly Ala Phe Ala Val Val Leu Glu Met Val Pro 180 185 190		
Ala Glu Ala Ala Arg Glu Val Thr Glu Asp Leu Ser Ile Thr Thr Ile 195 200 205		
Gly Ile Gly Ala Gly Asn Gly Thr Asp Gly Gln Val Leu Val Trp Gln 210 215 220		
Asp Ala Phe Gly Leu Asn Arg Gly Lys Lys Pro Arg Phe Val Arg Glu 225 230 235 240		
Tyr Ala Thr Leu Gly Asp Ser Leu His Asp Ala Ala Gln Ala Tyr Ile 245 250 255		
Ala Asp Ile His Ala Gly Thr Phe Pro Gly Glu Ala Glu Ser Phe 260 265 270		

&lt;210&gt; 281

&lt;211&gt; 930

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(907)

&lt;223&gt; FRXA01929

&lt;400&gt; 281

tgactccata acgagaactt aatcgagcaa cacccttgaa cagtgaatca aatcggaatt 60

tatttattct gagctgggtca tcacatctat actcatgccc atg tca ggc att gat	115
Met Ser Gly Ile Asp	5
1	

gca aag aaa atc cgc acc cgt cat ttc cgc gaa gct aaa gta aac ggc	163
Ala Lys Lys Ile Arg Thr Arg His Phe Arg Glu Ala Lys Val Asn Gly	20
10 15	

cag aaa gtt tcg gtt ctc acc agc tat gat gcg ctt tcg gcg cgc att	211
Gln Lys Val Ser Val Leu Thr Ser Tyr Asp Ala Leu Ser Ala Arg Ile	35
25 30	

ttt gat gag gct ggc gtc gat atg ctc ctt gtt ggt gat tcc gct gcc	259
Phe Asp Glu Ala Gly Val Asp Met Leu Leu Val Gly Asp Ser Ala Ala	50
40 45	

aac gtt gtg ctg ggt cgc gat acc acc ttg tcg atc acc ttg gat gag	307
Asn Val Val Leu Gly Arg Asp Thr Thr Leu Ser Ile Thr Leu Asp Glu	65
55 60	

atg att gtg ctg gcc aag gcg gtg acg atc gct acg aag cgt gcg ctt	355
---	-----

Met	Ile	Val	Leu	Ala	Lys	Ala	Val	Thr	Ile	Ala	Thr	Lys	Arg	Ala	Leu	
70					75					80					85	
gtg	gtg	gtt	gat	ctg	ccg	ttt	ggg	acc	tat	gag	gtg	agc	cca	aat	cag	403
Val	Val	Val	Asp	Leu	Pro	Phe	Gly	Thr	Tyr	Glu	Val	Ser	Pro	Asn	Gln	
				90					95					100		
gcg	gtg	gag	tcc	gcg	atc	cgg	gtc	atg	cgt	gaa	acg	ggg	gcg	gct	gcg	451
Ala	Val	Glu	Ser	Ala	Ile	Arg	Val	Met	Arg	Glu	Thr	Gly	Ala	Ala	Ala	
			105					110					115			
gtg	aag	atc	gag	ggg	ggc	gtg	gag	atc	gcg	cag	acg	att	cga	cgc	att	499
Val	Lys	Ile	Glu	Gly	Gly	Val	Glu	Ile	Ala	Gln	Thr	Ile	Arg	Arg	Ile	
		120					125					130				
gtt	gat	gct	gga	att	ccg	gtt	gtc	ggc	cac	atc	ggg	tac	acc	ccg	cag	547
Val	Asp	Ala	Gly	Ile	Pro	Val	Val	Gly	His	Ile	Gly	Tyr	Thr	Pro	Gln	
	135					140					145					
tcc	gag	cat	tcc	ttg	ggc	ggc	cac	gtg	gtt	cag	ggg	cgt	ggc	gcg	agt	595
Ser	Glu	His	Ser	Leu	Gly	Gly	His	Val	Val	Gln	Gly	Arg	Gly	Ala	Ser	
150					155					160					165	
tct	gga	aag	ctc	atc	gcc	gat	gcc	cgc	gcg	ttg	gag	cag	gcg	ggg	gcg	643
Ser	Gly	Lys	Leu	Ile	Ala	Asp	Ala	Arg	Ala	Leu	Glu	Gln	Ala	Gly	Ala	
			170					175						180		
ttt	gcg	gtt	gtg	ttg	gag	atg	gtt	cca	gca	gag	gca	gcg	cgc	gag	gtt	691
Phe	Ala	Val	Val	Leu	Glu	Met	Val	Pro	Ala	Glu	Ala	Ala	Arg	Glu	Val	
			185					190					195			
acc	gag	gat	ctt	tcc	atc	acc	act	atc	gga	atc	ggg	gcc	ggc	aat	ggc	739
Thr	Glu	Asp	Leu	Ser	Ile	Thr	Thr	Ile	Gly	Ile	Gly	Ala	Gly	Asn	Gly	
		200					205					210				
aca	gat	ggg	cag	gtt	ttg	gtg	tgg	cag	gat	gcc	ttc	ggc	ctc	aac	cgc	787
Thr	Asp	Gly	Gln	Val	Leu	Val	Trp	Gln	Asp	Ala	Phe	Gly	Leu	Asn	Arg	
	215					220					225					
ggc	aag	aag	cca	cgc	ttc	gtc	cgc	gag	tac	gcc	acc	ttg	ggc	gat	tcc	835
Gly	Lys	Lys	Pro	Arg	Phe	Val	Arg	Glu	Tyr	Ala	Thr	Leu	Gly	Asp	Ser	
230					235					240					245	
ttg	cac	gac	gcc	gcg	cag	gcc	tac	atc	gcc	gat	atc	cac	gcg	ggg	acc	883
Leu	His	Asp	Ala	Ala	Gln	Ala	Tyr	Ile	Ala	Asp	Ile	His	Ala	Gly	Thr	
			250					255					260			
ttc	cca	ggc	gaa	gcg	gag	tcc	ttt	taatgcaggt	agcaaccaca	aag						930
Phe	Pro	Gly	Glu	Ala	Glu	Ser	Phe									
			265													

&lt;210&gt; 282

&lt;211&gt; 269

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 282

Met	Ser	Gly	Ile	Asp	Ala	Lys	Lys	Ile	Arg	Thr	Arg	His	Phe	Arg	Glu
1				5					10					15	

Ala Lys Val Asn Gly Gln Lys Val Ser Val Leu Thr Ser Tyr Asp Ala  
                   20                                  25                                  30  
 Leu Ser Ala Arg Ile Phe Asp Glu Ala Gly Val Asp Met Leu Leu Val  
                   35                                  40                                  45  
 Gly Asp Ser Ala Ala Asn Val Val Leu Gly Arg Asp Thr Thr Leu Ser  
                   50                                  55                                  60  
 Ile Thr Leu Asp Glu Met Ile Val Leu Ala Lys Ala Val Thr Ile Ala  
                   65                                  70                                  75                                  80  
 Thr Lys Arg Ala Leu Val Val Val Asp Leu Pro Phe Gly Thr Tyr Glu  
                                   85                                  90                                  95  
 Val Ser Pro Asn Gln Ala Val Glu Ser Ala Ile Arg Val Met Arg Glu  
                                  100                                 105                                 110  
 Thr Gly Ala Ala Ala Val Lys Ile Glu Gly Gly Val Glu Ile Ala Gln  
                   115                                 120                                 125  
 Thr Ile Arg Arg Ile Val Asp Ala Gly Ile Pro Val Val Gly His Ile  
                   130                                 135                                 140  
 Gly Tyr Thr Pro Gln Ser Glu His Ser Leu Gly Gly His Val Val Gln  
                   145                                 150                                 155                                 160  
 Gly Arg Gly Ala Ser Ser Gly Lys Leu Ile Ala Asp Ala Arg Ala Leu  
                                  165                                 170                                 175  
 Glu Gln Ala Gly Ala Phe Ala Val Val Leu Glu Met Val Pro Ala Glu  
                                  180                                 185                                 190  
 Ala Ala Arg Glu Val Thr Glu Asp Leu Ser Ile Thr Thr Ile Gly Ile  
                   195                                 200                                 205  
 Gly Ala Gly Asn Gly Thr Asp Gly Gln Val Leu Val Trp Gln Asp Ala  
                   210                                 215                                 220  
 Phe Gly Leu Asn Arg Gly Lys Lys Pro Arg Phe Val Arg Glu Tyr Ala  
                   225                                 230                                 235                                 240  
 Thr Leu Gly Asp Ser Leu His Asp Ala Ala Gln Ala Tyr Ile Ala Asp  
                                  245                                 250                                 255  
 Ile His Ala Gly Thr Phe Pro Gly Glu Ala Glu Ser Phe  
                                  260                                 265

&lt;210&gt; 283

&lt;211&gt; 1065

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1042)

&lt;223&gt; RXN01420

&lt;400&gt; 283

cgaagttcac gactacaggc attacctggg tgctgatttt gcgcgagtaa agctgtggct .60



gcggaatgcg	ctgctcatcc	acacgtggaa	tcctgattgg	gtg	acg	ctg	ggt	gga	115
				Val	Thr	Leu	Gly	Gly	
				1				5	
ttg	aat	gta	cca	tcg	tgg	tcg	ctg	ggc	163
Leu	Asn	Val	Pro	Ser	Trp	Ser	Leu	Gly	
				10				15	
acg	ttc	ccg	ctg	ttt	att	ccg	tta	gtg	211
Thr	Phe	Pro	Leu	Phe	Ile	Pro	Leu	Val	
			25					30	
aac	tgg	tgg	gca	ttt	ggc	atc	acc	ttt	259
Asn	Trp	Trp	Ala	Phe	Gly	Ile	Thr	Phe	
			40					45	
aca	gtg	att	cac	ttt	tat	gcg	gac	gga	307
Thr	Val	Ile	His	Phe	Tyr	Ala	Asp	Gly	
			55					60	
ttt	gtt	cct	cg	ctg	tgg	gac	acc	aat	355
Phe	Val	Pro	Arg	Leu	Trp	Asp	Thr	Asn	
					75			80	
cac	gcc	gat	cca	gtg	tgg	ttt	atg	cag	403
His	Ala	Asp	Pro	Val	Trp	Phe	Met	Gln	
				90				95	
tct	tac	tgg	ctg	tct	tac	tac	ttc	ccg	451
Ser	Tyr	Trp	Leu	Ser	Tyr	Tyr	Phe	Pro	
			105					110	
tac	ctc	ggt	gtg	ttt	ggc	gcg	aag	ctg	499
Tyr	Leu	Gly	Val	Phe	Gly	Ala	Lys	Leu	
			120				125		
aac	acc	aac	atc	acc	atc	ccg	ctg	atc	547
Asn	Thr	Asn	Ile	Thr	Ile	Pro	Leu	Ile	
			135				140		
gct	act	tgg	ttt	gtg	cca	ctg	gca	ttc	595
Ala	Thr	Trp	Phe	Val	Pro	Leu	Ala	Phe	
					155			160	
ctg	cca	atg	gct	ttt	gtt	gtg	gca	acg	643
Leu	Pro	Met	Ala	Phe	Val	Val	Ala	Thr	
				170				175	
ggc	aag	agt	ggg	gaa	atc	gcc	tcg	cct	691
Gly	Lys	Ser	Gly	Glu	Ile	Ala	Ser	Pro	
			185					190	
att	tcc	ttt	gcc	ttc	tac	atg	gtg	caa	739
Ile	Ser	Phe	Ala	Phe	Tyr	Met	Val	Gln	
			200					205	
cag	cg	tat	ttc	att	gct	ggc	aaa	gaa	787
Gln	Arg	Tyr	Phe	Ile	Ala	Gly	Lys	Glu	
			215					220	

ttc tat gca gtg gtg tgt ttc atc gtg tcg gtc att ctc gcg tgg gtg 835  
 Phe Tyr Ala Val Val Cys Phe Ile Val Ser Val Ile Leu Ala Trp Val  
 230 235 240 245

ctg ttt acc ttc gtt gat gat cct ttg atg aag gcc acg gcg cgc aag 883  
 Leu Phe Thr Phe Val Asp Asp Pro Leu Met Lys Ala Thr Ala Arg Lys  
 250 255 260

aag ggg agt agg cgc ttg aag cag tcc aat att ttg gtc cgt gac ctg 931  
 Lys Gly Ser Arg Arg Leu Lys Gln Ser Asn Ile Leu Val Arg Asp Leu  
 265 270 275

aaa gtt ctc ttc ggc aaa agc ccc gaa aag ccg tta aaa gtt gag act 979  
 Lys Val Leu Phe Gly Lys Ser Pro Glu Lys Pro Leu Lys Val Glu Thr  
 280 285 290

cgc gct gag aat ctc aca gaa aac tcc gaa gct ccc gct aag gta gct  
 1027  
 Arg Ala Glu Asn Leu Thr Glu Asn Ser Glu Ala Pro Ala Lys Val Ala  
 295 300 305

acc gga atc aaa tct tagggaagga aaacatatgg cta  
 1065  
 Thr Gly Ile Lys Ser  
 310

<210> 284  
 <211> 314  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 284  
 Val Thr Leu Gly Gly Leu Asn Val Pro Ser Trp Ser Leu Gly Ala Glu  
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Met Leu Phe Tyr Leu Thr Phe Pro Leu Phe Ile Pro Leu Val Arg Lys  
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Val Lys Gly Val Gly Asn Trp Trp Ala Phe Gly Ile Thr Phe Ala Val  
 35 40 45

Ser Leu Ala Leu Ile Thr Val Ile His Phe Tyr Ala Asp Gly Pro Lys  
 50 55 60

Gly Ile Glu Asn Phe Phe Val Pro Arg Leu Trp Asp Thr Asn Val Ser  
 65 70 75 80

Pro Val Ala Glu Val His Ala Asp Pro Val Trp Phe Met Gln Glu Glu  
 85 90 95

Ile Pro Val Leu Glu Ser Tyr Trp Leu Ser Tyr Tyr Phe Pro Leu Thr  
 100 105 110

Arg Leu Ile Glu Phe Tyr Leu Gly Val Phe Gly Ala Lys Leu Val Ala  
 115 120 125

Glu Gly Met Phe Lys Asn Thr Asn Ile Thr Ile Pro Leu Ile Ala Leu  
 130 135 140

Ala Val Ser Phe Val Ala Thr Trp Phe Val Pro Leu Ala Phe Lys Met

145		150		155		160
Ser Val Ile Met	Ser Leu Pro Met	Ala Phe Val Val	Ala Thr Leu Ala			
	165	170	175			
Val Arg Asp Ile	Glu Gly Lys Ser	Gly Glu Ile Ala	Ser Pro Arg Ala			
	180	185	190			
Val Leu Leu Gly	Asn Ile Ser Phe	Ala Phe Tyr Met	Val Gln Phe Pro			
	195	200	205			
Val Met Val Phe	Val Gln Arg Tyr	Phe Ile Ala Gly	Lys Glu Tyr Gly			
	210	215	220			
Phe Leu Gly Trp	Ala Phe Tyr Ala	Val Val Cys Phe	Ile Val Ser Val			
225	230	235	240			
Ile Leu Ala Trp	Val Leu Phe Thr	Phe Val Asp Asp	Pro Leu Met Lys			
	245	250	255			
Ala Thr Ala Arg	Lys Lys Gly Ser	Arg Arg Leu Lys	Gln Ser Asn Ile			
	260	265	270			
Leu Val Arg Asp	Leu Lys Val Leu	Phe Gly Lys Ser	Pro Glu Lys Pro			
	275	280	285			
Leu Lys Val Glu	Thr Arg Ala Glu	Asn Leu Thr Glu	Asn Ser Glu Ala			
	290	295	300			
Pro Ala Lys Val	Ala Thr Gly Ile	Lys Ser				
305	310					

&lt;210&gt; 285

&lt;211&gt; 1137

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1114)

&lt;223&gt; RXS01145

&lt;400&gt; 285

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cttttcacca aaattttttac gaaaggcgag attttctccc atg gct att gaa ctg 115  
 Met Ala Ile Glu Leu  
 1 5

ctt tat gat gct gac gct gac ctc tcc ttg atc cag ggc cgt aag gtt 163  
 Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile Gln Gly Arg Lys Val  
 10 15 20

gcc atc gtt ggc tac ggc tcc cag ggc cac gca cac tcc cag aac ctc 211  
 Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala His Ser Gln Asn Leu  
 25 30 35

cgc gat tct ggc gtt gag gtt gtc att ggt ctg cgc gag ggc tcc aag 259  
 Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu Arg Glu Gly Ser Lys  
 40 45 50

tcc gca gag aag gca aag gaa gca ggc ttc gag gtc aag acc acc gct	307
Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu Val Lys Thr Thr Ala	
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gag gct gca gct tgg gct gac gtc atc atg ctc ctg gct cca gac acc	355
Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu Leu Ala Pro Asp Thr	
70 75 80 85	
tcc cag gca gaa atc ttc acc aac gac atc gag cca aac ctg aac gca	403
Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu Pro Asn Leu Asn Ala	
90 95 100	
ggc gac gca ctg ctg ttc ggc cac ggc ctg aac att cac ttc gac ctg	451
Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn Ile His Phe Asp Leu	
105 110 115	
atc aag cca gct gac gac atc atc gtt ggc atg gtt gcg cca aag ggc	499
Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met Val Ala Pro Lys Gly	
120 125 130	
cca ggc cac ttg gtt cgc cgt cag ttc gtt gat ggc aag ggt gtt cct	547
Pro Gly His Leu Val Arg Arg Gln Phe Val Asp Gly Lys Gly Val Pro	
135 140 145	
tgc ctc atc gca gtc gac cag gac cca acc gga acc gca cag gct ctg	595
Cys Leu Ile Ala Val Asp Gln Asp Pro Thr Gly Thr Ala Gln Ala Leu	
150 155 160 165	
acc ctg tcc tac gca gca gca atc ggt ggc gca cgc gca ggc gtt atc	643
Thr Leu Ser Tyr Ala Ala Ala Ile Gly Gly Ala Arg Ala Gly Val Ile	
170 175 180	
cca acc acc ttc gaa gct gag acc gtc acc gac ctc ttc ggc gag cag	691
Pro Thr Thr Phe Glu Ala Glu Thr Val Thr Asp Leu Phe Gly Glu Gln	
185 190 195	
gct gtt ctc tgc ggt ggc acc gag gaa ctg gtc aag gtt ggc ttc gag	739
Ala Val Leu Cys Gly Gly Thr Glu Glu Leu Val Lys Val Gly Phe Glu	
200 205 210	
gtt ctc acc gaa gct ggc tac gag cca gag atg gca tac ttc gag gtt	787
Val Leu Thr Glu Ala Gly Tyr Glu Pro Glu Met Ala Tyr Phe Glu Val	
215 220 225	
ctt cac gag ctc aag ctc atc gtt gac ctc atg ttc gaa ggt ggc atc	835
Leu His Glu Leu Lys Leu Ile Val Asp Leu Met Phe Glu Gly Gly Ile	
230 235 240 245	
agc aac atg aac tac tct gtt tct gac acc gct gag ttc ggt ggc tac	883
Ser Asn Met Asn Tyr Ser Val Ser Asp Thr Ala Glu Phe Gly Gly Tyr	
250 255 260	
ctc tcc ggc cca cgc gtc atc gat gca gac acc aag tcc cgc atg aag	931
Leu Ser Gly Pro Arg Val Ile Asp Ala Asp Thr Lys Ser Arg Met Lys	
265 270 275	
gac atc ctg acc gat atc cag gac ggc acc ttc acc aag cgc ctc atc	979
Asp Ile Leu Thr Asp Ile Gln Asp Gly Thr Phe Thr Lys Arg Leu Ile	
280 285 290	

gca aac gtt gag aac ggc aac acc gag ctt gag ggc ctt cgt gct tcc  
 1027  
 Ala Asn Val Glu Asn Gly Asn Thr Glu Leu Glu Gly Leu Arg Ala Ser  
 295 300 305

tac aac aac cac cca atc gag gag acc ggc gct aag ctc cgc gac ctc  
 1075  
 Tyr Asn Asn His Pro Ile Glu Glu Thr Gly Ala Lys Leu Arg Asp Leu  
 310 315 320 325

atg agc tgg gtc aag gtt gac gct cgc gca gaa acc gct taagtttcac  
 1124  
 Met Ser Trp Val Lys Val Asp Ala Arg Ala Glu Thr Ala  
 330 335

ccctttgacg gct  
 1137

<210> 286  
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 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 286  
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 20 25 30

His Ser Gln Asn Leu Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu  
 35 40 45

Arg Glu Gly Ser Lys Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu  
 50 55 60

Val Lys Thr Thr Ala Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu  
 65 70 75 80

Leu Ala Pro Asp Thr Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu  
 85 90 95

Pro Asn Leu Asn Ala Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn  
 100 105 110

Ile His Phe Asp Leu Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met  
 115 120 125

Val Ala Pro Lys Gly Pro Gly His Leu Val Arg Arg Gln Phe Val Asp  
 130 135 140

Gly Lys Gly Val Pro Cys Leu Ile Ala Val Asp Gln Asp Pro Thr Gly  
 145 150 155 160

Thr Ala Gln Ala Leu Thr Leu Ser Tyr Ala Ala Ala Ile Gly Gly Ala  
 165 170 175

Arg Ala Gly Val Ile Pro Thr Thr Phe Glu Ala Glu Thr Val Thr Asp  
 180 185 190

Leu Phe Gly Glu Gln Ala Val Leu Cys Gly Gly Thr Glu Glu Leu Val  
 195 200 205  
 Lys Val Gly Phe Glu Val Leu Thr Glu Ala Gly Tyr Glu Pro Glu Met  
 210 215 220  
 Ala Tyr Phe Glu Val Leu His Glu Leu Lys Leu Ile Val Asp Leu Met  
 225 230 235 240  
 Phe Glu Gly Gly Ile Ser Asn Met Asn Tyr Ser Val Ser Asp Thr Ala  
 245 250 255  
 Glu Phe Gly Gly Tyr Leu Ser Gly Pro Arg Val Ile Asp Ala Asp Thr  
 260 265 270  
 Lys Ser Arg Met Lys Asp Ile Leu Thr Asp Ile Gln Asp Gly Thr Phe  
 275 280 285  
 Thr Lys Arg Leu Ile Ala Asn Val Glu Asn Gly Asn Thr Glu Leu Glu  
 290 295 300  
 Gly Leu Arg Ala Ser Tyr Asn Asn His Pro Ile Glu Glu Thr Gly Ala  
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 Lys Leu Arg Asp Leu Met Ser Trp Val Lys Val Asp Ala Arg Ala Glu  
 325 330 335

Thr Ala

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 <211> 556  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(556)  
 <223> FRXA01145

<400> 287  
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 Met Ala Ile Glu Leu  
 1 5  
 ctt tat gat gct gac gct gac ctc tcc ttg atc cag ggc cgt aag gtt 163  
 Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile Gln Gly Arg Lys Val  
 10 15 20  
 gcc atc gtt ggc tac ggc tcc cag ggc cac gca cac tcc cag aac ctc 211  
 Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala His Ser Gln Asn Leu  
 25 30 35  
 cgc gat tct ggc gtt gag gtt gtc att ggt ctg cgc gag ggc tcc aag 259  
 Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu Arg Glu Gly Ser Lys  
 40 45 50  
 tcc gca gag aag gca aag gaa gca ggc ttc gag gtc aag acc acc gct 307

Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu Val Lys Thr Thr Ala  
55 60 65

gag gct gca gct tgg gct gac gtc atc atg ctc ctg gct cca gac acc 355  
Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu Leu Ala Pro Asp Thr  
70 75 80 85

tcc cag gca gaa atc ttc acc aac gac atc gag cca aac ctg aac gca 403  
Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu Pro Asn Leu Asn Ala  
90 95 100

ggc gac gca ctg ctg ttc ggc cac ggc ctg aac att cac ttc gac ctg 451  
Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn Ile His Phe Asp Leu  
105 110 115

atc aag cca gct gac gac atc atc gtt ggc atg gtt gcg cca aag ggc 499  
Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met Val Ala Pro Lys Gly  
120 125 130

cca ggc cac ttg gtt cgc cgt cag ttc gtt gat ggc aag ggt gtt cct 547  
Pro Gly His Leu Val Arg Arg Gln Phe Val Asp Gly Lys Gly Val Pro  
135 140 145

tgc ctc atc 556  
Cys Leu Ile  
150

&lt;210&gt; 288

&lt;211&gt; 152

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 288

Met Ala Ile Glu Leu Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile  
1 5 10 15

Gln Gly Arg Lys Val Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala  
20 25 30

His Ser Gln Asn Leu Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu  
35 40 45

Arg Glu Gly Ser Lys Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu  
50 55 60

Val Lys Thr Thr Ala Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu  
65 70 75 80

Leu Ala Pro Asp Thr Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu  
85 90 95

Pro Asn Leu Asn Ala Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn  
100 105 110

Ile His Phe Asp Leu Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met  
115 120 125

Val Ala Pro Lys Gly Pro Gly His Leu Val Arg Arg Gln Phe Val Asp  
130 135 140

Gly Lys Gly Val Pro Cys Leu Ile  
145 150

<210> 289

<211> 1350

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1327)

<223> RXA02375

<400> 289

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aagcgttcga ttacgggata atctcccaac gccaacccaa atg gcg ccg gtg aca 115
                Met Ala Pro Val Thr
                1 5

ggg ctt cct gtc acc ccc tac agc cag gaa gca agc atc ggt gcg agc 163
Gly Leu Pro Val Thr Pro Tyr Ser Gln Glu Ala Ser Ile Gly Ala Ser
                10 15 20

ttc ccg gca gtg gat ccg gac acc aaa gac agc gcc gca tac gga cat 211
Phe Pro Ala Val Asp Pro Asp Thr Lys Asp Ser Ala Ala Tyr Gly His
                25 30 35

gaa tcc gga atg cgt gag cgc atc tcc aac gct aag cga gtg gtg gtg 259
Glu Ser Gly Met Arg Glu Arg Ile Ser Asn Ala Lys Arg Val Val Val
                40 45 50

aaa att ggt tcg tcc tca ttg act aac gat gag gac gga cac acc gtc 307
Lys Ile Gly Ser Ser Ser Leu Thr Asn Asp Glu Asp Gly His Thr Val
                55 60 65

gat ccc aac cgc atc aac act att gtc aat gcc ttg caa gca cgc atg 355
Asp Pro Asn Arg Ile Asn Thr Ile Val Asn Ala Leu Gln Ala Arg Met
                70 75 80 85

gaa gct ggc tcg gac ctc atc gtt gtg tcc tct ggc gca gtg gcc gcg 403
Glu Ala Gly Ser Asp Leu Ile Val Val Ser Ser Gly Ala Val Ala Ala
                90 95 100

gga atg gcc ccg ctt gga ttg agc acc cgg ccc acg gaa ttg gca gtc 451
Gly Met Ala Pro Leu Gly Leu Ser Thr Arg Pro Thr Glu Leu Ala Val
                105 110 115

aag cag gct gca gca gca gtg ggg caa gtt cac ctc atg cac cag tgg 499
Lys Gln Ala Ala Ala Val Gly Gln Val His Leu Met His Gln Trp
                120 125 130

gga cgt tct ttt gcc cgg tat ggt cgc ccc atc ggc cag gtg ctt ctt 547
Gly Arg Ser Phe Ala Arg Tyr Gly Arg Pro Ile Gly Gln Val Leu Leu
                135 140 145

acc gca gct gat gca gga aag cgt gat cgt gcg agg aat gcg cag cgt 595
Thr Ala Ala Asp Ala Gly Lys Arg Asp Arg Ala Arg Asn Ala Gln Arg
150 155 160 165

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acc atc gac aag ctg cgc att ttg ggc gcg gtt cct atc gtc aat gaa	643
Thr Ile Asp Lys Leu Arg Ile Leu Gly Ala Val Pro Ile Val Asn Glu	
170 175 180	
aat gac acc gtg gca acc acc ggt gtg aat ttt ggt gac aac gac cga	691
Asn Asp Thr Val Ala Thr Thr Gly Val Asn Phe Gly Asp Asn Asp Arg	
185 190 195	
ctt gct gca att gtg gcg cac ctg gtg tcg gct gat gct ttg gtg ctg	739
Leu Ala Ala Ile Val Ala His Leu Val Ser Ala Asp Ala Leu Val Leu	
200 205 210	
ctc agt gac gtg gat gga ctt ttt gat aaa aac cct act gat ccc acc	787
Leu Ser Asp Val Asp Gly Leu Phe Asp Lys Asn Pro Thr Asp Pro Thr	
215 220 225	
gcg aag ttt att tcc gag gtt cgt gac ggc aat gat ttg aaa ggt gtc	835
Ala Lys Phe Ile Ser Glu Val Arg Asp Gly Asn Asp Leu Lys Gly Val	
230 235 240 245	
att gcc ggc gac ggc gga aaa gtg ggc acc ggt ggc atg gca tca aag	883
Ile Ala Gly Asp Gly Gly Lys Val Gly Thr Gly Gly Met Ala Ser Lys	
250 255 260	
gtg tct gct gca cgt ttg gct tcc cga agt ggc gtg cct gtg ctg ttg	931
Val Ser Ala Ala Arg Leu Ala Ser Arg Ser Gly Val Pro Val Leu Leu	
265 270 275	
acc tct gcg gca aac att ggc cca gca ctg gaa gac gcc cag gtg ggc	979
Thr Ser Ala Ala Asn Ile Gly Pro Ala Leu Glu Asp Ala Gln Val Gly	
280 285 290	
act gta ttc cac ccc aag gac aac cgc ctc tcc gcg tgg aag ttc tgg	
1027 Thr Val Phe His Pro Lys Asp Asn Arg Leu Ser Ala Trp Lys Phe Trp	
295 300 305	
gct ttg tat gcc gca gat act gca gga aag atc cga ctc gat gac ggc	
1075 Ala Leu Tyr Ala Ala Asp Thr Ala Gly Lys Ile Arg Leu Asp Asp Gly	
310 315 320 325	
gcg gtg gaa gca gtg acc tcc ggt ggt aaa tct ttg ctg gct gtg ggc	
1123 Ala Val Glu Ala Val Thr Ser Gly Gly Lys Ser Leu Leu Ala Val Gly	
330 335 340	
att act gaa atc att ggt gat ttc cag cag ggt gag atc gtg gag atc	
1171 Ile Thr Glu Ile Ile Gly Asp Phe Gln Gln Gly Glu Ile Val Glu Ile	
345 350 355	
ttg gga cct gcc ggc caa atc atc ggg cga ggc gag gtg tcc tac gat	
1219 Leu Gly Pro Ala Gly Gln Ile Ile Gly Arg Gly Glu Val Ser Tyr Asp	
360 365 370	
tct gat acc ttg caa tca atg gtt ggt atg caa acg cag gac ctt cca	
1267 Ser Asp Thr Leu Gln Ser Met Val Gly Met Gln Thr Gln Asp Leu Pro	
375 380 385	

gat ggc atg cag cgc ccg gta gtg cat gca gat tat ctg tcc aac tac  
 1315  
 Asp Gly Met Gln Arg Pro Val Val His Ala Asp Tyr Leu Ser Asn Tyr  
 390 395 400 405

gcc agc cgc gcg taaagcgcgg gcctgctggt ggc  
 1350  
 Ala Ser Arg Ala

<210> 290  
 <211> 409  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 290  
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 20 25 30  
 Ala Ala Tyr Gly His Glu Ser Gly Met Arg Glu Arg Ile Ser Asn Ala  
 35 40 45  
 Lys Arg Val Val Val Lys Ile Gly Ser Ser Ser Leu Thr Asn Asp Glu  
 50 55 60  
 Asp Gly His Thr Val Asp Pro Asn Arg Ile Asn Thr Ile Val Asn Ala  
 65 70 75 80  
 Leu Gln Ala Arg Met Glu Ala Gly Ser Asp Leu Ile Val Val Ser Ser  
 85 90 95  
 Gly Ala Val Ala Ala Gly Met Ala Pro Leu Gly Leu Ser Thr Arg Pro  
 100 105 110  
 Thr Glu Leu Ala Val Lys Gln Ala Ala Ala Ala Val Gly Gln Val His  
 115 120 125  
 Leu Met His Gln Trp Gly Arg Ser Phe Ala Arg Tyr Gly Arg Pro Ile  
 130 135 140  
 Gly Gln Val Leu Leu Thr Ala Ala Asp Ala Gly Lys Arg Asp Arg Ala  
 145 150 155 160  
 Arg Asn Ala Gln Arg Thr Ile Asp Lys Leu Arg Ile Leu Gly Ala Val  
 165 170 175  
 Pro Ile Val Asn Glu Asn Asp Thr Val Ala Thr Thr Gly Val Asn Phe  
 180 185 190  
 Gly Asp Asn Asp Arg Leu Ala Ala Ile Val Ala His Leu Val Ser Ala  
 195 200 205  
 Asp Ala Leu Val Leu Leu Ser Asp Val Asp Gly Leu Phe Asp Lys Asn  
 210 215 220  
 Pro Thr Asp Pro Thr Ala Lys Phe Ile Ser Glu Val Arg Asp Gly Asn

225		230		235		240
Asp Leu Lys Gly Val Ile Ala Gly Asp Gly Gly Lys Val Gly Thr Gly						
	245			250		255
Gly Met Ala Ser Lys Val Ser Ala Ala Arg Leu Ala Ser Arg Ser Gly						
	260		265			270
Val Pro Val Leu Leu Thr Ser Ala Ala Asn Ile Gly Pro Ala Leu Glu						
	275		280			285
Asp Ala Gln Val Gly Thr Val Phe His Pro Lys Asp Asn Arg Leu Ser						
	290		295		300	
Ala Trp Lys Phe Trp Ala Leu Tyr Ala Ala Asp Thr Ala Gly Lys Ile						
305		310		315		320
Arg Leu Asp Asp Gly Ala Val Glu Ala Val Thr Ser Gly Gly Lys Ser						
	325		330			335
Leu Leu Ala Val Gly Ile Thr Glu Ile Ile Gly Asp Phe Gln Gln Gly						
	340		345			350
Glu Ile Val Glu Ile Leu Gly Pro Ala Gly Gln Ile Ile Gly Arg Gly						
	355		360		365	
Glu Val Ser Tyr Asp Ser Asp Thr Leu Gln Ser Met Val Gly Met Gln						
	370		375		380	
Thr Gln Asp Leu Pro Asp Gly Met Gln Arg Pro Val Val His Ala Asp						
385		390		395		400
Tyr Leu Ser Asn Tyr Ala Ser Arg Ala						
	405					

<210> 291  
 <211> 1419  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1396)  
 <223> RXN02382

<400> 291  
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 Met Ser Ser Thr Thr  
 1 5  
 cta act gat gac caa att cgc gac aat gag cgg acc gaa gtt cta gct 163  
 Leu Thr Asp Asp Gln Ile Arg Asp Asn Glu Arg Thr Glu Val Leu Ala  
 10 15 20  
 aaa gca act gca gct aag aac atc gtc ccg gat att gca gtg ttg ggc 211  
 Lys Ala Thr Ala Ala Lys Asn Ile Val Pro Asp Ile Ala Val Leu Gly  
 25 30 35

acc gga ccg aag aac gca atc ctg cgt gcg gcg gca gat gaa ctc gtt	259
Thr Gly Pro Lys Asn Ala Ile Leu Arg Ala Ala Ala Asp Glu Leu Val	
40 45 50	
gca cgc agc gca gaa atc atc gaa gcc aac gct tcc gat atc gaa gcg	307
Ala Arg Ser Ala Glu Ile Ile Glu Ala Asn Ala Ser Asp Ile Glu Ala	
55 60 65	
ggc cgc gca aac ggc atg gaa gaa tcc atg att gat cgc ctt gcc ctt	355
Gly Arg Ala Asn Gly Met Glu Glu Ser Met Ile Asp Arg Leu Ala Leu	
70 75 80 85	
gat gaa tct cgc att gag ggc atc gct ggc ggt ttg cgc cag gtt gct	403
Asp Glu Ser Arg Ile Glu Gly Ile Ala Gly Gly Leu Arg Gln Val Ala	
90 95 100	
ggc ctg acc gac cca gtg ggt gaa gta ctg cgc gga cat gtc atg gaa	451
Gly Leu Thr Asp Pro Val Gly Glu Val Leu Arg Gly His Val Met Glu	
105 110 115	
aac ggc att cag atg aag cag gtc cgt gtg cct ttg ggc gtg atg ggc	499
Asn Gly Ile Gln Met Lys Gln Val Arg Val Pro Leu Gly Val Met Gly	
120 125 130	
atg gtc tat gaa gcc cgc cct aac gtc acc gtc gac gcc ttc ggc ctg	547
Met Val Tyr Glu Ala Arg Pro Asn Val Thr Val Asp Ala Phe Gly Leu	
135 140 145	
gca ctc aag tcc gga aac gta gct ttg ctg cgc ggt tcc tcc aca gct	595
Ala Leu Lys Ser Gly Asn Val Ala Leu Leu Arg Gly Ser Ser Thr Ala	
150 155 160 165	
gtg cat tcc aac acc aag ctc gtg gaa atc ctg cag gac gtc ctc gag	643
Val His Ser Asn Thr Lys Leu Val Glu Ile Leu Gln Asp Val Leu Glu	
170 175 180	
cgt ttc gag ctg cca cgc gaa acc gtg cag ttg ctg cct tgc caa acc	691
Arg Phe Glu Leu Pro Arg Glu Thr Val Gln Leu Leu Pro Cys Gln Thr	
185 190 195	
cgc gga tcc gtc caa gat ttg atc acc gca cgc ggc ctc gtt gac gtg	739
Arg Gly Ser Val Gln Asp Leu Ile Thr Ala Arg Gly Leu Val Asp Val	
200 205 210	
gtc atc cca cgc ggc ggc gca gga cta atc aac gca gtg gtc acc ggt	787
Val Ile Pro Arg Gly Gly Ala Gly Leu Ile Asn Ala Val Val Thr Gly	
215 220 225	
gcg acc gtg ccc acc att gaa acc ggc acc ggc aac tgc cac ttc tac	835
Ala Thr Val Pro Thr Ile Glu Thr Gly Thr Gly Asn Cys His Phe Tyr	
230 235 240 245	
atc gat gcc gaa gcc aag ctt gat cag gca atc gcc atg gtc atc aac	883
Ile Asp Ala Glu Ala Lys Leu Asp Gln Ala Ile Ala Met Val Ile Asn	
250 255 260	
ggc aag acc cgc cgc tgc agc gtg tgc aac gct act gaa acc gcg ctt	931
Gly Lys Thr Arg Arg Cys Ser Val Cys Asn Ala Thr Glu Thr Ala Leu	
265 270 275	
ctc gac gcc gcc ctc agc gac tca gac aag ctt gca gtc gtc cag gcg	979

Leu Asp Ala Ala Leu Ser Asp Ser Asp Lys Leu Ala Val Val Gln Ala  
280 285 290

ctc cag gaa gca gga gtc aca att cat gga cgg gtg gcc gaa ttg gaa  
1027

Leu Gln Glu Ala Gly Val Thr Ile His Gly Arg Val Ala Glu Leu Glu  
295 300 305

gca ttc ggt gca acc gac gtg gtg gaa gca act gaa act gac tgg gat  
1075

Ala Phe Gly Ala Thr Asp Val Val Glu Ala Thr Glu Thr Asp Trp Asp  
310 315 320 325

tct gag tac ctg tcc ttc gat atc gct gtc gct gtg gtt gac ggt gtg  
1123

Ser Glu Tyr Leu Ser Phe Asp Ile Ala Val Ala Val Val Asp Gly Val  
330 335 340

gat gga gct ctg gca cac atc gct aag tac agc acc aag cac acc gaa  
1171

Asp Gly Ala Leu Ala His Ile Ala Lys Tyr Ser Thr Lys His Thr Glu  
345 350 355

gcg atc gcc acc caa aac att gaa acc gct cag cgc ttt gca gat cgc  
1219

Ala Ile Ala Thr Gln Asn Ile Glu Thr Ala Gln Arg Phe Ala Asp Arg  
360 365 370

gtc gat gca gca gcg gtg atg ata aac gca tcc acc gcc tac acc gat  
1267

Val Asp Ala Ala Ala Val Met Ile Asn Ala Ser Thr Ala Tyr Thr Asp  
375 380 385

ggg gag cag tac ggc atg ggc gcg gag atc ggc att tcc acc cag aaa  
1315

Gly Glu Gln Tyr Gly Met Gly Ala Glu Ile Gly Ile Ser Thr Gln Lys  
390 395 400 405

ctg cat gca cgt gga cca atg gcc ctg cca gag ctg acc tcc acc aag  
1363

Leu His Ala Arg Gly Pro Met Ala Leu Pro Glu Leu Thr Ser Thr Lys  
410 415 420

tgg att ctg cag ggc aca gga caa att agg cct taagtttgaa gaagtaatca  
1416

Trp Ile Leu Gln Gly Thr Gly Gln Ile Arg Pro  
425 430

agc  
1419

<210> 292

<211> 432

<212> PRT

<213> Corynebacterium glutamicum

<400> 292

Met Ser Ser Thr Thr Leu Thr Asp Asp Gln Ile Arg Asp Asn Glu Arg  
1 5 10 15

Thr Glu Val Leu Ala Lys Ala Thr Ala Ala Lys Asn Ile Val Pro Asp  
 20 25 30  
 Ile Ala Val Leu Gly Thr Gly Pro Lys Asn Ala Ile Leu Arg Ala Ala  
 35 40 45  
 Ala Asp Glu Leu Val Ala Arg Ser Ala Glu Ile Ile Glu Ala Asn Ala  
 50 55 60  
 Ser Asp Ile Glu Ala Gly Arg Ala Asn Gly Met Glu Glu Ser Met Ile  
 65 70 75 80  
 Asp Arg Leu Ala Leu Asp Glu Ser Arg Ile Glu Gly Ile Ala Gly Gly  
 85 90 95  
 Leu Arg Gln Val Ala Gly Leu Thr Asp Pro Val Gly Glu Val Leu Arg  
 100 105 110  
 Gly His Val Met Glu Asn Gly Ile Gln Met Lys Gln Val Arg Val Pro  
 115 120 125  
 Leu Gly Val Met Gly Met Val Tyr Glu Ala Arg Pro Asn Val Thr Val  
 130 135 140  
 Asp Ala Phe Gly Leu Ala Leu Lys Ser Gly Asn Val Ala Leu Leu Arg  
 145 150 155 160  
 Gly Ser Ser Thr Ala Val His Ser Asn Thr Lys Leu Val Glu Ile Leu  
 165 170 175  
 Gln Asp Val Leu Glu Arg Phe Glu Leu Pro Arg Glu Thr Val Gln Leu  
 180 185 190  
 Leu Pro Cys Gln Thr Arg Gly Ser Val Gln Asp Leu Ile Thr Ala Arg  
 195 200 205  
 Gly Leu Val Asp Val Val Ile Pro Arg Gly Gly Ala Gly Leu Ile Asn  
 210 215 220  
 Ala Val Val Thr Gly Ala Thr Val Pro Thr Ile Glu Thr Gly Thr Gly  
 225 230 235 240  
 Asn Cys His Phe Tyr Ile Asp Ala Glu Ala Lys Leu Asp Gln Ala Ile  
 245 250 255  
 Ala Met Val Ile Asn Gly Lys Thr Arg Arg Cys Ser Val Cys Asn Ala  
 260 265 270  
 Thr Glu Thr Ala Leu Leu Asp Ala Ala Leu Ser Asp Ser Asp Lys Leu  
 275 280 285  
 Ala Val Val Gln Ala Leu Gln Glu Ala Gly Val Thr Ile His Gly Arg  
 290 295 300  
 Val Ala Glu Leu Glu Ala Phe Gly Ala Thr Asp Val Val Glu Ala Thr  
 305 310 315 320  
 Glu Thr Asp Trp Asp Ser Glu Tyr Leu Ser Phe Asp Ile Ala Val Ala  
 325 330 335  
 Val Val Asp Gly Val Asp Gly Ala Leu Ala His Ile Ala Lys Tyr Ser

			340					345					350				
Thr	Lys	His	Thr	Glu	Ala	Ile	Ala	Thr	Gln	Asn	Ile	Glu	Thr	Ala	Gln		
		355					360					365					
Arg	Phe	Ala	Asp	Arg	Val	Asp	Ala	Ala	Ala	Val	Met	Ile	Asn	Ala	Ser		
	370					375					380						
Thr	Ala	Tyr	Thr	Asp	Gly	Glu	Gln	Tyr	Gly	Met	Gly	Ala	Glu	Ile	Gly		
385					390					395					400		
Ile	Ser	Thr	Gln	Lys	Leu	His	Ala	Arg	Gly	Pro	Met	Ala	Leu	Pro	Glu		
				405					410					415			
Leu	Thr	Ser	Thr	Lys	Trp	Ile	Leu	Gln	Gly	Thr	Gly	Gln	Ile	Arg	Pro		
			420					425					430				

<210> 293  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(709)  
 <223> FRXA02378

<400> 293  
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cgacactggt gcttcttaag ggtctgtata gtgggcaacc atg agt tca acg acc 115  
 Met Ser Ser Thr Thr  
 1 5

cta act gat gac caa att cgc gac aat gag cgg acc gaa gtt cta gct 163  
 Leu Thr Asp Asp Gln Ile Arg Asp Asn Glu Arg Thr Glu Val Leu Ala  
 10 15 20

aaa gca act gca gct aag aac atc gtc ccg gat att gca gtg ttg ggc 211  
 Lys Ala Thr Ala Ala Lys Asn Ile Val Pro Asp Ile Ala Val Leu Gly  
 25 30 35

acc gga ccg aag aac gca atc ctg cgt gcg gcg gca gat gaa ctc gtt 259  
 Thr Gly Pro Lys Asn Ala Ile Leu Arg Ala Ala Ala Asp Glu Leu Val  
 40 45 50

gca cgc agc gca gaa atc atc gaa gcc aac gct tcc gat atc gaa gcg 307  
 Ala Arg Ser Ala Glu Ile Ile Glu Ala Asn Ala Ser Asp Ile Glu Ala  
 55 60 65

ggt cgc gca aac ggc atg gaa gaa tcc atg att gat cgc ctt gcc ctt 355  
 Gly Arg Ala Asn Gly Met Glu Glu Ser Met Ile Asp Arg Leu Ala Leu  
 70 75 80 85

gat gaa tct cgc att gag ggc atc gct ggc ggt ttg cgc cag gtt gct 403  
 Asp Glu Ser Arg Ile Glu Gly Ile Ala Gly Gly Leu Arg Gln Val Ala  
 90 95 100

ggc ctg acc gac cca gtg ggt gaa gta ctg cgc gga cat gtc atg gaa 451  
 Gly Leu Thr Asp Pro Val Gly Glu Val Leu Arg Gly His Val Met Glu  
 105 110 115  
 aac ggc att cag atg aag cag gtc cgt gtg cct ttg ggc gtg atg ggc 499  
 Asn Gly Ile Gln Met Lys Gln Val Arg Val Pro Leu Gly Val Met Gly  
 120 125 130  
 atg gtc tat gaa gcc cgc cct aac gtc acc gtc gac gcc ttc ggc ctg 547  
 Met Val Tyr Glu Ala Arg Pro Asn Val Thr Val Asp Ala Phe Gly Leu  
 135 140 145  
 gca ctc aag tcc gga aac gta gct ttg ctg cgc ggt tcc tcc aca gct 595  
 Ala Leu Lys Ser Gly Asn Val Ala Leu Leu Arg Gly Ser Ser Thr Ala  
 150 155 160 165  
 gtg cat tcc aac acc aag ctc gtg gaa atc ctg cag gac gta ctc gag 643  
 Val His Ser Asn Thr Lys Leu Val Glu Ile Leu Gln Asp Val Leu Glu  
 170 175 180  
 cgt ttc gag ctg cca cgc gaa acc gtg cag ttg ctg ctt gcc aaa ccc 691  
 Arg Phe Glu Leu Pro Arg Glu Thr Val Gln Leu Leu Leu Ala Lys Pro  
 185 190 195  
 gcg gat ccg tcc aag att tgatcaccgg acgcg 724  
 Ala Asp Pro Ser Lys Ile  
 200

&lt;210&gt; 294

&lt;211&gt; 203

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 294

Met Ser Ser Thr Thr Leu Thr Asp Asp Gln Ile Arg Asp Asn Glu Arg  
 1 5 10 15  
 Thr Glu Val Leu Ala Lys Ala Thr Ala Ala Lys Asn Ile Val Pro Asp  
 20 25 30  
 Ile Ala Val Leu Gly Thr Gly Pro Lys Asn Ala Ile Leu Arg Ala Ala  
 35 40 45  
 Ala Asp Glu Leu Val Ala Arg Ser Ala Glu Ile Ile Glu Ala Asn Ala  
 50 55 60  
 Ser Asp Ile Glu Ala Gly Arg Ala Asn Gly Met Glu Glu Ser Met Ile  
 65 70 75 80  
 Asp Arg Leu Ala Leu Asp Glu Ser Arg Ile Glu Gly Ile Ala Gly Gly  
 85 90 95  
 Leu Arg Gln Val Ala Gly Leu Thr Asp Pro Val Gly Glu Val Leu Arg  
 100 105 110  
 Gly His Val Met Glu Asn Gly Ile Gln Met Lys Gln Val Arg Val Pro  
 115 120 125  
 Leu Gly Val Met Gly Met Val Tyr Glu Ala Arg Pro Asn Val Thr Val



130	135	140
Asp Ala Phe Gly Leu Ala Leu Lys Ser Gly Asn Val Ala Leu Leu Arg		
145	150	155 160
Gly Ser Ser Thr Ala Val His Ser Asn Thr Lys Leu Val Glu Ile Leu		
	165	170 175
Gln Asp Val Leu Glu Arg Phe Glu Leu Pro Arg Glu Thr Val Gln Leu		
	180	185 190
Leu Leu Ala Lys Pro Ala Asp Pro Ser Lys Ile		
195	200	

&lt;210&gt; 295

&lt;211&gt; 623

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(600)

&lt;223&gt; FRXA02382

&lt;400&gt; 295

ccc acc att gaa acc ggc acc ggc aac tgc cac ttc tac atc gat gcc	48
Pro Thr Ile Glu Thr Gly Thr Gly Asn Cys His Phe Tyr Ile Asp Ala	
1 5 10 15	

gaa gcc aag ctt gat cag gca atc gcc atg gtc atc aac ggc aag acc	96
Glu Ala Lys Leu Asp Gln Ala Ile Ala Met Val Ile Asn Gly Lys Thr	
20 25 30	

cgc cgc tgc agc gtg tgc aac gct act gaa acc gcg ctt ctc gac gcc	144
Arg Arg Cys Ser Val Cys Asn Ala Thr Glu Thr Ala Leu Leu Asp Ala	
35 40 45	

gcc ctc agc gac tca gac aag ctt gca gtc gtc cag gcg ctc cag gaa	192
Ala Leu Ser Asp Ser Asp Lys Leu Ala Val Val Gln Ala Leu Gln Glu	
50 55 60	

gca gga gtc aca att cat gga cgg gtg gcc gaa ttg gaa gca ttc ggt	240
Ala Gly Val Thr Ile His Gly Arg Val Ala Glu Leu Glu Ala Phe Gly	
65 70 75 80	

gca acc gac gtg gtg gaa gca act gaa act gac tgg gat tct gag tac	288
Ala Thr Asp Val Val Glu Ala Thr Glu Thr Asp Trp Asp Ser Glu Tyr	
85 90 95	

ctg tcc ttc gat atc gct gtc gct gtg gtt gac ggt gtg gat gga gct	336
Leu Ser Phe Asp Ile Ala Val Ala Val Val Asp Gly Val Asp Gly Ala	
100 105 110	

ctg gca cac atc gct aag tac agc acc aag cac acc gaa gcg atc gcc	384
Leu Ala His Ile Ala Lys Tyr Ser Thr Lys His Thr Glu Ala Ile Ala	
115 120 125	

acc caa aac att gaa acc gct cag cgc ttt gca gat cgc gtc gat gca	432
Thr Gln Asn Ile Glu Thr Ala Gln Arg Phe Ala Asp Arg Val Asp Ala	
130 135 140	

gca gcg gtg atg ata aac gca tcc acc gcc tac acc gat ggg gag cag 480  
 Ala Ala Val Met Ile Asn Ala Ser Thr Ala Tyr Thr Asp Gly Glu Gln  
 145 150 155 160

tac ggc atg ggc gcg gag atc ggc att tcc acc cag aaa ctg cat gca 528  
 Tyr Gly Met Gly Ala Glu Ile Gly Ile Ser Thr Gln Lys Leu His Ala  
 165 170 175

cgt gga cca atg gcc ctg cca gag ctg acc tcc acc aag tgg att ctg 576  
 Arg Gly Pro Met Ala Leu Pro Glu Leu Thr Ser Thr Lys Trp Ile Leu  
 180 185 190

cag ggc aca gga caa att agg cct taagtttgaa gaagtaatca agc 623  
 Gln Gly Thr Gly Gln Ile Arg Pro  
 195 200

<210> 296

<211> 200

<212> PRT

<213> Corynebacterium glutamicum

<400> 296

Pro Thr Ile Glu Thr Gly Thr Gly Asn Cys His Phe Tyr Ile Asp Ala  
 1 5 10 15

Glu Ala Lys Leu Asp Gln Ala Ile Ala Met Val Ile Asn Gly Lys Thr  
 20 25 30

Arg Arg Cys Ser Val Cys Asn Ala Thr Glu Thr Ala Leu Leu Asp Ala  
 35 40 45

Ala Leu Ser Asp Ser Asp Lys Leu Ala Val Val Gln Ala Leu Gln Glu  
 50 55 60

Ala Gly Val Thr Ile His Gly Arg Val Ala Glu Leu Glu Ala Phe Gly  
 65 70 75 80

Ala Thr Asp Val Val Glu Ala Thr Glu Thr Asp Trp Asp Ser Glu Tyr  
 85 90 95

Leu Ser Phe Asp Ile Ala Val Ala Val Val Asp Gly Val Asp Gly Ala  
 100 105 110

Leu Ala His Ile Ala Lys Tyr Ser Thr Lys His Thr Glu Ala Ile Ala  
 115 120 125

Thr Gln Asn Ile Glu Thr Ala Gln Arg Phe Ala Asp Arg Val Asp Ala  
 130 135 140

Ala Ala Val Met Ile Asn Ala Ser Thr Ala Tyr Thr Asp Gly Glu Gln  
 145 150 155 160

Tyr Gly Met Gly Ala Glu Ile Gly Ile Ser Thr Gln Lys Leu His Ala  
 165 170 175

Arg Gly Pro Met Ala Leu Pro Glu Leu Thr Ser Thr Lys Trp Ile Leu  
 180 185 190

Gln Gly Thr Gly Gln Ile Arg Pro

195

200

<210> 297  
 <211> 933  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(910)  
 <223> RXA02499

<400> 297  
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ctgctgcaaaa acaggggtgg ttagtggcag tgtgggaacc atg aca aca att gct 115  
 Met Thr Thr Ile Ala  
 1 5

gta atc ggc ggc gga caa atc ggc gag gct tta gtc tca ggt ttg atc 163  
 Val Ile Gly Gly Gly Gln Ile Gly Glu Ala Leu Val Ser Gly Leu Ile  
 10 15 20

gcg gcc aac atg aat cca caa aat att cgc gtc acc aac cgt tcg gaa 211  
 Ala Ala Asn Met Asn Pro Gln Asn Ile Arg Val Thr Asn Arg Ser Glu  
 25 30 35

gag cgc ggc caa gag ctg cgt gac cgc tac ggc atc ctc aac atg acg 259  
 Glu Arg Gly Gln Glu Leu Arg Asp Arg Tyr Gly Ile Leu Asn Met Thr  
 40 45 50

gat aat tcc caa gcc gca gac gaa gcc gac gtg gtg ttc ctg tgc gtg 307  
 Asp Asn Ser Gln Ala Ala Asp Glu Ala Asp Val Val Phe Leu Cys Val  
 55 60 65

aag ccg aaa ttt atc gtc gaa gtg ctc tcc gaa atc acc ggc act ttg 355  
 Lys Pro Lys Phe Ile Val Glu Val Leu Ser Glu Ile Thr Gly Thr Leu  
 70 75 80 85

gat aac aac tcc gca caa agt gtt gtg gtc agc atg gcc gca ggc atc 403  
 Asp Asn Asn Ser Ala Gln Ser Val Val Val Ser Met Ala Ala Gly Ile  
 90 95 100

agc atc gct gcc atg gaa gaa agc gcc tct gcg ggg ctc ccc gtc gtg 451  
 Ser Ile Ala Ala Met Glu Glu Ser Ala Ser Ala Gly Leu Pro Val Val  
 105 110 115

cgc gtc atg ccg aac act cca atg ctc gtg ggc aag ggc atg tcg act 499  
 Arg Val Met Pro Asn Thr Pro Met Leu Val Gly Lys Gly Met Ser Thr  
 120 125 130

gtc acc aaa ggc cgc tac gtt gac gcg gaa cag ttg gaa caa gtc aag 547  
 Val Thr Lys Gly Arg Tyr Val Asp Ala Glu Gln Leu Glu Gln Val Lys  
 135 140 145

gac ttg ttg agc acc gtt gga gac gtc ctc gaa gtc gcg gaa tca gac 595  
 Asp Leu Leu Ser Thr Val Gly Asp Val Leu Glu Val Ala Glu Ser Asp  
 150 155 160 165

atc gac gca gtc acc gcg atg tcc gga tcc tcc cct gca tac ctg ttc 643

Ile	Asp	Ala	Val	Thr	Ala	Met	Ser	Gly	Ser	Ser	Pro	Ala	Tyr	Leu	Phe	
				170					175					180		
ctt	gtg	acc	gaa	gcg	ctc	att	gag	gca	gga	gtt	aat	cta	ggc	ctg	ccc	691
Leu	Val	Thr	Glu	Ala	Leu	Ile	Glu	Ala	Gly	Val	Asn	Leu	Gly	Leu	Pro	
			185					190					195			
cgc	gcg	acc	gct	aaa	aag	ctc	gct	gtg	gcc	tca	ttc	gaa	ggg	gct	gca	739
Arg	Ala	Thr	Ala	Lys	Lys	Leu	Ala	Val	Ala	Ser	Phe	Glu	Gly	Ala	Ala	
		200					205					210				
acc	atg	atg	aag	gaa	acc	ggc	aaa	gaa	ccc	tca	gaa	ttg	cgc	gca	ggc	787
Thr	Met	Met	Lys	Glu	Thr	Gly	Lys	Glu	Pro	Ser	Glu	Leu	Arg	Ala	Gly	
	215					220					225					
gtt	tcc	tca	ccc	gca	ggc	acc	acc	gtc	gca	gcc	atc	cga	gaa	ctc	gaa	835
Val	Ser	Ser	Pro	Ala	Gly	Thr	Thr	Val	Ala	Ala	Ile	Arg	Glu	Leu	Glu	
230					235				240							
gaa	agc	gga	atc	cga	ggc	gct	ttc	tac	cgc	gca	gcc	caa	gct	tgc	gcc	883
Glu	Ser	Gly	Ile	Arg	Gly	Ala	Phe	Tyr	Arg	Ala	Ala	Gln	Ala	Cys	Ala	
				250					255					260		
gac	cga	tct	gaa	gaa	ctc	gga	aag	cgc	tagaaaccgt	tatttccccg						930
Asp	Arg	Ser	Glu	Glu	Leu	Gly	Lys	Arg								
			265					270								
tta																933

&lt;210&gt; 298

&lt;211&gt; 270

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 298

Met	Thr	Thr	Ile	Ala	Val	Ile	Gly	Gly	Gly	Gln	Ile	Gly	Glu	Ala	Leu	
1				5					10					15		
Val	Ser	Gly	Leu	Ile	Ala	Ala	Asn	Met	Asn	Pro	Gln	Asn	Ile	Arg	Val	
			20					25					30			
Thr	Asn	Arg	Ser	Glu	Glu	Arg	Gly	Gln	Glu	Leu	Arg	Asp	Arg	Tyr	Gly	
		35					40					45				
Ile	Leu	Asn	Met	Thr	Asp	Asn	Ser	Gln	Ala	Ala	Asp	Glu	Ala	Asp	Val	
		50				55					60					
Val	Phe	Leu	Cys	Val	Lys	Pro	Lys	Phe	Ile	Val	Glu	Val	Leu	Ser	Glu	
65					70					75					80	
Ile	Thr	Gly	Thr	Leu	Asp	Asn	Asn	Ser	Ala	Gln	Ser	Val	Val	Val	Ser	
				85					90					95		
Met	Ala	Ala	Gly	Ile	Ser	Ile	Ala	Ala	Met	Glu	Glu	Ser	Ala	Ser	Ala	
			100					105					110			
Gly	Leu	Pro	Val	Val	Arg	Val	Met	Pro	Asn	Thr	Pro	Met	Leu	Val	Gly	
		115					120					125				
Lys	Gly	Met	Ser	Thr	Val	Thr	Lys	Gly	Arg	Tyr	Val	Asp	Ala	Glu	Gln	

130	135	140
Leu Glu Gln Val Lys Asp	Leu Leu Ser Thr Val Gly Asp Val Leu Glu	
145	150	155
Val Ala Glu Ser Asp Ile Asp Ala Val Thr Ala Met Ser Gly Ser Ser		
	165	170
Pro Ala Tyr Leu Phe Leu Val Thr Glu Ala Leu Ile Glu Ala Gly Val		
	180	185
Asn Leu Gly Leu Pro Arg Ala Thr Ala Lys Lys Leu Ala Val Ala Ser		
	195	200
Phe Glu Gly Ala Ala Thr Met Met Lys Glu Thr Gly Lys Glu Pro Ser		
	210	215
Glu Leu Arg Ala Gly Val Ser Ser Pro Ala Gly Thr Thr Val Ala Ala		
	225	230
Ile Arg Glu Leu Glu Glu Ser Gly Ile Arg Gly Ala Phe Tyr Arg Ala		
	245	250
Ala Gln Ala Cys Ala Asp Arg Ser Glu Glu Leu Gly Lys Arg		
	260	265
		270

&lt;210&gt; 299

&lt;211&gt; 1296

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1273)

&lt;223&gt; RXS02157

&lt;400&gt; 299

gggtggaatt ggcacgatgg tgctgccgga tgtttttgat cgggagaatt atcctgaagg 60

caccgttttt	agaaaagacg	acaaggatgg	ggaactgtaa	atg	agc	acg	ctg	gaa	115
				Met	Ser	Thr	Leu	Glu	
				1				5	

act	tgg	cca	cag	gtc	att	att	aat	acg	tac	ggc	acc	cca	cca	gtt	gag	163
Thr	Trp	Pro	Gln	Val	Ile	Ile	Asn	Thr	Tyr	Gly	Thr	Pro	Pro	Val	Glu	
				10					15					20		

ctg	gtg	tcc	ggc	aag	ggc	gca	acc	gtc	act	gat	gac	cag	ggc	aat	gtc	211
Leu	Val	Ser	Gly	Lys	Gly	Ala	Thr	Val	Thr	Asp	Asp	Gln	Gly	Asn	Val	
			25					30					35			

tac	atc	gac	ttg	ctc	gcg	ggc	atc	gca	gtc	aac	gcg	ttg	ggc	cac	gcc	259
Tyr	Ile	Asp	Leu	Leu	Ala	Gly	Ile	Ala	Val	Asn	Ala	Leu	Gly	His	Ala	
		40				45						50				

cac	ccg	gcg	atc	atc	gag	gcg	gtc	acc	aac	cag	atc	ggc	caa	ctt	ggt	307
His	Pro	Ala	Ile	Ile	Glu	Ala	Val	Thr	Asn	Gln	Ile	Gly	Gln	Leu	Gly	
	55					60					65					

cac	gtc	tca	aac	ttg	ttc	gca	tcc	agg	ccc	gtc	gtc	gag	gtc	gcc	gag	355
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

His 70	Val	Ser	Asn	Leu	Phe 75	Ala	Ser	Arg	Pro	Val 80	Val	Glu	Val	Ala	Glu 85	
gag	ctc	atc	aag	cgt	ttt	tcg	ctt	gac	gac	gcc	acc	ctc	gcc	gcg	caa	403
Glu	Leu	Ile	Lys	Arg 90	Phe	Ser	Leu	Asp	Asp 95	Ala	Thr	Leu	Ala	Ala	Gln 100	
acc	cgg	gtt	ttc	ttc	tgc	aac	tcg	ggc	gcc	gaa	gca	aac	gag	gct	gct	451
Thr	Arg	Val	Phe 105	Phe	Cys	Asn	Ser	Gly 110	Ala	Glu	Ala	Asn	Glu 115	Ala	Ala	
ttc	aag	att	gca	cgc	ttg	act	ggc	cgt	tcc	cgg	att	ctg	gct	gca	gtt	499
Phe	Lys	Ile 120	Ala	Arg	Leu	Thr	Gly 125	Arg	Ser	Arg	Ile	Leu 130	Ala	Ala	Val	
cat	ggc	ttc	cac	ggc	cgc	acc	atg	ggc	tcc	ctc	gcg	ctg	act	ggc	cag	547
His	Gly 135	Phe	His	Gly	Arg	Thr 140	Met	Gly	Ser	Leu	Ala 145	Leu	Thr	Gly	Gln	
cca	gac	aag	cgt	gaa	gcg	ttc	ctg	cca	atg	cca	agc	ggc	gtg	gag	ttc	595
Pro	Asp	Lys	Arg	Glu 150	Ala 155	Phe	Leu	Pro	Met	Pro 160	Ser	Gly	Val	Glu	Phe 165	
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ggc	gtt	gtt	cca	gca	cct	gaa	gga	ttc	ctc	aag	gca	gtg	cgc	gag	ctg	739
Gly	Val	Val 200	Pro	Ala	Pro	Glu	Gly 205	Phe	Leu	Lys	Ala	Val 210	Arg	Glu	Leu	
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Cys	Asp 215	Glu	Tyr	Gly	Ile	Leu 220	Met	Ile	Thr	Asp	Glu 225	Val	Gln	Thr	Gly	
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Val	Gly	Arg	Thr	Gly	Asp 235	Phe	Phe	Ala	His	Gln 240	His	Asp	Gly	Val 245	Val	
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Pro	Asp	Val	Val	Thr 250	Met	Ala	Lys	Gly	Leu 255	Gly	Gly	Gly	Leu	Pro 260	Ile	
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Gly	Ala	Cys 265	Leu	Ala	Thr	Gly	Arg	Ala 270	Ala	Glu	Leu	Met	Thr 275	Pro	Gly	
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Lys	His	Gly 280	Thr	Thr	Phe	Gly	Gly	Asn 285	Pro	Val	Ala	Cys	Ala 290	Ala	Ala	
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 Ala Asn Glu Ala Ala Phe Lys Ile Ala Arg Leu Thr Gly Arg Ser Arg  
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Ser Gly Val Glu Phe Tyr Pro Tyr Gly Asp Thr Asp Tyr Leu Arg Lys
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Met Val Glu Thr Asn Pro Thr Asp Val Ala Ala Ile Phe Leu Glu Pro
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Ile Gln Gly Glu Thr Gly Val Val Pro Ala Pro Glu Gly Phe Leu Lys
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His Asp Gly Val Val Pro Asp Val Val Thr Met Ala Lys Gly Leu Gly
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Gly Gly Leu Pro Ile Gly Ala Cys Leu Ala Thr Gly Arg Ala Ala Glu
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Ala Cys Ala Ala Ala Lys Ala Val Leu Ser Val Val Asp Asp Ala Phe
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Cys Ala Glu Val Ala Arg Lys Gly Glu Leu Phe Lys Glu Leu Leu Ala
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Lys Val Asp Gly Val Val Asp Val Arg Gly Arg Gly Leu Met Leu Gly
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Lys His Gly Val Ile Leu Asn Ala Pro Ala Asp Asn Ile Ile Arg Leu
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 Gly Ser Asn Ala Glu Asn Lys Ala Ser Gly Leu Pro Arg Ser Ile His  
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Tyr	Phe	Lys	Lys	Glu	Trp	Leu	Lys	Pro	Gly	Ala	Leu	Leu	Leu	Leu	Pro	
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Ala	Ala	Gly	Arg	Phe	Asp	Asp	Ala	Tyr	Leu	Leu	Asp	Asp	Ala	Arg	Leu	
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 Val Asp Val Met Glu Glu Thr Leu Val Leu Leu Ala Gln Gly Asp Tyr  
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 Pro Glu Asn Pro Glu Phe Glu Gly Met Pro Lys Asp Gly Pro Asp Arg  
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 Gly Val Lys Trp Tyr Gly Ser Asn Ala Glu Asn Lys Ala Ser Gly Leu  
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 Pro Arg Ser Ile His Thr Phe Val Leu Asn Asp Thr Val Thr Gly Ala  
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 Pro Lys Ala Ile Met Ser Ala Asn Leu Leu Ser Ala Tyr Arg Thr Gly  
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 Thr Leu Ala Val Val Gly Pro Gly Val Met Ala Lys Thr Ile Thr Glu  
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 Arg Ser Glu Arg Gly Ile Asn Ala Phe Ala Thr Trp Ala Leu Glu Lys  
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 Phe Pro Glu Ile Glu Val Val Ala Val Gly Ser Glu Glu Asp Val Val  
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 Lys Asp Ala Asp Ile Val Ile Ala Ala Thr Thr Thr Asp Ala Ala Gly  
 225 230 235 240  
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 Asp Asp Ala Arg Leu Val Val Asp Tyr Met Gly Leu Tyr Glu Ala Trp  
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 Ala Glu Glu Tyr Gly Pro Gln Ala Tyr Gln Leu Leu Gly Ile Pro Gly  
 290 295 300  
 Thr His Trp Tyr Asp Leu Ala Leu Gln Gly Lys Leu Asp Leu Ala Lys  
 305 310 315 320  
 Ile Ser Gln Ile Gly Asp Ile Cys Ser Gly Lys Leu Pro Gly Arg Thr  
 325 330 335

Asn Asp Glu Glu Ile Ile Leu Tyr Ser Val Gly Gly Met Pro Val Glu  
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 Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala  
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 Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe  
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cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct 259  
 His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala  
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gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac 307  
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tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac 403  
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 Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly  
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gca ggt tac tta aat ggc gtg cgc gaa ctt tgc aac aag cac ggc atc Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile 250 255 260			883
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 1315  
 Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu  
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 Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser Gly Asn Arg Phe His  
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 Asp Ala Val Glu Ala Ala Ala Gln Ala Val Glu Leu Thr Phe Ala Gly  
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 Ala Leu Phe  
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&lt;211&gt; 456

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

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 Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro  
 35 40 45  
 Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly  
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 Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly  
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 His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg  
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 Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val  
 100 105 110  
 Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe

115					120					125					
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His	Gly	Ala	Thr	Gly	Ser	Ala	Met	Met	Leu	Thr	Gly	Glu	His	Arg	Arg
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Phe	Leu	His	His	Ser	Ser	Phe	Phe	Ala	Thr	Thr	Gln	Glu	Glu	Glu	Cys
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Gly	Met	Ile	Ala	Ala	Ile	Val	Leu	Glu	Pro	Val	Val	Gly	Ser	Ser	Gly
225					230					235					240
Ile	Ile	Leu	Pro	Pro	Ala	Gly	Tyr	Leu	Asn	Gly	Val	Arg	Glu	Leu	Cys
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Asn	Lys	His	Gly	Ile	Leu	Phe	Ile	Ala	Asp	Glu	Val	Met	Val	Gly	Phe
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Gly	Arg	Thr	Gly	Lys	Leu	Phe	Ala	Tyr	Glu	His	Ala	Gly	Asp	Asp	Phe
		275					280					285			
Gln	Pro	Asp	Met	Ile	Thr	Phe	Ala	Lys	Gly	Val	Asn	Ala	Gly	Tyr	Ala
	290					295					300				
Pro	Leu	Gly	Gly	Ile	Val	Met	Thr	Gln	Ser	Ile	Arg	Asp	Thr	Phe	Gly
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Ser	Glu	Ala	Tyr	Ser	Gly	Gly	Leu	Thr	Tyr	Ser	Gly	His	Pro	Leu	Ala
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Val	Ala	Pro	Ala	Lys	Ala	Ala	Leu	Glu	Ile	Tyr	Ala	Glu	Gly	Glu	Ile
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Ile	Pro	Arg	Val	Ala	Arg	Leu	Gly	Ala	Glu	Leu	Ile	Glu	Pro	Arg	Leu
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Arg	Glu	Leu	Ala	Glu	Glu	Asn	Val	Ala	Ile	Ala	Asp	Val	Arg	Gly	Ile
	370					375					380				
Gly	Phe	Phe	Trp	Ala	Val	Glu	Phe	Asn	Ala	Asp	Ala	Thr	Ala	Met	Ala
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Ala	Gly	Ala	Ala	Glu	Phe	Lys	Glu	Arg	Gly	Val	Trp	Pro	Met	Ile	Ser
				405					410					415	
Gly	Asn	Arg	Phe	His	Ile	Ala	Pro	Pro	Leu	Thr	Thr	Thr	Asp	Asp	Glu
			420				425						430		
Leu	Val	Ala	Leu	Leu	Asp	Ala	Val	Glu	Ala	Ala	Ala	Gln	Ala	Val	Glu
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Leu Ala Leu Lys Gly  
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Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala  
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Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe  
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Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val  
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Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly  
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Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly  
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Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly  
150 155 160 165



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Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr	
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Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser	
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Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys	
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His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala	
215 220 225	
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Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro	
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Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile	
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 Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro  
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 Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly  
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 Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly  
   65                                      70                                      75                                      80  
 His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg  
                                     85                                      90                                      95  
 Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val  
                                     100                                      105                                      110  
 Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe  
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 Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala  
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 Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr  
 145                                      150                                      155                                      160  
 His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg  
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 Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro  
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 Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys  
                                     195                                      200                                      205  
 Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala  
                                     210                                      215                                      220

Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly  
 225 230 235 240  
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 245 250 255  
 Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe  
 260 265 270  
 Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe  
 275 280 285  
 Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala  
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 325 330 335  
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 Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu  
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 Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile  
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 Met Thr Ser Met Asn  
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 ctg cct att gag ttg gct acg ctg tct gac cag gct gtg gac aag gtg 163  
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Ser Phe Leu Asp Arg Ala Gln Ile Gln Ala Gly Ser Leu Val Gly Arg	
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Ala Leu Pro Gln Val Val Val Pro Ala Ala Arg Ala Arg Ile Arg Gln	
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Met Val Gly His Met Ile Val Asp Ala Arg Asp Lys Gln Phe Ala Lys	
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Ala Val Ala Glu Ile Gln Ser Asp Gly His Arg Leu Asn Ile Asn Leu	
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Asp Thr Val Arg Leu Leu Arg Arg Pro Asp Val Glu Tyr Val Ser Ile	
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Lys Val Ser Ser Val Ala Ser Gln Ile Ser Met Trp Gly Phe Glu Asp	
185 190 195	
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Thr Val Asn Tyr Val Val Glu Gln Leu Thr Pro Leu Tyr Ile Glu Ala	
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Tyr Arg Asp Leu Arg Leu Thr Met Glu Val Phe Lys Arg Leu Leu Ser	
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Asn Pro Glu Leu His Glu Leu Glu Ala Gly Ile Val Leu Gln Ala Tyr	
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Leu Pro Asp Ala Leu Gly Ala Ile Gln Asp Leu Ala Gln Phe Gly Arg	
265 270 275	

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 Glu Arg Val Asn Thr Gly Gly Ala Gly Val Lys Val Arg Leu Val Lys  
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 295 300 305

cca gtt gcc aca gaa cct tcc aaa caa gcc acc gat gcc aat tac aag  
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ctg ggc gtt gcc ggc cac aac ctt ttc gac ata gca ttc gca cat ttg  
 1171  
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 1219  
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 1267  
 Gln Gly Met Ala Ser Asp Gln Ala Arg Ala Val Ser Val Asp Val Gly  
 375 380 385

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 1315  
 Glu Leu Leu Leu Tyr Val Pro Ala Val Arg Pro Gln Glu Phe Asp Val  
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gcc att tct tac ctc gtg cgc cgc ctc gag gaa aac gcc gcg agc gaa  
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aac ttc atg tcc gcc atc ttc gac ctc gac gcc gac aac ccg tcc ttc  
 1411  
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 1507  
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 455 460 465

aaa gag acg ctt ctc gac gcc ccc ctc gtc cca ttt atc aac gag ccc  
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Lys Glu Thr Leu Leu Asp Ala Pro Leu Val Pro Phe Ile Asn Glu Pro  
 470 475 480 485  
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 Asp Thr Asn Pro Ala Leu Ile Gln Asn Gln Gln Trp Ala Thr Lys Ala  
 490 495 500  
 gtc gcc acc gca gca gag ccc ggt tgg ttg gaa aaa caa aca aag ccg  
 1651  
 Val Ala Thr Ala Ala Glu Pro Gly Trp Leu Glu Lys Gln Thr Lys Pro  
 505 510 515  
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 Glu Val Leu Glu Glu Gly Asp Val Asp Lys Leu Ile Asn Asp Val Arg  
 520 525 530  
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 Asp Ala Ala Glu Ala Trp Ala Ala Arg Pro Ala Arg Glu Arg Ala Glu  
 535 540 545  
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 1795  
 Ile Leu Tyr Lys Thr Ala Glu Ile Leu Arg Val Arg Arg Gly His Leu  
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 1843  
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 570 575 580  
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 1891  
 Pro Glu Ile Ser Glu Ala Ile Asp Phe Ala Arg Tyr Tyr Ala His Leu  
 585 590 595  
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 1987  
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 615 620 625  
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 Gly Ser Thr Phe Ala Ala Leu Ala Ala Gly Ala Gly Val Ile His Lys  
 630 635 640 645  
 ccc tca aag cct agc caa cat tgc tcc gct gca gtg gtc gaa gcc ctc  
 2083  
 Pro Ser Lys Pro Ser Gln His Cys Ser Ala Ala Val Val Glu Ala Leu  
 650 655 660  
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 2131  
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665	670	675
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Val Ile Leu Thr Gly Ser Ser Glu Thr Ala Ala Met Phe Ser Ser Trp 695 700 705		
cga cca gaa ctc acc atc aac ggc gaa acc tcc ggc aaa aac gcc atc 2275		
Arg Pro Glu Leu Thr Ile Asn Gly Glu Thr Ser Gly Lys Asn Ala Ile 710 715 720 725		
gtg gtc acc cca tct gcc gac cgc gac ctc gcc gtc gcc gac ctg gtg 2323		
Val Val Thr Pro Ser Ala Asp Arg Asp Leu Ala Val Ala Asp Leu Val 730 735 740		
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Lys Ser Ala Phe Gly His Ala Gly Gln Lys Cys Ser Ala Ala Ser Leu 745 750 755		
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tcc gca acc gtc gga cca ctc acc gaa ctc ccc agc gat aaa ctc cac 2515		
Ser Ala Thr Val Gly Pro Leu Thr Glu Leu Pro Ser Asp Lys Leu His 790 795 800 805		
cac gcc cta acc acc ctc gaa gaa gga gaa agc tgg ctg ctg aaa ccc 2563		
His Ala Leu Thr Thr Leu Glu Glu Gly Glu Ser Trp Leu Leu Lys Pro 810 815 820		
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Gly Val Lys Pro Gly Thr Phe Phe His Leu Thr Glu Val Phe Gly Pro 840 845 850		
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Val Leu Gly Leu Met Lys Ala Thr Asp Leu Asn Glu Ala Ile Glu Phe 855 860 865		

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gcc gac gaa gtc cgc acc tgg ctt gac cac gtc gat gtc gga aac gcc  
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 905 910 915

gga ggc tgg aaa aaa tcc tcc gtc ggc ctc gga tcc aaa gcc gga gga  
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 920 925 930

ccc aac tat gtc atg ctc atg gga acc tgg gcc gac gcg cca agc cac  
 2947  
 Pro Asn Tyr Val Met Leu Met Gly Thr Trp Ala Asp Ala Pro Ser His  
 935 940 945

cac gcc cca cgc gaa aca aac ccg ctg atc agc aaa ctg gat ctc ccc  
 2995  
 His Ala Pro Arg Glu Thr Asn Pro Leu Ile Ser Lys Leu Asp Leu Pro  
 950 955 960 965

gga gaa gag ctc gaa tgg ctc gaa aaa gcc aac gcc agc gat gaa aca  
 3043  
 Gly Glu Glu Leu Glu Trp Leu Glu Lys Ala Asn Ala Ser Asp Glu Thr  
 970 975 980

gca tgg aac acg gaa ttc ggc agc cca cgc gac ccc tcc ggc ctc gat  
 3091  
 Ala Trp Asn Thr Glu Phe Gly Ser Pro Arg Asp Pro Ser Gly Leu Asp  
 985 990 995

gta gaa gcc aac att ttc cgc tac cga cca gca gag gta gta ctc cga  
 3139  
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 3187  
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gcc cgt cgc gcc ggg gtt act ccg cga gtt ctt caa aca cca ggt gtt  
 3235  
 Ala Arg Arg Ala Gly Val Thr Pro Arg Val Leu Gln Thr Pro Gly Val  
 1030 1035 1040 1045

tca gag caa gtc cgc gaa gta ttg tcc gct gct gga gtg agt gca gaa  
 3283  
 Ser Glu Gln Val Arg Glu Val Leu Ser Ala Ala Gly Val Ser Ala Glu  
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aca gtc gat gat tcg gta ttt att tcc aac gtg ttg cgc ggc gaa tac  
3331

Thr Val Asp Asp Ser Val Phe Ile Ser Asn Val Leu Arg Gly Glu Tyr  
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3379

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3427

Thr Val Arg Glu Arg Leu Ser Val Arg Pro Glu Val Val Leu Leu Asp  
1095 1100 1105

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3475

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3523

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<211> 1152

<212> PRT

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35 40 45

Asn Gly Leu Glu Phe Thr Val Gly Phe Val Asp Arg Val Val Arg Thr  
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Glu Asp Arg Glu Ala Ala Ala His Ala Leu Tyr Glu Leu Gly Lys Ile  
65 70 75 80

Ala Pro Ser Thr Met Ser Phe Leu Asp Arg Ala Gln Ile Gln Ala Gly  
85 90 95

Ser Leu Val Gly Arg Ala Leu Pro Gln Val Val Val Pro Ala Ala Arg  
100 105 110

Ala	Arg	Ile	Arg	Gln	Met	Val	Gly	His	Met	Ile	Val	Asp	Ala	Arg	Asp	115	120	125
Lys	Gln	Phe	Ala	Lys	Ala	Val	Ala	Glu	Ile	Gln	Ser	Asp	Gly	His	Arg	130	135	140
Leu	Asn	Ile	Asn	Leu	Leu	Gly	Glu	Ala	Val	Leu	Gly	Arg	Lys	Glu	Ala	145	150	155
Ala	Lys	His	Leu	Asp	Asp	Thr	Val	Arg	Leu	Leu	Arg	Arg	Pro	Asp	Val	165	170	175
Glu	Tyr	Val	Ser	Ile	Lys	Val	Ser	Ser	Val	Ala	Ser	Gln	Ile	Ser	Met	180	185	190
Trp	Gly	Phe	Glu	Asp	Thr	Val	Asn	Tyr	Val	Val	Glu	Gln	Leu	Thr	Pro	195	200	205
Leu	Tyr	Ile	Glu	Ala	Ala	Arg	Ala	Pro	Lys	Gly	Thr	Lys	Phe	Ile	Asn	210	215	220
Leu	Asp	Met	Glu	Glu	Tyr	Arg	Asp	Leu	Arg	Leu	Thr	Met	Glu	Val	Phe	225	230	235
Lys	Arg	Leu	Leu	Ser	Asn	Pro	Glu	Leu	His	Glu	Leu	Glu	Ala	Gly	Ile	245	250	255
Val	Leu	Gln	Ala	Tyr	Leu	Pro	Asp	Ala	Leu	Gly	Ala	Ile	Gln	Asp	Leu	260	265	270
Ala	Gln	Phe	Gly	Arg	Glu	Arg	Val	Asn	Thr	Gly	Gly	Ala	Gly	Val	Lys	275	280	285
Val	Arg	Leu	Val	Lys	Gly	Ala	Asn	Leu	Pro	Met	Glu	His	Val	His	Ala	290	295	300
Gln	Ile	Thr	Gly	Trp	Pro	Val	Ala	Thr	Glu	Pro	Ser	Lys	Gln	Ala	Thr	305	310	315
Asp	Ala	Asn	Tyr	Lys	Arg	Val	Leu	Tyr	Trp	Thr	Met	Arg	Lys	Glu	Asn	325	330	335
Met	Glu	Gly	Leu	Arg	Leu	Gly	Val	Ala	Gly	His	Asn	Leu	Phe	Asp	Ile	340	345	350
Ala	Phe	Ala	His	Leu	Leu	Ser	Val	Glu	Arg	Gly	Val	Ala	Asp	Arg	Val	355	360	365
Glu	Phe	Glu	Met	Leu	Gln	Gly	Met	Ala	Ser	Asp	Gln	Ala	Arg	Ala	Val	370	375	380
Ser	Val	Asp	Val	Gly	Glu	Leu	Leu	Leu	Tyr	Val	Pro	Ala	Val	Arg	Pro	385	390	395
Gln	Glu	Phe	Asp	Val	Ala	Ile	Ser	Tyr	Leu	Val	Arg	Arg	Leu	Glu	Glu	405	410	415
Asn	Ala	Ala	Ser	Glu	Asn	Phe	Met	Ser	Ala	Ile	Phe	Asp	Leu	Asp	Ala	420	425	430
Asp	Asn	Pro	Ser	Phe	Lys	Arg	Glu	Glu	Ser	Arg	Phe	Arg	Ala	Ser	Ile			

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Ser	Asp	Leu	Ala	Thr	Leu	Ile	Asp	Val	Pro	Ala	Pro	Gly	Pro	Asn	His
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Phe	Ile	Asn	Glu	Pro	Asp	Thr	Asn	Pro	Ala	Leu	Ile	Gln	Asn	Gln	Gln
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Lys	Gln	Thr	Lys	Pro	Glu	Val	Leu	Glu	Glu	Gly	Asp	Val	Asp	Lys	Leu
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Val	Glu	Gln	Thr	Asp	Pro	Glu	Ile	Ser	Glu	Ala	Ile	Asp	Phe	Ala	Arg
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Tyr	Tyr	Ala	His	Leu	Ala	Leu	Glu	Leu	Asp	Asp	Val	Asp	Asn	Ala	Glu
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Phe	Thr	Pro	Asp	Arg	Val	Val	Val	Val	Thr	Pro	Pro	Trp	Asn	Phe	Pro
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Gly	Val	Ile	His	Lys	Pro	Ser	Lys	Pro	Ser	Gln	His	Cys	Ser	Ala	Ala
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Cys	Ile	Tyr	Pro	Ala	Asn	Arg	Asp	Val	Gly	Cys	Ala	Leu	Ile	Ser	His
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Glu	His	Val	Asp	Arg	Val	Ile	Leu	Thr	Gly	Ser	Ser	Glu	Thr	Ala	Ala
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Met	Phe	Ser	Ser	Trp	Arg	Pro	Glu	Leu	Thr	Ile	Asn	Gly	Glu	Thr	Ser
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 Gln Arg Gln Ser Phe Gly Gly Trp Lys Lys Ser Ser Val Gly Leu Gly  
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 Ser Lys Ala Gly Gly Pro Asn Tyr Val Met Leu Met Gly Thr Trp Ala  
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 Asp Ala Pro Ser His His Ala Pro Arg Glu Thr Asn Pro Leu Ile Ser  
 945 950 955 960  
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 Ala Ser Asp Glu Thr Ala Trp Asn Thr Glu Phe Gly Ser Pro Arg Asp  
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 Pro Ser Gly Leu Asp Val Glu Ala Asn Ile Phe Arg Tyr Arg Pro Ala  
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Ala	Thr	Pro	Arg	Glu	Thr	Ala	Arg	Ala	Leu	Leu	Ala	Ala	Arg	Arg	Ala	
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Gly	Val	Thr	Pro	Arg	Val	Leu	Gln	Thr	Pro	Gly	Val	Ser	Glu	Gln	Val	
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Ser	Val	Arg	Val	Arg	Tyr	Leu	Gly	Lys	Val	Ser	Asp	Thr	Val	Arg	Glu	
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cgc	cta	tct	gta	cgg	ccc	gaa	gtt	gtt	ctg	ctt	gac	gat	gca	gta	act	336
Arg	Leu	Ser	Val	Arg	Pro	Glu	Val	Val	Leu	Leu	Asp	Asp	Ala	Val	Thr	
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Ala	Ser	Gly	Arg	Val	Glu	Leu	Arg	Tyr	Trp	Leu	Lys	Glu	Gln	Ala	Ile	
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Ser	Met	Thr	Leu	His	Arg	Phe	Gly	Asn	Pro	Val	Ala	Ala	Phe	His	Glu	

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 Met Thr Ser Met Asn  
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Arg Ser Trp Leu Glu Tyr Ser Lys Lys Glu Ser Val Pro Asn Ala Asp	
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Ala Lys Arg Leu Ala Ala Val Leu Gln Asp Pro Asn Gly Leu Glu Phe	
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Thr Val Gly Phe Val Asp Arg Val Val Arg Thr Glu Asp Arg Glu Ala	
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Ala Ala His Ala Leu Tyr Glu Leu Gly Lys Ile Ala Pro Ser Thr Met	
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Ser Phe Leu Asp Arg Ala Gln Ile Gln Ala Gly Ser Leu Val Gly Arg	
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Ala Leu Pro Gln Val Val Val Pro Ala Ala Arg Ala Arg Ile Arg Gln	
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Met Val Gly His Met Ile Val Asp Ala Arg Asp Lys Gln Phe Ala Lys	
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Ala Val Ala Glu Ile Gln Ser Asp Gly His Arg Leu Asn Ile Asn Leu	
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Leu Gly Glu Ala Val Leu Gly Arg Lys Glu Ala Ala Lys His Leu Asp	
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Asp Thr Val Arg Leu Leu Arg Arg Pro Asp Val Glu Tyr Val Ser Xaa	
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Xaa Xaa Ser Ser Val Ala Ser Gln Ile Ser Met Trp Gly Phe Glu Asp	
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Thr Val Asn Tyr Val Val Glu Gln Leu Thr Pro Leu Tyr Ile Glu Pro	
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Ala Arg Ala Pro Lys Gly Thr Lys Phe Ile Asn Leu Asp Met Glu Glu	
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Tyr Arg Asp Leu Arg Leu Thr Met Glu Val Phe Lys Arg Leu Leu Ser	
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Glu	Arg	Val	Asn	Thr	Gly	Gly	Ala	Gly	Val	Lys	Val	Arg	Leu	Val	Lys		
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1459																	
Lys	Arg	Glu	Glu	Ser	Arg	Phe	Arg	Ala	Ser	Ile	Ser	Asp	Leu	Ala	Thr		
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gtc gcc acc gca gca gag ccc ggt tgg ttg gaa aaa caa aca aag ccg  
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 Pro Glu Ile Ser Glu Ala Ile Asp Phe Ala Arg Tyr Tyr Ala His Leu  
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 1987  
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 Pro Ser Lys Pro Ser Gln His Cys Ser Ala Ala Val Val Glu Ala Leu  
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 Trp Glu Ala Gly Val Pro Arg Glu Val Leu His Cys Ile Tyr Pro Ala  
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 680 685 690

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 Arg Gln Leu Asp Asp Thr Gly Arg Leu Trp Ser Pro Gly Ile Lys Glu  
 825 830 835

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 Gly Val Lys Pro Gly Thr Phe Phe His Leu Thr Glu Val Phe Gly Pro  
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 2803  
 Ala Asp Glu Val Arg Thr Trp Leu Asp His Val Asp Val Gly Asn Ala  
                                   890                                  895                                  900

tac gtc aac cgc ggc atc acc ggc gcc att gtc caa cgc caa tcc ttc  
 2851  
 Tyr Val Asn Arg Gly Ile Thr Gly Ala Ile Val Gln Arg Gln Ser Phe  
                                   905                                  910                                  915

gga ggc tgg aaa aaa tcc tcc gtc ggc ctc gga tcc aaa gcc gga gga  
 2899  
 Gly Gly Trp Lys Lys Ser Ser Val Gly Leu Gly Ser Lys Ala Gly Gly  
           920                                  925                                  930

ccc aac tat gtc atg ctc atg gga acc tgg gcc gac gcg cca agc cac  
 2947  
 Pro Asn Tyr Val Met Leu Met Gly Thr Trp Ala Asp Ala Pro Ser His  
           935                                  940                                  945

cac gcc cca cgc gaa aca aac ccg ctg atc agc aaa ctg gat ctc ccc  
 2995  
 His Ala Pro Arg Glu Thr Asn Pro Leu Ile Ser Lys Leu Asp Leu Pro  
           950                                  955                                  960                                  965

gga gaa gag ctc gaa tgg ctc gaa aaa gcc aac gcc agc gat gaa aca  
 3043  
 Gly Glu Glu Leu Glu Trp Leu Glu Lys Ala Asn Ala Ser Asp Glu Thr  
                                   970                                  975                                  980

gca tgg aac acg gaa ttc ggc agc cca cgc gac ccc tcc ggc ctc gat  
 3091  
 Ala Trp Asn Thr Glu Phe Gly Ser Pro Arg Asp Pro Ser Gly Leu Asp  
                                   985                                  990                                  995

gta gaa gcc aac att ttc cgc tac cga cca gca  
 3124  
 Val Glu Ala Asn Ile Phe Arg Tyr Arg Pro Ala  
           1000                                  1005

<210> 312

<211> 1008

<212> PRT

<213> Corynebacterium glutamicum

&lt;400&gt; 312

Met	Thr	Ser	Met	Asn	Leu	Pro	Ile	Glu	Leu	Ala	Thr	Leu	Ser	Asp	Gln
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Ala	Val	Asp	Lys	Val	Arg	Ser	Trp	Leu	Glu	Tyr	Ser	Lys	Lys	Glu	Ser
			20					25					30		
Val	Pro	Asn	Ala	Asp	Ala	Lys	Arg	Leu	Ala	Ala	Val	Leu	Gln	Asp	Pro
		35					40					45			
Asn	Gly	Leu	Glu	Phe	Thr	Val	Gly	Phe	Val	Asp	Arg	Val	Val	Arg	Thr
	50					55				60					
Glu	Asp	Arg	Glu	Ala	Ala	Ala	His	Ala	Leu	Tyr	Glu	Leu	Gly	Lys	Ile
65					70					75					80
Ala	Pro	Ser	Thr	Met	Ser	Phe	Leu	Asp	Arg	Ala	Gln	Ile	Gln	Ala	Gly
				85				90						95	
Ser	Leu	Val	Gly	Arg	Ala	Leu	Pro	Gln	Val	Val	Val	Pro	Ala	Ala	Arg
			100					105					110		
Ala	Arg	Ile	Arg	Gln	Met	Val	Gly	His	Met	Ile	Val	Asp	Ala	Arg	Asp
		115					120					125			
Lys	Gln	Phe	Ala	Lys	Ala	Val	Ala	Glu	Ile	Gln	Ser	Asp	Gly	His	Arg
	130					135					140				
Leu	Asn	Ile	Asn	Leu	Leu	Gly	Glu	Ala	Val	Leu	Gly	Arg	Lys	Glu	Ala
145					150					155					160
Ala	Lys	His	Leu	Asp	Asp	Thr	Val	Arg	Leu	Leu	Arg	Arg	Pro	Asp	Val
				165				170						175	
Glu	Tyr	Val	Ser	Xaa	Xaa	Xaa	Ser	Ser	Val	Ala	Ser	Gln	Ile	Ser	Met
			180					185					190		
Trp	Gly	Phe	Glu	Asp	Thr	Val	Asn	Tyr	Val	Val	Glu	Gln	Leu	Thr	Pro
		195					200					205			
Leu	Tyr	Ile	Glu	Pro	Ala	Arg	Ala	Pro	Lys	Gly	Thr	Lys	Phe	Ile	Asn
	210					215					220				
Leu	Asp	Met	Glu	Glu	Tyr	Arg	Asp	Leu	Arg	Leu	Thr	Met	Glu	Val	Phe
225					230					235					240
Lys	Arg	Leu	Leu	Ser	Asn	Pro	Glu	Leu	His	Glu	Leu	Glu	Ala	Gly	Ile
				245					250					255	
Val	Leu	Gln	Ala	Tyr	Leu	Pro	Asp	Ala	Leu	Gly	Ala	Ile	Gln	Asp	Leu
			260					265					270		
Ala	Gln	Phe	Gly	Arg	Glu	Arg	Val	Asn	Thr	Gly	Gly	Ala	Gly	Val	Lys
		275					280					285			
Val	Arg	Leu	Val	Lys	Gly	Ala	Asn	Leu	Pro	Met	Glu	His	Val	His	Ala
	290					295					300				
Gln	Ile	Thr	Gly	Trp	Pro	Val	Ala	Thr	Glu	Pro	Ser	Lys	Gln	Ala	Thr
305					310					315					320

Asp Ala Asn Tyr Lys Arg Val Leu Tyr Trp Thr Met Arg Lys Glu Asn  
 325 330 335  
 Met Glu Gly Leu Arg Leu Gly Val Ala Gly His Asn Leu Phe Asp Ile  
 340 345 350  
 Ala Phe Ala His Leu Leu Ser Val Glu Arg Gly Val Ala Asp Arg Val  
 355 360 365  
 Glu Phe Glu Met Leu Gln Gly Met Ala Ser Asp Gln Ala Arg Ala Val  
 370 375 380  
 Ser Val Asp Val Gly Glu Leu Leu Leu Tyr Val Pro Ala Val Arg Pro  
 385 390 395 400  
 Gln Glu Phe Asp Val Ala Ile Ser Tyr Leu Val Arg Arg Leu Glu Glu  
 405 410 415  
 Asn Ala Ala Ser Glu Asn Phe Met Ser Ala Ile Phe Asp Leu Asp Ala  
 420 425 430  
 Asp Asn Pro Ser Phe Lys Arg Glu Glu Ser Arg Phe Arg Ala Ser Ile  
 435 440 445  
 Ser Asp Leu Ala Thr Leu Ile Asp Val Pro Ala Pro Gly Pro Asn His  
 450 455 460  
 Thr Gln Asp Arg Ser Lys Glu Thr Leu Leu Asp Ala Pro Leu Val Pro  
 465 470 475 480  
 Phe Ile Asn Glu Pro Asp Thr Asn Pro Ala Leu Ile Gln Asn Gln Gln  
 485 490 495  
 Trp Ala Thr Lys Ala Val Ala Thr Ala Ala Glu Pro Gly Trp Leu Glu  
 500 505 510  
 Lys Gln Thr Lys Pro Glu Val Leu Glu Glu Gly Asp Val Asp Lys Leu  
 515 520 525  
 Ile Asn Asp Val Arg Asp Ala Ala Glu Ala Trp Ala Ala Arg Pro Ala  
 530 535 540  
 Arg Glu Arg Ala Glu Ile Leu Tyr Lys Thr Ala Glu Ile Leu Arg Val  
 545 550 555 560  
 Arg Arg Gly His Leu Ile Ser Val Thr Ala Ala Glu Val Gly Lys Ala  
 565 570 575  
 Val Glu Gln Thr Asp Pro Glu Ile Ser Glu Ala Ile Asp Phe Ala Arg  
 580 585 590  
 Tyr Tyr Ala His Leu Ala Leu Glu Leu Asp Asp Val Asp Asn Ala Glu  
 595 600 605  
 Phe Thr Pro Asp Arg Val Val Val Val Thr Pro Pro Trp Asn Phe Pro  
 610 615 620  
 Ile Ala Ile Pro Ala Gly Ser Thr Phe Ala Ala Leu Ala Ala Gly Ala  
 625 630 635 640  
 Gly Val Ile His Lys Pro Ser Lys Pro Ser Gln His Cys Ser Ala Ala

645								650				655			
Val	Val	Glu	Ala	Leu	Trp	Glu	Ala	Gly	Val	Pro	Arg	Glu	Val	Leu	His
			660					665					670		
Cys	Ile	Tyr	Pro	Ala	Asn	Arg	Asp	Val	Gly	Cys	Ala	Leu	Ile	Ser	His
		675					680					685			
Glu	His	Val	Asp	Arg	Val	Ile	Leu	Thr	Gly	Ser	Ser	Glu	Thr	Ala	Ala
	690					695					700				
Met	Phe	Ser	Ser	Trp	Arg	Pro	Glu	Leu	Thr	Ile	Asn	Gly	Glu	Thr	Ser
705					710					715					720
Gly	Lys	Asn	Ala	Ile	Val	Val	Thr	Pro	Ser	Ala	Asp	Arg	Asp	Leu	Ala
				725					730					735	
Val	Ala	Asp	Leu	Val	Lys	Ser	Ala	Phe	Gly	His	Ala	Gly	Gln	Lys	Cys
			740					745					750		
Ser	Ala	Ala	Ser	Leu	Gly	Ile	Leu	Val	Gly	Ser	Val	Tyr	Glu	Ser	Glu
		755					760					765			
Arg	Phe	Arg	Lys	Gln	Leu	Val	Asp	Ala	Ala	Ser	Ser	Leu	Ile	Val	Asp
	770					775					780				
Trp	Pro	Thr	Asn	Pro	Ser	Ala	Thr	Val	Gly	Pro	Leu	Thr	Glu	Leu	Pro
785					790					795					800
Ser	Asp	Lys	Leu	His	His	Ala	Leu	Thr	Thr	Leu	Glu	Glu	Gly	Glu	Ser
				805					810					815	
Trp	Leu	Leu	Lys	Pro	Arg	Gln	Leu	Asp	Asp	Thr	Gly	Arg	Leu	Trp	Ser
			820					825					830		
Pro	Gly	Ile	Lys	Glu	Gly	Val	Lys	Pro	Gly	Thr	Phe	Phe	His	Leu	Thr
		835					840					845			
Glu	Val	Phe	Gly	Pro	Val	Leu	Gly	Leu	Met	Lys	Ala	Thr	Asp	Leu	Asn
	850					855					860				
Glu	Ala	Ile	Glu	Phe	Gln	Asn	Gly	Asn	Asp	Phe	Gly	Leu	Thr	Gly	Gly
865					870				875						880
Leu	Gln	Ser	Leu	Asp	Ala	Asp	Glu	Val	Arg	Thr	Trp	Leu	Asp	His	Val
				885					890					895	
Asp	Val	Gly	Asn	Ala	Tyr	Val	Asn	Arg	Gly	Ile	Thr	Gly	Ala	Ile	Val
			900					905					910		
Gln	Arg	Gln	Ser	Phe	Gly	Gly	Trp	Lys	Lys	Ser	Ser	Val	Gly	Leu	Gly
		915					920					925			
Ser	Lys	Ala	Gly	Gly	Pro	Asn	Tyr	Val	Met	Leu	Met	Gly	Thr	Trp	Ala
	930					935					940				
Asp	Ala	Pro	Ser	His	His	Ala	Pro	Arg	Glu	Thr	Asn	Pro	Leu	Ile	Ser
945					950					955					960
Lys	Leu	Asp	Leu	Pro	Gly	Glu	Glu	Leu	Glu	Trp	Leu	Glu	Lys	Ala	Asn
				965					970					975	

Ala Ser Asp Glu Thr Ala Trp Asn Thr Glu Phe Gly Ser Pro Arg Asp  
 980 985 990

Pro Ser Gly Leu Asp Val Glu Ala Asn Ile Phe Arg Tyr Arg Pro Ala  
 995 1000 1005

<210> 313

<211> 927

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(904)

<223> RXC02498

<400> 313

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aggactcgag taacatttac ccggaaagga gttggcgaaa atg agt gaa gag aaa 115  
 Met Ser Glu Glu Lys  
 1 5

ctc aca gtc gct gag ctg atg gcg cgt gcc gcg aaa gag gga cgc tcc 163  
 Leu Thr Val Ala Glu Leu Met Ala Arg Ala Ala Lys Glu Gly Arg Ser  
 10 15 20

acc gat gct ccc cga cga cgc agg cgc cgc agc atc gaa gac ggt ggc 211  
 Thr Asp Ala Pro Arg Arg Arg Arg Arg Arg Ser Ile Glu Asp Gly Gly  
 25 30 35

gta tcc gtt gct gag ctg acc ggc tcc att cct gcc gtt aag gaa aag 259  
 Val Ser Val Ala Glu Leu Thr Gly Ser Ile Pro Ala Val Lys Glu Lys  
 40 45 50

ccc gcg gag tcc aag cac tcc agc gtg ccc atc gat gca cca gca gaa 307  
 Pro Ala Glu Ser Lys His Ser Ser Val Pro Ile Asp Ala Pro Ala Glu  
 55 60 65

cct gag gtt gtt gag gcc ccc aag cct gag ccc gcc gaa gaa gta gaa 355  
 Pro Glu Val Val Glu Ala Pro Lys Pro Glu Pro Ala Glu Glu Val Glu  
 70 75 80 85

gtg gct tcg gtg gag ggc gac gtc gat aag cag gaa acc cct gag cgt 403  
 Val Ala Ser Val Glu Gly Asp Val Asp Lys Gln Glu Thr Pro Glu Arg  
 90 95 100

ccg gcg ccg agc aac gaa gaa acc atg gtg ctg cgc atc gtg gat gaa 451  
 Pro Ala Pro Ser Asn Glu Glu Thr Met Val Leu Arg Ile Val Asp Glu  
 105 110 115

aaa gat cca att agc ttg acg acg ggc gcg ttc ccc gtg gtt ccg gca 499  
 Lys Asp Pro Ile Ser Leu Thr Thr Gly Ala Phe Pro Val Val Pro Ala  
 120 125 130

gtt gcc gcc aag ccg gcg ccc gta gtg cgc gcg gag aag gac gcc gat 547

Val	Ala	Ala	Lys	Pro	Ala	Pro	Val	Val	Arg	Ala	Glu	Lys	Asp	Ala	Asp	
135						140					145					
gtg	gag	act	gcc	gta	aag	gca	gat	ttc	gca	gag	gtg	gaa	gtc	gat	aac	595
Val	Glu	Thr	Ala	Val	Lys	Ala	Asp	Phe	Ala	Glu	Val	Glu	Val	Asp	Asn	
150					155					160					165	
act	gac	acc	acg	cag	atg	gct	gtg	gtg	gaa	gaa	gtt	gac	gag	gag	cca	643
Thr	Asp	Thr	Thr	Gln	Met	Ala	Val	Val	Glu	Glu	Val	Asp	Glu	Glu	Pro	
				170					175					180		
gag	caa	gaa	aac	aaa	atg	tcc	gta	ttc	gcg	atc	atc	atg	atg	gcg	atc	691
Glu	Gln	Glu	Asn	Lys	Met	Ser	Val	Phe	Ala	Ile	Ile	Met	Met	Ala	Ile	
			185					190					195			
gtc	gga	gtt	gtt	ctc	ggt	gtc	gtt	gta	ttc	ctc	ggc	ttt	gaa	atg	ctg	739
Val	Gly	Val	Val	Leu	Gly	Val	Val	Val	Phe	Leu	Gly	Phe	Glu	Met	Leu	
		200					205					210				
tgg	gag	cgc	ctg	aac	aag	tgg	atc	gtc	gct	gtt	ctg	gca	gtc	ggc	gtg	787
Trp	Glu	Arg	Leu	Asn	Lys	Trp	Ile	Val	Ala	Val	Leu	Ala	Val	Gly	Val	
	215					220					225					
acc	ttg	gga	atg	gtg	ggc	atc	atc	cac	gct	ttg	cgc	acc	tca	cgt	gat	835
Thr	Leu	Gly	Met	Val	Gly	Ile	Ile	His	Ala	Leu	Arg	Thr	Ser	Arg	Asp	
230					235					240					245	
ggt	ttc	agc	atg	gtt	ctc	gca	gga	atc	gtg	ggc	ctg	gtc	atg	acg	ttc	883
Gly	Phe	Ser	Met	Val	Leu	Ala	Gly	Ile	Val	Gly	Leu	Val	Met	Thr	Phe	
				250				255						260		
ggg	ccg	ctg	gca	atc	gtc	atg	taatttgtcg ttttgggccc ccg									927
Gly	Pro	Leu	Ala	Ile	Val	Met										
			265													

&lt;210&gt; 314

&lt;211&gt; 268

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 314

Met	Ser	Glu	Glu	Lys	Leu	Thr	Val	Ala	Glu	Leu	Met	Ala	Arg	Ala	Ala	
1				5					10					15		
Lys	Glu	Gly	Arg	Ser	Thr	Asp	Ala	Pro	Arg	Arg	Arg	Arg	Arg	Arg	Ser	
			20					25					30			
Ile	Glu	Asp	Gly	Gly	Val	Ser	Val	Ala	Glu	Leu	Thr	Gly	Ser	Ile	Pro	
		35					40					45				
Ala	Val	Lys	Glu	Lys	Pro	Ala	Glu	Ser	Lys	His	Ser	Ser	Val	Pro	Ile	
		50				55					60					
Asp	Ala	Pro	Ala	Glu	Pro	Glu	Val	Val	Glu	Ala	Pro	Lys	Pro	Glu	Pro	
65					70				75					80		
Ala	Glu	Glu	Val	Glu	Val	Ala	Ser	Val	Glu	Gly	Asp	Val	Asp	Lys	Gln	
				85					90					95		
Glu	Thr	Pro	Glu	Arg	Pro	Ala	Pro	Ser	Asn	Glu	Glu	Thr	Met	Val	Leu	



100					105					110						
Arg	Ile	Val	Asp	Glu	Lys	Asp	Pro	Ile	Ser	Leu	Thr	Thr	Gly	Ala	Phe	
115					120					125						
Pro	Val	Val	Pro	Ala	Val	Ala	Ala	Lys	Pro	Ala	Pro	Val	Val	Arg	Ala	
130					135					140						
Glu	Lys	Asp	Ala	Asp	Val	Glu	Thr	Ala	Val	Lys	Ala	Asp	Phe	Ala	Glu	
145					150					155					160	
Val	Glu	Val	Asp	Asn	Thr	Asp	Thr	Thr	Gln	Met	Ala	Val	Val	Glu	Glu	
165					170					175						
Val	Asp	Glu	Glu	Pro	Glu	Gln	Glu	Asn	Lys	Met	Ser	Val	Phe	Ala	Ile	
180					185					190						
Ile	Met	Met	Ala	Ile	Val	Gly	Val	Val	Leu	Gly	Val	Val	Val	Phe	Leu	
195					200					205						
Gly	Phe	Glu	Met	Leu	Trp	Glu	Arg	Leu	Asn	Lys	Trp	Ile	Val	Ala	Val	
210					215					220						
Leu	Ala	Val	Gly	Val	Thr	Leu	Gly	Met	Val	Gly	Ile	Ile	His	Ala	Leu	
225					230					235					240	
Arg	Thr	Ser	Arg	Asp	Gly	Phe	Ser	Met	Val	Leu	Ala	Gly	Ile	Val	Gly	
245					250					255						
Leu	Val	Met	Thr	Phe	Gly	Pro	Leu	Ala	Ile	Val	Met					
260					265											

&lt;210&gt; 315

&lt;211&gt; 774

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(751)

&lt;223&gt; RXA01491

&lt;400&gt; 315

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gggcagcatg	tgtggccata	tccagtgatg	gaggtggaca	atg	ctg	gat	gag	tct		115
				Met	Leu	Asp	Glu	Ser		
				1				5		

ttg	ttt	cca	aat	tcg	gca	aag	ttt	tct	ttc	att	aaa	act	ggc	gat	gct	163
Leu	Phe	Pro	Asn	Ser	Ala	Lys	Phe	Ser	Phe	Ile	Lys	Thr	Gly	Asp	Ala	
			10					15						20		

gtt	aat	tta	gac	cat	ttc	cat	cag	ttg	cat	ccg	ttg	gaa	aag	gca	ctg	211
Val	Asn	Leu	Asp	His	Phe	His	Gln	Leu	His	Pro	Leu	Glu	Lys	Ala	Leu	
			25				30						35			

gta	gcg	cac	tcg	gtt	gat	att	aga	aaa	gca	gag	ttt	gga	gat	gcc	agg	259
Val	Ala	His	Ser	Val	Asp	Ile	Arg	Lys	Ala	Glu	Phe	Gly	Asp	Ala	Arg	
			40				45					50				

tgg tgt gca cat cag gca ctc caa gct ttg gga cga gat agc ggt gat	307
Trp Cys Ala His Gln Ala Leu Gln Ala Leu Gly Arg Asp Ser Gly Asp	
55 60 65	
ccc att ttg cgt ggg gaa cga gga atg cca ttg tgg cct tct tcg gtg	355
Pro Ile Leu Arg Gly Glu Arg Gly Met Pro Leu Trp Pro Ser Ser Val	
70 75 80 85	
tct ggt tca ttg acc cac act gac gga ttc cga gct gct gtt gtg gcg	403
Ser Gly Ser Leu Thr His Thr Asp Gly Phe Arg Ala Ala Val Val Ala	
90 95 100	
cca cga ttg ttg gtg cgt tct atg gga ttg gat gcc gaa cct gcg gag	451
Pro Arg Leu Leu Val Arg Ser Met Gly Leu Asp Ala Glu Pro Ala Glu	
105 110 115	
ccg ttg ccc aag gat gtt ttg ggt tca atc gct cgg gtg ggg gag att	499
Pro Leu Pro Lys Asp Val Leu Gly Ser Ile Ala Arg Val Gly Glu Ile	
120 125 130	
cct caa ctt aag cgc ttg gag gaa caa ggt gtg cac tgc gcg gat cgc	547
Pro Gln Leu Lys Arg Leu Glu Glu Gln Gly Val His Cys Ala Asp Arg	
135 140 145	
ctg ctg ttt tgt gcc aag gaa gca aca tac aaa gcg tgg ttc ccg ctg	595
Leu Leu Phe Cys Ala Lys Glu Ala Thr Tyr Lys Ala Trp Phe Pro Leu	
150 155 160 165	
acg cat agg tgg ctt ggt ttt gaa caa gct gag atc gac ttg cgt gat	643
Thr His Arg Trp Leu Gly Phe Glu Gln Ala Glu Ile Asp Leu Arg Asp	
170 175 180	
gat ggc act ttt gtg tcc tat ttg ctg gtt cga cca act cca gtg ccg	691
Asp Gly Thr Phe Val Ser Tyr Leu Leu Val Arg Pro Thr Pro Val Pro	
185 190 195	
ttt att tca ggt aaa tgg gta ctg cgt gat ggt tat gtc ata gct gcg	739
Phe Ile Ser Gly Lys Trp Val Leu Arg Asp Gly Tyr Val Ile Ala Ala	
200 205 210	
act gca gtg act tgaactggat ggagaggata cct	774
Thr Ala Val Thr	
215	

&lt;210&gt; 316

&lt;211&gt; 217

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 316

Met Leu Asp Glu Ser Leu Phe Pro Asn Ser Ala Lys Phe Ser Phe Ile
1 5 10 15

Lys Thr Gly Asp Ala Val Asn Leu Asp His Phe His Gln Leu His Pro
20 25 30

Leu Glu Lys Ala Leu Val Ala His Ser Val Asp Ile Arg Lys Ala Glu
35 40 45

Phe Gly Asp Ala Arg Trp Cys Ala His Gln Ala Leu Gln Ala Leu Gly  
 50 55 60  
 Arg Asp Ser Gly Asp Pro Ile Leu Arg Gly Glu Arg Gly Met Pro Leu  
 65 70 75 80  
 Trp Pro Ser Ser Val Ser Gly Ser Leu Thr His Thr Asp Gly Phe Arg  
 85 90 95  
 Ala Ala Val Val Ala Pro Arg Leu Leu Val Arg Ser Met Gly Leu Asp  
 100 105 110  
 Ala Glu Pro Ala Glu Pro Leu Pro Lys Asp Val Leu Gly Ser Ile Ala  
 115 120 125  
 Arg Val Gly Glu Ile Pro Gln Leu Lys Arg Leu Glu Glu Gln Gly Val  
 130 135 140  
 His Cys Ala Asp Arg Leu Leu Phe Cys Ala Lys Glu Ala Thr Tyr Lys  
 145 150 155 160  
 Ala Trp Phe Pro Leu Thr His Arg Trp Leu Gly Phe Glu Gln Ala Glu  
 165 170 175  
 Ile Asp Leu Arg Asp Asp Gly Thr Phe Val Ser Tyr Leu Leu Val Arg  
 180 185 190  
 Pro Thr Pro Val Pro Phe Ile Ser Gly Lys Trp Val Leu Arg Asp Gly  
 195 200 205  
 Tyr Val Ile Ala Ala Thr Ala Val Thr  
 210 215

&lt;210&gt; 317

&lt;211&gt; 1287

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1264)

&lt;223&gt; RXA02155

&lt;400&gt; 317

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gcaaacacaa caaacacatc taattcagta ggagttccac atg gca gaa aaa ggc 115  
 Met Ala Glu Lys Gly  
 1 5

att acc gcg ccg aaa ggc ttc gtt gct tct gca acg acc gcg ggt att 163  
 Ile Thr Ala Pro Lys Gly Phe Val Ala Ser Ala Thr Thr Ala Gly Ile  
 10 15 20

aaa gct tct ggc aat cct gac atg gcg ttg gtg gtt aac cag ggt cca 211  
 Lys Ala Ser Gly Asn Pro Asp Met Ala Leu Val Val Asn Gln Gly Pro  
 25 30 35

gag ttt tcc gca gcg gcc gtg ttt aca cgt aac cga gtt ttc gca gcg 259  
 Glu Phe Ser Ala Ala Ala Val Phe Thr Arg Asn Arg Val Phe Ala Ala

40					45					50						
cct	gtg	aag	gtg	agc	cga	gag	aac	gtt	gct	gat	ggc	cag	atc	agg	gct	307
Pro	Val	Lys	Val	Ser	Arg	Glu	Asn	Val	Ala	Asp	Gly	Gln	Ile	Arg	Ala	
	55					60					65					
gtt	ttg	tac	aac	gct	ggg	aat	gct	aat	gcg	tgt	aat	ggg	ctg	cag	ggg	355
Val	Leu	Tyr	Asn	Ala	Gly	Asn	Ala	Asn	Ala	Cys	Asn	Gly	Leu	Gln	Gly	
70					75					80					85	
gag	aag	gat	gct	cgt	gag	tct	gtt	tct	cat	cta	gct	caa	aat	ttg	ggc	403
Glu	Lys	Asp	Ala	Arg	Glu	Ser	Val	Ser	His	Leu	Ala	Gln	Asn	Leu	Gly	
				90					95					100		
ttg	gag	gat	tcc	gat	att	ggg	gtg	tgt	tcc	act	ggg	ctt	att	ggg	gag	451
Leu	Glu	Asp	Ser	Asp	Ile	Gly	Val	Cys	Ser	Thr	Gly	Leu	Ile	Gly	Glu	
			105					110					115			
ttg	ctt	ccg	atg	gat	aag	ctc	aat	gca	ggg	att	gat	cag	ctg	acc	gct	499
Leu	Leu	Pro	Met	Asp	Lys	Leu	Asn	Ala	Gly	Ile	Asp	Gln	Leu	Thr	Ala	
		120					125					130				
gag	ggc	gct	ttg	ggg	gac	aat	ggg	gca	gct	gct	gcc	aag	gcg	atc	atg	547
Glu	Gly	Ala	Leu	Gly	Asp	Asn	Gly	Ala	Ala	Ala	Ala	Lys	Ala	Ile	Met	
	135					140					145					
acc	act	gac	acg	gtg	gat	aag	gaa	acc	gtc	gtg	ttt	gct	gat	ggg	tgg	595
Thr	Thr	Asp	Thr	Val	Asp	Lys	Glu	Thr	Val	Val	Phe	Ala	Asp	Gly	Trp	
150					155					160					165	
act	gtc	ggc	gga	atg	ggc	aag	ggc	gtg	ggc	atg	atg	gcg	ccg	tct	ctt	643
Thr	Val	Gly	Gly	Met	Gly	Lys	Gly	Val	Gly	Met	Met	Ala	Pro	Ser	Leu	
				170					175					180		
gcc	acc	atg	ctg	gtc	tgc	ttg	acc	act	gat	gca	tcc	gtt	act	cag	gaa	691
Ala	Thr	Met	Leu	Val	Cys	Leu	Thr	Thr	Asp	Ala	Ser	Val	Thr	Gln	Glu	
			185					190					195			
atg	gct	cag	atc	gcg	ctg	gct	aat	gct	acg	gcc	gtt	acg	ttt	gac	acc	739
Met	Ala	Gln	Ile	Ala	Leu	Ala	Asn	Ala	Thr	Ala	Val	Thr	Phe	Asp	Thr	
		200					205					210				
ctg	gat	att	gat	gga	tca	acc	tcc	acc	aat	gac	acc	gtg	ttc	ctg	ctg	787
Leu	Asp	Ile	Asp	Gly	Ser	Thr	Ser	Thr	Asn	Asp	Thr	Val	Phe	Leu	Leu	
	215					220					225					
gca	tct	ggc	gct	agc	gga	atc	acc	cca	act	cag	gat	gaa	ctc	aac	gat	835
Ala	Ser	Gly	Ala	Ser	Gly	Ile	Thr	Pro	Thr	Gln	Asp	Glu	Leu	Asn	Asp	
230					235					240					245	
gcg	gtg	tac	gca	gct	tgt	tct	gat	atc	gca	gcg	aag	ctt	cag	gct	gat	883
Ala	Val	Tyr	Ala	Ala	Cys	Ser	Asp	Ile	Ala	Ala	Lys	Leu	Gln	Ala	Asp	
				250					255					260		
gca	gag	ggg	gtg	acc	aag	cgc	gtt	gct	gtg	aca	gtg	gtg	gga	acc	acc	931
Ala	Glu	Gly	Val	Thr	Lys	Arg	Val	Ala	Val	Thr	Val	Val	Gly	Thr	Thr	
			265					270					275			
aac	aac	gag	cag	gcg	att	aat	gcg	gct	cgc	act	gtt	gct	cgt	gac	aat	979
Asn	Asn	Glu	Gln	Ala	Ile	Asn	Ala	Ala	Arg	Thr	Val	Ala	Arg	Asp	Asn	
		280					285					290				

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 310 315 320 325

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 1123  
 Ser Val Phe Phe Asn Gly Gln Ala Val Cys Leu Asp Ser Thr Gly Ala  
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cct ggt gct cgt gag gtg gat ctt tcc ggc gct gac att gat gtc cga  
 1171  
 Pro Gly Ala Arg Glu Val Asp Leu Ser Gly Ala Asp Ile Asp Val Arg  
 345 350 355

att gat ttg ggc acc agt ggg gaa ggc cag gca aca gtt cga acc act  
 1219  
 Ile Asp Leu Gly Thr Ser Gly Glu Gly Gln Ala Thr Val Arg Thr Thr  
 360 365 370

gac ctg agc ttc tcc tac gtg gag atc aac tcc gcg tac agc tct  
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 375 380 385

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 <213> Corynebacterium glutamicum

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 35 40 45

Arg Val Phe Ala Ala Pro Val Lys Val Ser Arg Glu Asn Val Ala Asp  
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Gly Gln Ile Arg Ala Val Leu Tyr Asn Ala Gly Asn Ala Asn Ala Cys  
 65 70 75 80

Asn Gly Leu Gln Gly Glu Lys Asp Ala Arg Glu Ser Val Ser His Leu  
 85 90 95

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 115 120 125  
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 130 135 140  
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 145 150 155 160  
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 165 170 175  
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 180 185 190  
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 Val Thr Phe Asp Thr Leu Asp Ile Asp Gly Ser Thr Ser Thr Asn Asp  
 210 215 220  
 Thr Val Phe Leu Leu Ala Ser Gly Ala Ser Gly Ile Thr Pro Thr Gln  
 225 230 235 240  
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 245 250 255  
 Lys Leu Gln Ala Asp Ala Glu Gly Val Thr Lys Arg Val Ala Val Thr  
 260 265 270  
 Val Val Gly Thr Thr Asn Asn Glu Gln Ala Ile Asn Ala Ala Arg Thr  
 275 280 285  
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 Asn Trp Gly Arg Val Leu Ala Ala Val Gly Met Ala Asp Ala Asp Met  
 305 310 315 320  
 Glu Pro Glu Lys Ile Ser Val Phe Phe Asn Gly Gln Ala Val Cys Leu  
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 Asp Ser Thr Gly Ala Pro Gly Ala Arg Glu Val Asp Leu Ser Gly Ala  
 340 345 350  
 Asp Ile Asp Val Arg Ile Asp Leu Gly Thr Ser Gly Glu Gly Gln Ala  
 355 360 365  
 Thr Val Arg Thr Thr Asp Leu Ser Phe Ser Tyr Val Glu Ile Asn Ser  
 370 375 380  
 Ala Tyr Ser Ser  
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&lt;210&gt; 319

&lt;211&gt; 1074

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1051)

&lt;223&gt; RXA02156

&lt;400&gt; 319

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 Met Asn Asp Leu Ile  
 1 5

aaa gat tta ggc tct gag gtg cgc gca aat gtc ctc gct gag gcg ttg 163  
 Lys Asp Leu Gly Ser Glu Val Arg Ala Asn Val Leu Ala Glu Ala Leu  
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cca tgg ttg cag cac ttc cgc gac aag att gtt gtc gtg aaa tat ggc 211  
 Pro Trp Leu Gln His Phe Arg Asp Lys Ile Val Val Val Lys Tyr Gly  
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gga aac gcc atg gtg gat gat gat ctc aag gct gct ttt gct gcc gac 259  
 Gly Asn Ala Met Val Asp Asp Asp Leu Lys Ala Ala Phe Ala Ala Asp  
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atg gtc ttc ttg cgc acc gtg ggc gca aaa cca gtg gtg gtg cac ggt 307  
 Met Val Phe Leu Arg Thr Val Gly Ala Lys Pro Val Val Val His Gly  
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ggt gga cct cag att tct gag atg cta aac cgt gtg ggt ctc cag ggc 355  
 Gly Gly Pro Gln Ile Ser Glu Met Leu Asn Arg Val Gly Leu Gln Gly  
 70 75 80 85

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 Glu Phe Lys Gly Gly Phe Arg Val Thr Thr Pro Glu Val Met Asp Ile  
 90 95 100

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 Val Arg Met Val Leu Phe Gly Gln Val Gly Arg Asp Leu Val Gly Leu  
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 Ile Asn Ser His Gly Pro Tyr Ala Val Gly Thr Ser Gly Glu Asp Ala  
 120 125 130

ggc ctg ttt acc gcg cag aag cgc atg gtc aac atc gat ggc gta ccc 547  
 Gly Leu Phe Thr Ala Gln Lys Arg Met Val Asn Ile Asp Gly Val Pro  
 135 140 145

act gat att ggt ttg gtc gga gac atc att aat gtc gat gcc tct tcc 595  
 Thr Asp Ile Gly Leu Val Gly Asp Ile Ile Asn Val Asp Ala Ser Ser  
 150 155 160 165

ttg atg gat atc atc gag gcc ggt cgc att cct gtg gtc tct acg att 643  
 Leu Met Asp Ile Ile Glu Ala Gly Arg Ile Pro Val Val Ser Thr Ile  
 170 175 180

gct cca ggc gaa gac ggc cag att tac aac att aac gcc gat acc gca 691  
 Ala Pro Gly Glu Asp Gly Gln Ile Tyr Asn Ile Asn Ala Asp Thr Ala  
 185 190 195

gca ggt gct ttg gct gca gcg att ggt gca gaa cgc ctg ctg gtt ctc 739

Ala Gly Ala Leu Ala Ala Ala Ile Gly Ala Glu Arg Leu Leu Val Leu  
 200 205 210

acc aat gtg gaa ggt ctg tac acc gat tgg cct gat aag agc tca ctg 787  
 Thr Asn Val Glu Gly Leu Tyr Thr Asp Trp Pro Asp Lys Ser Ser Leu  
 215 220 225

gtg tcc aag atc aag gcc acc gag ctg gag gcc att ctt ccg gga ctt 835  
 Val Ser Lys Ile Lys Ala Thr Glu Leu Glu Ala Ile Leu Pro Gly Leu  
 230 235 240 245

gat tcc ggc atg att cca aag atg gag tct tgc ttg aac gcg gtg cgt 883  
 Asp Ser Gly Met Ile Pro Lys Met Glu Ser Cys Leu Asn Ala Val Arg  
 250 255 260

ggg gga gta agc gct gct cat gtc att gac ggc cgc atc gcg cac tcg 931  
 Gly Gly Val Ser Ala Ala His Val Ile Asp Gly Arg Ile Ala His Ser  
 265 270 275

gtg ttg ctg gag ctt ttg acc atg ggt gga att ggc acg atg gtg ctg 979  
 Val Leu Leu Glu Leu Leu Thr Met Gly Gly Ile Gly Thr Met Val Leu  
 280 285 290

ccg gat gtt ttt gat cgg gag aat tat cct gaa ggc acc gtt ttt aga  
 1027  
 Pro Asp Val Phe Asp Arg Glu Asn Tyr Pro Glu Gly Thr Val Phe Arg  
 295 300 305

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 1074  
 Lys Asp Asp Lys Asp Gly Glu Leu  
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 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 320  
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Leu Ala Glu Ala Leu Pro Trp Leu Gln His Phe Arg Asp Lys Ile Val  
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Val Val Lys Tyr Gly Gly Asn Ala Met Val Asp Asp Asp Leu Lys Ala  
 35 40 45

Ala Phe Ala Ala Asp Met Val Phe Leu Arg Thr Val Gly Ala Lys Pro  
 50 55 60

Val Val Val His Gly Gly Gly Pro Gln Ile Ser Glu Met Leu Asn Arg  
 65 70 75 80

Val Gly Leu Gln Gly Glu Phe Lys Gly Gly Phe Arg Val Thr Thr Pro  
 85 90 95

Glu Val Met Asp Ile Val Arg Met Val Leu Phe Gly Gln Val Gly Arg  
 100 105 110



Asp Leu Val Gly Leu Ile Asn Ser His Gly Pro Tyr Ala Val Gly Thr  
 115 120 125  
 Ser Gly Glu Asp Ala Gly Leu Phe Thr Ala Gln Lys Arg Met Val Asn  
 130 135 140  
 Ile Asp Gly Val Pro Thr Asp Ile Gly Leu Val Gly Asp Ile Ile Asn  
 145 150 155 160  
 Val Asp Ala Ser Ser Leu Met Asp Ile Ile Glu Ala Gly Arg Ile Pro  
 165 170 175  
 Val Val Ser Thr Ile Ala Pro Gly Glu Asp Gly Gln Ile Tyr Asn Ile  
 180 185 190  
 Asn Ala Asp Thr Ala Ala Gly Ala Leu Ala Ala Ala Ile Gly Ala Glu  
 195 200 205  
 Arg Leu Leu Val Leu Thr Asn Val Glu Gly Leu Tyr Thr Asp Trp Pro  
 210 215 220  
 Asp Lys Ser Ser Leu Val Ser Lys Ile Lys Ala Thr Glu Leu Glu Ala  
 225 230 235 240  
 Ile Leu Pro Gly Leu Asp Ser Gly Met Ile Pro Lys Met Glu Ser Cys  
 245 250 255  
 Leu Asn Ala Val Arg Gly Gly Val Ser Ala Ala His Val Ile Asp Gly  
 260 265 270  
 Arg Ile Ala His Ser Val Leu Leu Glu Leu Leu Thr Met Gly Gly Ile  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(880)  
 <223> RXN02153

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 Met Ile Met His Asn  
 1 5  
 gtg tat ggt gta act atg aca atc aag gtt gca atc gca gga gcc agt 163  
 Val Tyr Gly Val Thr Met Thr Ile Lys Val Ala Ile Ala Gly Ala Ser  
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gga tat gcc ggc gga gaa atc ctt cgt ctc ctt tta ggc cat cca gct	211
Gly Tyr Ala Gly Gly Glu Ile Leu Arg Leu Leu Leu Gly His Pro Ala	
25 30 35	
tat gca tct ggt gaa cta gaa atc gga gca ctc acc gcg gca tca acc	259
Tyr Ala Ser Gly Glu Leu Glu Ile Gly Ala Leu Thr Ala Ala Ser Thr	
40 45 50	
gca ggc agc acg ctc ggt gaa ttg atg cca cac att ccg cag ttg gcg	307
Ala Gly Ser Thr Leu Gly Glu Leu Met Pro His Ile Pro Gln Leu Ala	
55 60 65	
gat cgt gtt att caa gac acc aca gct gaa act cta gcc ggt cat gat	355
Asp Arg Val Ile Gln Asp Thr Thr Ala Glu Thr Leu Ala Gly His Asp	
70 75 80 85	
gtc gta ttt cta gga ctt cca cac gga ttc tct gca gaa att gca ctt	403
Val Val Phe Leu Gly Leu Pro His Gly Phe Ser Ala Glu Ile Ala Leu	
90 95 100	
cag ctc gga cca gat gtc aca gtg att gac tgt gca gct gac ttt cgt	451
Gln Leu Gly Pro Asp Val Thr Val Ile Asp Cys Ala Ala Asp Phe Arg	
105 110 115	
ctg caa aat gct gca gat tgg gag aag ttc tac ggc tca gag cac cag	499
Leu Gln Asn Ala Ala Asp Trp Glu Lys Phe Tyr Gly Ser Glu His Gln	
120 125 130	
gga aca tgg cct tat ggc att cca gaa atg cca gga cac cgc gag gct	547
Gly Thr Trp Pro Tyr Gly Ile Pro Glu Met Pro Gly His Arg Glu Ala	
135 140 145	
ctt cgt ggt gct aag cgt gta gca gtg cca gga tgt ttc cca acc ggt	595
Leu Arg Gly Ala Lys Arg Val Ala Val Pro Gly Cys Phe Pro Thr Gly	
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gca acc ttg gct ctt ctt cct gcg gtt caa gcg gga ctt atc gag cca	643
Ala Thr Leu Ala Leu Leu Pro Ala Val Gln Ala Gly Leu Ile Glu Pro	
170 175 180	
gat gtt tcc gta gtg tcc atc acc ggc gta tca ggt gca ggt aag aaa	691
Asp Val Ser Val Val Ser Ile Thr Gly Val Ser Gly Ala Gly Lys Lys	
185 190 195	
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Ala Ser Val Ala Leu Leu Gly Ser Glu Thr Met Gly Ser Leu Lys Ala	
200 205 210	
tac aac acc tcc gga aag cac cgc cac acc ccg gaa att gcc cag aac	787
Tyr Asn Thr Ser Gly Lys His Arg His Thr Pro Glu Ile Ala Gln Asn	
215 220 225	
ctc ggc gaa gtc agc gac aag cca gtc aag gtg agc ttc acc cca gtg	835
Leu Gly Glu Val Ser Asp Lys Pro Val Lys Val Ser Phe Thr Pro Val	
230 235 240 245	
ctt gca ccg tta cct cgc gaa ttc tca cca ctg caa ccg cac ctt	880
Leu Ala Pro Leu Pro Arg Glu Phe Ser Pro Leu Gln Pro His Leu	
250 255 260	
tgaaagaagg cgttaccgca gaa	903

&lt;210&gt; 322

&lt;211&gt; 260

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 322

Met Ile Met His Asn Val Tyr Gly Val Thr Met Thr Ile Lys Val Ala  
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Ile Ala Gly Ala Ser Gly Tyr Ala Gly Gly Glu Ile Leu Arg Leu Leu  
 20 25 30

Leu Gly His Pro Ala Tyr Ala Ser Gly Glu Leu Glu Ile Gly Ala Leu  
 35 40 45

Thr Ala Ala Ser Thr Ala Gly Ser Thr Leu Gly Glu Leu Met Pro His  
 50 55 60

Ile Pro Gln Leu Ala Asp Arg Val Ile Gln Asp Thr Thr Ala Glu Thr  
 65 70 75 80

Leu Ala Gly His Asp Val Val Phe Leu Gly Leu Pro His Gly Phe Ser  
 85 90 95

Ala Glu Ile Ala Leu Gln Leu Gly Pro Asp Val Thr Val Ile Asp Cys  
 100 105 110

Ala Ala Asp Phe Arg Leu Gln Asn Ala Ala Asp Trp Glu Lys Phe Tyr  
 115 120 125

Gly Ser Glu His Gln Gly Thr Trp Pro Tyr Gly Ile Pro Glu Met Pro  
 130 135 140

Gly His Arg Glu Ala Leu Arg Gly Ala Lys Arg Val Ala Val Pro Gly  
 145 150 155 160

Cys Phe Pro Thr Gly Ala Thr Leu Ala Leu Leu Pro Ala Val Gln Ala  
 165 170 175

Gly Leu Ile Glu Pro Asp Val Ser Val Val Ser Ile Thr Gly Val Ser  
 180 185 190

Gly Ala Gly Lys Lys Ala Ser Val Ala Leu Leu Gly Ser Glu Thr Met  
 195 200 205

Gly Ser Leu Lys Ala Tyr Asn Thr Ser Gly Lys His Arg His Thr Pro  
 210 215 220

Glu Ile Ala Gln Asn Leu Gly Glu Val Ser Asp Lys Pro Val Lys Val  
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Ser Phe Thr Pro Val Leu Ala Pro Leu Pro Arg Glu Phe Ser Pro Leu  
 245 250 255

Gln Pro His Leu  
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&lt;210&gt; 323

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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(880)  
 <223> FRXA02153

<400> 323

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                                         Met Ile Met His Asn
                                         1 5

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Val Tyr Gly Val Thr Met Thr Ile Lys Val Ala Ile Ala Gly Ala Ser
                        10 15 20

gga tat gcc ggc gga gaa atc ctt cgt ctc ctt tta ggc cat cca gct 211
Gly Tyr Ala Gly Gly Glu Ile Leu Arg Leu Leu Leu Gly His Pro Ala
                        25 30 35

tat gca tct ggt gaa cta gaa atc gga gca ctc acc gcg gca tca acc 259
Tyr Ala Ser Gly Glu Leu Glu Ile Gly Ala Leu Thr Ala Ala Ser Thr
                        40 45 50

gca ggc agc acg ctc ggt gaa ttg atg cca cac att ccg cag ttg gcg 307
Ala Gly Ser Thr Leu Gly Glu Leu Met Pro His Ile Pro Gln Leu Ala
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gat cgt gtt att caa gac acc aca gct gaa act cta gcc ggt cat gat 355
Asp Arg Val Ile Gln Asp Thr Thr Ala Glu Thr Leu Ala Gly His Asp
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gtc gta ttt cta gga ctt cca cac gga ttc tct gca gaa att gca ctt 403
Val Val Phe Leu Gly Leu Pro His Gly Phe Ser Ala Glu Ile Ala Leu
                        90 95 100

cag ctc gga cca gat gtc aca gtg att gac tgt gca gct gac ttt cgt 451
Gln Leu Gly Pro Asp Val Thr Val Ile Asp Cys Ala Ala Asp Phe Arg
                        105 110 115

ctg caa aat gct gca gat tgg gag aag ttc tac ggc tca gag cac cag 499
Leu Gln Asn Ala Ala Asp Trp Glu Lys Phe Tyr Gly Ser Glu His Gln
                        120 125 130

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Gly Thr Trp Pro Tyr Gly Ile Pro Glu Met Pro Gly His Arg Glu Ala
                        135 140 145

ctt cgt ggt gct aag cgt gta gca gtg cca gga tgt ttc cca acc ggt 595
Leu Arg Gly Ala Lys Arg Val Ala Val Pro Gly Cys Phe Pro Thr Gly
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gca acc ttg gct ctt ctt cct gcg gtt caa gcg gga ctt atc gag cca 643
Ala Thr Leu Ala Leu Leu Pro Ala Val Gln Ala Gly Leu Ile Glu Pro
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gat gtt tcc gta gtg tcc atc acc ggc gta tca ggt gca ggt aag aaa 691

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Asp Val Ser Val Val Ser Ile Thr Gly Val Ser Gly Ala Gly Lys Lys  
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 gca tct gtt gca cta ctt ggc tcg gaa acc atg ggt tca ctc aag gcg 739  
 Ala Ser Val Ala Leu Leu Gly Ser Glu Thr Met Gly Ser Leu Lys Ala  
 200 205 210  
 tac aac acc tcc gga aag cac cgc cac acc ccg gaa att gcc cag aac 787  
 Tyr Asn Thr Ser Gly Lys His Arg His Thr Pro Glu Ile Ala Gln Asn  
 215 220 225  
 ctc ggc gaa gtc agc gac aag cca gtc aag gtg agc ttc acc cca gtg 835  
 Leu Gly Glu Val Ser Asp Lys Pro Val Lys Val Ser Phe Thr Pro Val  
 230 235 240 245  
 ctt gca ccg tta cct cgc gaa ttc tca cca ctg caa ccg cac ctt 880  
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 35 40 45  
 Thr Ala Ala Ser Thr Ala Gly Ser Thr Leu Gly Glu Leu Met Pro His  
 50 55 60  
 Ile Pro Gln Leu Ala Asp Arg Val Ile Gln Asp Thr Thr Ala Glu Thr  
 65 70 75 80  
 Leu Ala Gly His Asp Val Val Phe Leu Gly Leu Pro His Gly Phe Ser  
 85 90 95  
 Ala Glu Ile Ala Leu Gln Leu Gly Pro Asp Val Thr Val Ile Asp Cys  
 100 105 110  
 Ala Ala Asp Phe Arg Leu Gln Asn Ala Ala Asp Trp Glu Lys Phe Tyr  
 115 120 125  
 Gly Ser Glu His Gln Gly Thr Trp Pro Tyr Gly Ile Pro Glu Met Pro  
 130 135 140  
 Gly His Arg Glu Ala Leu Arg Gly Ala Lys Arg Val Ala Val Pro Gly  
 145 150 155 160  
 Cys Phe Pro Thr Gly Ala Thr Leu Ala Leu Leu Pro Ala Val Gln Ala  
 165 170 175

Gly Leu Ile Glu Pro Asp Val Ser Val Val Ser Ile Thr Gly Val Ser  
 180 185 190  
 Gly Ala Gly Lys Lys Ala Ser Val Ala Leu Leu Gly Ser Glu Thr Met  
 195 200 205  
 Gly Ser Leu Lys Ala Tyr Asn Thr Ser Gly Lys His Arg His Thr Pro  
 210 215 220  
 Glu Ile Ala Gln Asn Leu Gly Glu Val Ser Asp Lys Pro Val Lys Val  
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 Gln Pro His Leu  
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 <212> DNA  
 <213> Corynebacterium glutamicum

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 <223> RXA02154

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 Leu Lys Glu Gly Val  
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 Thr Ala Glu Gln Ala Arg Ala Val Tyr Glu Glu Phe Tyr Ala Gln Glu  
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 Thr Phe Val His Val Leu Pro Glu Gly Ala Gln Pro Gln Thr Gln Ala  
 25 30 35  
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 Val Leu Gly Ser Asn Met Cys His Val Gln Val Glu Ile Asp Glu Glu  
 40 45 50  
 gca ggc aaa gtc ctt gtt acc tcc gca atc gat aac ctc acc aag gga 307  
 Ala Gly Lys Val Leu Val Thr Ser Ala Ile Asp Asn Leu Thr Lys Gly  
 55 60 65  
 act gcc ggc gcc gct gtt cag tgc atg aac tta agc gtt ggt ttt gat 355  
 Thr Ala Gly Ala Ala Val Gln Cys Met Asn Leu Ser Val Gly Phe Asp  
 70 75 80 85  
 gag gca gca ggc ctg cca cag gtc ggc gtc gca cct taaagtagcg 401  
 Glu Ala Ala Gly Leu Pro Gln Val Gly Val Ala Pro  
 90 95  
 ccttaaagcg gcg 414



55	60	65	
cac gtc tca aac ttg ttc gca tcc agg ccc gtc gtc gag gtc gcc gag His Val Ser Asn Leu Phe Ala Ser Arg Pro Val Val Glu Val Ala Glu 70 75 80 85			355
gag ctc atc aag cgt ttt tcg ctt gac gac gcc acc ctc gcc gcg caa Glu Leu Ile Lys Arg Phe Ser Leu Asp Asp Ala Thr Leu Ala Ala Gln 90 95 100			403
acc cgg gtt ttc ttc tgc aac tcg ggc gcc gaa gca aac gag gct gct Thr Arg Val Phe Phe Cys Asn Ser Gly Ala Glu Ala Asn Glu Ala Ala 105 110 115			451
ttc aag att gca cgc ttg act ggt cgt tcc cgg att ctg gct gca gtt Phe Lys Ile Ala Arg Leu Thr Gly Arg Ser Arg Ile Leu Ala Ala Val 120 125 130			499
cat ggt ttc cac ggc cgc acc atg ggt tcc ctc gcg ctg act ggc cag His Gly Phe His Gly Arg Thr Met Gly Ser Leu Ala Leu Thr Gly Gln 135 140 145			547
cca gac aag cgt gaa gcg ttc ctg cca atg cca agc ggt gtg gag ttc Pro Asp Lys Arg Glu Ala Phe Leu Pro Met Pro Ser Gly Val Glu Phe 150 155 160 165			595
tac cct tac ggc gac acc gat tac ttg cgc aaa atg gta gaa acc aac Tyr Pro Tyr Gly Asp Thr Asp Tyr Leu Arg Lys Met Val Glu Thr Asn 170 175 180			643
cca acg gat gtg gct gct atc ttc ctc gag cca atc cag ggt gaa acg Pro Thr Asp Val Ala Ala Ile Phe Leu Glu Pro Ile Gln Gly Glu Thr 185 190 195			691
ggc gtt gtt cca gca cct gaa gga ttc ctc aag gca gtg cgc gag ctg Gly Val Val Pro Ala Pro Glu Gly Phe Leu Lys Ala Val Arg Glu Leu 200 205 210			739
tgc gat gag tac ggc atc ttg atg atc acc gat gaa gtc cag act ggc Cys Asp Glu Tyr Gly Ile Leu Met Ile Thr Asp Glu Val Gln Thr Gly 215 220 225			787
gtt ggc cgt acc ggc gat ttc ttt gca cat cag cac gat ggc gtt gtt Val Gly Arg Thr Gly Asp Phe Phe Ala His Gln His Asp Gly Val Val 230 235 240 245			835
ccc gat gtg gtg acc atg gcc aag gga ctt ggc ggc ggt ctt ccc atc Pro Asp Val Val Thr Met Ala Lys Gly Leu Gly Gly Gly Leu Pro Ile 250 255 260			883
ggt gct tgt ttg gcc act ggc cgt gca gct gaa ttg atg acc cca ggc Gly Ala Cys Leu Ala Thr Gly Arg Ala Ala Glu Leu Met Thr Pro Gly 265 270 275			931
aag cac ggc acc act ttc ggt ggc aac cca gtt gct tgt gca gct gcc Lys His Gly Thr Thr Phe Gly Gly Asn Pro Val Ala Cys Ala Ala Ala 280 285 290			979
aag gca gtg ctg tct gtt gtc gat gac gct ttc tgc gca gaa gtt gcc 1027 Lys Ala Val Leu Ser Val Val Asp Asp Ala Phe Cys Ala Glu Val Ala			



295                                      300                                      305  
 cgc aag ggc gag ctg ttc aag gaa ctt ctt gcc aag gtt gac ggc gtt  
 1075  
 Arg Lys Gly Glu Leu Phe Lys Glu Leu Leu Ala Lys Val Asp Gly Val  
 310                                      315                                      320                                      325  
 gta gac gtc cgt ggc agg ggc ttg atg ttg ggc gtg gtg ctg gag cgc  
 1123  
 Val Asp Val Arg Gly Arg Gly Leu Met Leu Gly Val Val Leu Glu Arg  
 330                                      335                                      340  
 gac gtc gca aag caa gct gtt ctt gat ggt ttt aag cac ggc gtt att  
 1171  
 Asp Val Ala Lys Gln Ala Val Leu Asp Gly Phe Lys His Gly Val Ile  
 345                                      350                                      355  
 ttg aat gca ccg gcg gac aac att atc cgt ttg acc ccg ccg ctg gtg  
 1219  
 Leu Asn Ala Pro Ala Asp Asn Ile Ile Arg Leu Thr Pro Pro Leu Val  
 360                                      365                                      370  
 atc acc gac gaa gaa atc gca gac gca gtc aag gct att gcc gag aca  
 1267  
 Ile Thr Asp Glu Glu Ile Ala Asp Ala Val Lys Ala Ile Ala Glu Thr  
 375                                      380                                      385  
 atc gca taaaggactc aaacttatga ctt  
 1296  
 Ile Ala  
 390

&lt;210&gt; 328

&lt;211&gt; 391

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 328

Met Ser Thr Leu Glu Thr Trp Pro Gln Val Ile Ile Asn Thr Tyr Gly  
 1                                      5                                      10                                      15  
 Thr Pro Pro Val Glu Leu Val Ser Gly Lys Gly Ala Thr Val Thr Asp  
 20                                      25                                      30  
 Asp Gln Gly Asn Val Tyr Ile Asp Leu Leu Ala Gly Ile Ala Val Asn  
 35                                      40                                      45  
 Ala Leu Gly His Ala His Pro Ala Ile Ile Glu Ala Val Thr Asn Gln  
 50                                      55                                      60  
 Ile Gly Gln Leu Gly His Val Ser Asn Leu Phe Ala Ser Arg Pro Val  
 65                                      70                                      75                                      80  
 Val Glu Val Ala Glu Glu Leu Ile Lys Arg Phe Ser Leu Asp Asp Ala  
 85                                      90                                      95  
 Thr Leu Ala Ala Gln Thr Arg Val Phe Phe Cys Asn Ser Gly Ala Glu  
 100                                      105                                      110  
 Ala Asn Glu Ala Ala Phe Lys Ile Ala Arg Leu Thr Gly Arg Ser Arg

115					120					125					
Ile	Leu	Ala	Ala	Val	His	Gly	Phe	His	Gly	Arg	Thr	Met	Gly	Ser	Leu
130						135					140				
Ala	Leu	Thr	Gly	Gln	Pro	Asp	Lys	Arg	Glu	Ala	Phe	Leu	Pro	Met	Pro
145					150					155					160
Ser	Gly	Val	Glu	Phe	Tyr	Pro	Tyr	Gly	Asp	Thr	Asp	Tyr	Leu	Arg	Lys
				165					170					175	
Met	Val	Glu	Thr	Asn	Pro	Thr	Asp	Val	Ala	Ala	Ile	Phe	Leu	Glu	Pro
			180					185					190		
Ile	Gln	Gly	Glu	Thr	Gly	Val	Val	Pro	Ala	Pro	Glu	Gly	Phe	Leu	Lys
		195					200					205			
Ala	Val	Arg	Glu	Leu	Cys	Asp	Glu	Tyr	Gly	Ile	Leu	Met	Ile	Thr	Asp
		210				215					220				
Glu	Val	Gln	Thr	Gly	Val	Gly	Arg	Thr	Gly	Asp	Phe	Phe	Ala	His	Gln
225						230					235				240
His	Asp	Gly	Val	Val	Pro	Asp	Val	Val	Thr	Met	Ala	Lys	Gly	Leu	Gly
				245					250					255	
Gly	Gly	Leu	Pro	Ile	Gly	Ala	Cys	Leu	Ala	Thr	Gly	Arg	Ala	Ala	Glu
			260					265					270		
Leu	Met	Thr	Pro	Gly	Lys	His	Gly	Thr	Thr	Phe	Gly	Gly	Asn	Pro	Val
		275					280					285			
Ala	Cys	Ala	Ala	Ala	Lys	Ala	Val	Leu	Ser	Val	Val	Asp	Asp	Ala	Phe
		290				295					300				
Cys	Ala	Glu	Val	Ala	Arg	Lys	Gly	Glu	Leu	Phe	Lys	Glu	Leu	Leu	Ala
305						310					315				320
Lys	Val	Asp	Gly	Val	Val	Asp	Val	Arg	Gly	Arg	Gly	Leu	Met	Leu	Gly
				325					330					335	
Val	Val	Leu	Glu	Arg	Asp	Val	Ala	Lys	Gln	Ala	Val	Leu	Asp	Gly	Phe
			340					345					350		
Lys	His	Gly	Val	Ile	Leu	Asn	Ala	Pro	Ala	Asp	Asn	Ile	Ile	Arg	Leu
		355					360					365			
Thr	Pro	Pro	Leu	Val	Ile	Thr	Asp	Glu	Glu	Ile	Ala	Asp	Ala	Val	Lys
		370				375					380				
Ala	Ile	Ala	Glu	Thr	Ile	Ala									
385						390									

&lt;210&gt; 329

&lt;211&gt; 1491

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1468)

&lt;223&gt; RXS02970

&lt;400&gt; 329

aaccgacaaa acagccgttc acgtgctaaa gcagctcggc ttgatctagg gtgaggtgag 60

ttatttaaag	acttcataat	atthttgggga	gtgaactggg	ttg	gca	ttg	aag	ggg	115
				Leu	Ala	Leu	Lys	Gly	
				1				5	

tac	acc	aac	ttt	gac	ggg	gaa	ttc	atc	gaa	ttc	gga	tct	gtg	caa	gca	163
Tyr	Thr	Asn	Phe	Asp	Gly	Glu	Phe	Ile	Glu	Phe	Gly	Ser	Val	Gln	Ala	
				10					15					20		

aaa	gaa	gag	gaa	aaa	cgg	gca	ttc	gac	aac	gat	cgc	gcg	cac	gtt	ttc	211
Lys	Glu	Glu	Glu	Lys	Arg	Ala	Phe	Asp	Asn	Asp	Arg	Ala	His	Val	Phe	
			25					30					35			

cac	tcc	tgg	tcc	gcg	cag	gac	aaa	atc	agc	ccc	aaa	gta	tgg	gca	gct	259
His	Ser	Trp	Ser	Ala	Gln	Asp	Lys	Ile	Ser	Pro	Lys	Val	Trp	Ala	Ala	
		40					45					50				

gcc	gaa	ggg	tcc	acg	ctg	tac	gac	ttc	gac	ggc	aac	gcc	ttc	atc	gac	307
Ala	Glu	Gly	Ser	Thr	Leu	Tyr	Asp	Phe	Asp	Gly	Asn	Ala	Phe	Ile	Asp	
	55					60					65					

atg	ggg	tcc	caa	ctt	gtc	tcg	gca	aac	tta	ggc	cac	aac	aac	cct	cga	355
Met	Gly	Ser	Gln	Leu	Val	Ser	Ala	Asn	Leu	Gly	His	Asn	Asn	Pro	Arg	
70					75					80					85	

tta	gtt	gag	gcg	atc	cag	cgc	caa	gca	gcc	cgg	ttg	acc	aac	atc	aac	403
Leu	Val	Glu	Ala	Ile	Gln	Arg	Gln	Ala	Ala	Arg	Leu	Thr	Asn	Ile	Asn	
				90				95						100		

ccg	gcc	ttc	ggc	aac	gat	gtg	cgc	tct	gat	gtt	gct	gca	aag	atc	gtg	451
Pro	Ala	Phe	Gly	Asn	Asp	Val	Arg	Ser	Asp	Val	Ala	Ala	Lys	Ile	Val	
			105					110					115			

tcg	atg	gcc	cgt	ggc	gaa	ttc	tcc	cac	gtg	ttt	ttc	acc	aac	ggc	ggc	499
Ser	Met	Ala	Arg	Gly	Glu	Phe	Ser	His	Val	Phe	Phe	Thr	Asn	Gly	Gly	
		120					125					130				

gcc	gac	gcc	atc	gag	cac	tcc	atc	cgc	atg	gct	cgc	ctg	cac	acc	gga	547
Ala	Asp	Ala	Ile	Glu	His	Ser	Ile	Arg	Met	Ala	Arg	Leu	His	Thr	Gly	
	135					140					145					

cgc	aac	aaa	att	ctg	tcc	gca	tac	cgc	agc	tac	cac	ggc	gca	acc	gga	595
Arg	Asn	Lys	Ile	Leu	Ser	Ala	Tyr	Arg	Ser	Tyr	His	Gly	Ala	Thr	Gly	
150					155					160					165	

tcc	gcg	atg	atg	ctc	acc	ggc	gaa	cac	cgc	cgc	ctg	ggc	aac	ccc	acc	643
Ser	Ala	Met	Met	Leu	Thr	Gly	Glu	His	Arg	Arg	Leu	Gly	Asn	Pro	Thr	
				170					175					180		

acc	gac	cca	gat	atc	tac	cac	ttc	tgg	gca	cca	ttc	ctg	cac	cac	tcc	691
Thr	Asp	Pro	Asp	Ile	Tyr	His	Phe	Trp	Ala	Pro	Phe	Leu	His	His	Ser	
			185					190					195			

tca	ttc	ttt	gcc	acc	acc	caa	gaa	gaa	gaa	tgc	gaa	cgc	gca	ctc	aag	739
Ser	Phe	Phe	Ala	Thr	Thr	Gln	Glu	Glu	Glu	Cys	Glu	Arg	Ala	Leu	Lys	
		200					205					210				

cac ttg gaa gat gtc atc gcg ttt gaa ggt gct ggc atg atc gca gcg	787
His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala	
215 220 225	
atc gtc ctg gag cca gtg gtg gga tca tca gga atc atc ctg cca cca	835
Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro	
230 235 240 245	
gca ggt tac tta aat ggc gtg cgc gaa ctt tgc aac aag cac ggc atc	883
Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile	
250 255 260	
ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa	931
Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys	
265 270 275	
ctg ttt gct tac gag cat gct ggc gac gat ttc cag cca gac atg atc	979
Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile	
280 285 290	
acc ttc gcc aag ggt gtt aac gca ggt tac gcc cca ctc ggt ggc atc	
1027 Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile	
295 300 305	
gtg atg acc caa tca atc cgc gat acc ttc gga tca gag gca tac tcc	
1075 Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly Ser Glu Ala Tyr Ser	
310 315 320 325	
ggc gga ctc acc tac tcc gga cac cca ctt gca gta gca ccc gcc aag	
1123 Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys	
330 335 340	
gca gcg ctg gag att tac gcg gaa gga gag atc att cca cgc gta gct	
1171 Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala	
345 350 355	
cga ctt ggc gct gaa ctg atc gaa cct cgc ctt cgt gaa cta gcg gaa	
1219 Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu	
360 365 370	
gaa aac gta gcg atc gct gac gtg cgg ggc atc gga ttc ttc tgg gca	
1267 Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile Gly Phe Phe Trp Ala	
375 380 385	
gtg gag ttc aat gca gac gcc act gcc atg gct gcc ggt gct gca gaa	
1315 Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu	
390 395 400 405	
ttc aag gaa cgc ggc gtg tgg ccg atg atc tcc ggc aac cga ttc cac	
1363 Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser Gly Asn Arg Phe His	
410 415 420	

atc gcg ccg ccg ctg acc acc act gat gac gaa ttg gta gca ctg ctg  
 1411  
 Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu Leu Val Ala Leu Leu  
                   425                                  430                                  435

gac gcg gtg gaa gct gca gcc caa gct gtc gag ctg acc ttc gct ggg  
 1459  
 Asp Ala Val Glu Ala Ala Ala Gln Ala Val Glu Leu Thr Phe Ala Gly  
                   440                                  445                                  450

gcg ttg ttc taagttttct agataacaag gcc  
 1491  
 Ala Leu Phe  
                   455

<210> 330  
 <211> 456  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 330  
 Leu Ala Leu Lys Gly Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe  
   1                                  5                                  10                                  15  
 Gly Ser Val Gln Ala Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp  
                   20                                  25                                  30  
 Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro  
                   35                                  40                                  45  
 Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly  
                   50                                  55                                  60  
 Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly  
   65                                  70                                  75                                  80  
 His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg  
                   85                                  90                                  95  
 Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val  
                   100                                  105                                  110  
 Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe  
                   115                                  120                                  125  
 Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala  
                   130                                  135                                  140  
 Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr  
   145                                  150                                  155                                  160  
 His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg  
                   165                                  170                                  175  
 Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro  
                   180                                  185                                  190  
 Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys  
                   195                                  200                                  205

Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala  
210 215 220

Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly  
225 230 235 240

Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys  
245 250 255

Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe  
260 265 270

Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe  
275 280 285

Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala  
290 295 300

Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly  
305 310 315 320

Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala  
325 330 335

Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile  
340 345 350

Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu  
355 360 365

Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile  
370 375 380

Gly Phe Phe Trp Ala Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala  
385 390 395 400

Ala Gly Ala Ala Glu Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser  
405 410 415

Gly Asn Arg Phe His Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu  
420 425 430

Leu Val Ala Leu Leu Asp Ala Val Glu Ala Ala Ala Gln Ala Val Glu  
435 440 445

Leu Thr Phe Ala Gly Ala Leu Phe  
450 455

<210> 331

<211> 1330

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1330)

<223> FRXA01009

<400> 331

aaccgacaaa acagccgttc acgtgctaaa gcagctcggc ttgatctagg gtgagggtgag 60

ttattttaag acttcataat attttgggga gtgaactggt	115
Leu Ala Leu Lys Gly	5
1	
tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca	163
Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala	20
10 15	
aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc	211
Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe	35
25 30	
cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct	259
His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala	50
40 45	
gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac	307
Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp	65
55 60	
atg ggt tcc caa ctt gtc tcg gca aac tta ggc cac aac aac cct cga	355
Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg	85
70 75 80	
tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac	403
Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn	100
90 95	
ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg	451
Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val	115
105 110	
tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc	499
Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly	130
120 125	
gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga	547
Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly	145
135 140	
cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga	595
Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly	165
150 155 160	
tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc	643
Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr	180
170 175	
acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc	691
Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser	195
185 190	
tca ttc ttt gcc acc acc caa gaa gaa gaa tgc gaa cgc gca ctc aag	739
Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys	210
200 205 210	
cac ttg gaa gat gtc atc gcg ttt gaa ggt gct ggc atg atc gca gcg	787
His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala	225
215 220	

atc gtc ctg gag cca gtg gtg gga tca tca gga atc atc ctg cca cca 835  
 Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro  
 230 235 240 245

gca ggt tac tta aat ggc gtg cgc gaa ctt tgc aac aag cac ggc atc 883  
 Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile  
 250 255 260

ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa 931  
 Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys  
 265 270 275

ctg ttt gct tac gag cat gct ggc gac gat ttc cag cca gac atg atc 979  
 Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile  
 280 285 290

acc ttc gcc aag ggt gtt aac gca ggt tac gcc cca ctc ggt ggc atc  
 1027  
 Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile  
 295 300 305

gtg atg acc caa tca atc cgc gat acc ttc gga tca gag gca tac tcc  
 1075  
 Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly Ser Glu Ala Tyr Ser  
 310 315 320 325

ggc gga ctc acc tac tcc gga cac cca ctt gca gta gca ccc gcc aag  
 1123  
 Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys  
 330 335 340

gca gcg ctg gag att tac gcg gaa gga gag atc att cca cgc gta gct  
 1171  
 Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala  
 345 350 355

cga ctt ggc gct gaa ctg atc gaa cct cgc ctt cgt gaa cta gcg gaa  
 1219  
 Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu  
 360 365 370

gaa aac gta gcg atc gct gac gtg cgg ggc atc gga ttc ttc tgg gca  
 1267  
 Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile Gly Phe Phe Trp Ala  
 375 380 385

gtg gag ttc aat gca gac gcc act gcc atg gct gcc ggt gct gca gaa  
 1315  
 Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu  
 390 395 400 405

ttc aag gaa cgc ggc  
 1330  
 Phe Lys Glu Arg Gly  
 410

&lt;210&gt; 332

&lt;211&gt; 410

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum



&lt;400&gt; 332

Leu	Ala	Leu	Lys	Gly	Tyr	Thr	Asn	Phe	Asp	Gly	Glu	Phe	Ile	Glu	Phe
1				5					10					15	
Gly	Ser	Val	Gln	Ala	Lys	Glu	Glu	Glu	Lys	Arg	Ala	Phe	Asp	Asn	Asp
			20					25					30		
Arg	Ala	His	Val	Phe	His	Ser	Trp	Ser	Ala	Gln	Asp	Lys	Ile	Ser	Pro
		35					40					45			
Lys	Val	Trp	Ala	Ala	Ala	Glu	Gly	Ser	Thr	Leu	Tyr	Asp	Phe	Asp	Gly
	50					55					60				
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225					230					235					240
Ile	Ile	Leu	Pro	Pro	Ala	Gly	Tyr	Leu	Asn	Gly	Val	Arg	Glu	Leu	Cys
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Gln	Pro	Asp	Met	Ile	Thr	Phe	Ala	Lys	Gly	Val	Asn	Ala	Gly	Tyr	Ala
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Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala  
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Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile  
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Glu Thr Ser Thr Val Pro Leu Val Asn Ser Leu Ser Asp Asp Leu His	
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Pro Cys Gln Ile Leu Ala Asp Leu Gln Thr Ile Val Glu Asn Leu Ser	
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Tyr Arg Gly Lys Glu Val Ala Ala Ser Val Ile Asp Gly Pro Ala Ser	
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His	Cys	Leu	Pro	Ala	Tyr	Arg	Gly	Lys	Glu	Val	Ala	Ala	Ser	Val	Ile
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 Val Thr Ile Glu Arg Glu Leu Ala Arg Tyr Lys Arg Gly Val Asp Ala  
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Gln	Pro	Leu	Leu	Arg	Asp	Ile	Asp	Arg	Ile	Arg	Asp	Leu	Asp	Lys	Arg	
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265				270				275								

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 Ser Asp Ser Trp Ser Thr Gly Ser Ser Ile Met Pro Gln Lys Lys Asn  
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 Pro Asp Val Ala Glu Leu Thr Arg Gly Lys Ser Gly Arg Leu Ile Gly  
 295 300 305

aac ctc acc ggt ctg ctg gct acc ctg aag gca cag cct tta gcg tac  
 1075  
 Asn Leu Thr Gly Leu Leu Ala Thr Leu Lys Ala Gln Pro Leu Ala Tyr  
 310 315 320 325

aac cgc gac ctg cag gaa gat aag gaa cca atc gta gat tcc gtg gcg  
 1123  
 Asn Arg Asp Leu Gln Glu Asp Lys Glu Pro Ile Val Asp Ser Val Ala  
 330 335 340

cag ctc aac ctg ctg ctc cct gca atg act ggt ttg gtt tcc acc ttg  
 1171  
 Gln Leu Asn Leu Leu Leu Pro Ala Met Thr Gly Leu Val Ser Thr Leu  
 345 350 355

acc ttc aac acc gag cgc atg cgt gaa ctt gca cca gca ggt ttc acc  
 1219  
 Thr Phe Asn Thr Glu Arg Met Arg Glu Leu Ala Pro Ala Gly Phe Thr  
 360 365 370

ctt gcc acc gac ttg gct gag tgg atg gtg cgc cag ggc gtt cca ttc  
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cgt gag gca cac gaa gca tcc ggc gct tgc gtg cgg atc gcg gag tcc  
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 Arg Glu Ala His Glu Ala Ser Gly Ala Cys Val Arg Ile Ala Glu Ser  
 390 395 400 405

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 1363  
 Arg Gly Val Asp Leu Ile Asp Leu Thr Asp Glu Glu Leu Ser Gly Val  
 410 415 420

gat gca cgt ctg acc cca gag gta cgg gaa gtg ctc acc att gat ggt  
 1411  
 Asp Ala Arg Leu Thr Pro Glu Val Arg Glu Val Leu Thr Ile Asp Gly  
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gcg gag caa cgc gca cgt gtc gat gcc gca agt acc gct cac gcg gag  
 1507  
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 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 338  
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 35 40 45  
 Ala Lys Val Leu His Gln Ala Asp Leu Leu Ser Asp Glu Asp Leu Ala  
 50 55 60  
 Thr Met Leu Ala Gly Leu Asp Gln Leu Gly Lys Asp Val Ala Asp Gly  
 65 70 75 80  
 Thr Phe Gly Pro Leu Pro Ser Asp Glu Asp Val His Gly Ala Met Glu  
 85 90 95  
 Arg Gly Val Ile Asp Arg Val Gly Pro Glu Val Gly Gly Arg Leu Arg  
 100 105 110  
 Ala Gly Arg Ser Arg Asn Asp Gln Val Ala Thr Leu Phe Arg Met Trp  
 115 120 125  
 Val Arg Asp Ala Val Arg Asp Ile Ala Leu Gly Thr Thr Glu Leu Val  
 130 135 140  
 Asp Ala Leu Ser Ala Gln Ala Lys Ala His Ala Gly Ala Ile Met Pro  
 145 150 155 160  
 Gly Lys Thr His Phe Gln Ala Ala Gln Pro Val Leu Leu Ala His Gln  
 165 170 175  
 Leu Leu Ala His Ala Gln Pro Leu Leu Arg Asp Ile Asp Arg Ile Arg  
 180 185 190  
 Asp Leu Asp Lys Arg Leu Ala Val Ser Pro Tyr Gly Ser Gly Ala Leu  
 195 200 205  
 Ala Gly Ser Ser Leu Lys Leu Asn Pro Glu Ala Ile Ala Glu Glu Leu  
 210 215 220  
 Gly Phe Asp Ser Ala Ala Asp Asn Ser Ile Asp Ala Thr Ser Ser Arg  
 225 230 235 240  
 Asp Phe Ala Ser Glu Thr Ala Phe Val Leu Ala Gln Leu Ala Val Asp  
 245 250 255  
 Met Ser Arg Leu Ala Glu Glu Ile Ile Ala Trp Cys Thr Pro Glu Phe

260								265				270				
Gly	Tyr	Ile	Thr	Leu	Ser	Asp	Ser	Trp	Ser	Thr	Gly	Ser	Ser	Ile	Met	
275							280				285					
Pro	Gln	Lys	Lys	Asn	Pro	Asp	Val	Ala	Glu	Leu	Thr	Arg	Gly	Lys	Ser	
290							295				300					
Gly	Arg	Leu	Ile	Gly	Asn	Leu	Thr	Gly	Leu	Leu	Ala	Thr	Leu	Lys	Ala	
305							310				315				320	
Gln	Pro	Leu	Ala	Tyr	Asn	Arg	Asp	Leu	Gln	Glu	Asp	Lys	Glu	Pro	Ile	
325							330				335					
Val	Asp	Ser	Val	Ala	Gln	Leu	Asn	Leu	Leu	Leu	Pro	Ala	Met	Thr	Gly	
340							345				350					
Leu	Val	Ser	Thr	Leu	Thr	Phe	Asn	Thr	Glu	Arg	Met	Arg	Glu	Leu	Ala	
355							360				365					
Pro	Ala	Gly	Phe	Thr	Leu	Ala	Thr	Asp	Leu	Ala	Glu	Trp	Met	Val	Arg	
370							375				380					
Gln	Gly	Val	Pro	Phe	Arg	Glu	Ala	His	Glu	Ala	Ser	Gly	Ala	Cys	Val	
385							390				395				400	
Arg	Ile	Ala	Glu	Ser	Arg	Gly	Val	Asp	Leu	Ile	Asp	Leu	Thr	Asp	Glu	
405							410				415					
Glu	Leu	Ser	Gly	Val	Asp	Ala	Arg	Leu	Thr	Pro	Glu	Val	Arg	Glu	Val	
420							425				430					
Leu	Thr	Ile	Asp	Gly	Ala	Val	Ala	Ser	Arg	Ala	Thr	Arg	Gly	Gly	Thr	
435							440				445					
Ala	Gly	Val	Arg	Val	Ala	Glu	Gln	Arg	Ala	Arg	Val	Asp	Ala	Ala	Ser	
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Thr	Ala	His	Ala	Glu	Trp	Ala	Arg	Ala	Gly	Val	Arg	Arg				
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&lt;210&gt; 339

&lt;211&gt; 906

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(883)

&lt;223&gt; FRXA02161

&lt;400&gt; 339

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acc	aat	gaa	ggt	gcg	ctg	tgg	ggc	ggc	cgc	ttc	tcc	ggt	gga	ccc	tcc	163
Thr	Asn	Glu	Gly	Ala	Leu	Trp	Gly	Gly	Arg	Phe	Ser	Gly	Gly	Pro	Ser	

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gag	gcc	atg	ttc	gcc	ttg	agt	gtc	tcc	act	cat	ttc	gac	tgg	gtt	ttg	211	
Glu	Ala	Met	Phe	Ala	Leu	Ser	Val	Ser	Thr	His	Phe	Asp	Trp	Val	Leu		
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gcc	cct	tat	gat	gtg	ttg	gcc	tcc	aag	gca	cac	gcc	aag	gtt	ttg	cac	259	
Ala	Pro	Tyr	Asp	Val	Leu	Ala	Ser	Lys	Ala	His	Ala	Lys	Val	Leu	His		
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caa	gca	gat	cta	ctt	tct	gat	gaa	gat	cta	gcc	acc	atg	ctg	gct	ggg	307	
Gln	Ala	Asp	Leu	Leu	Ser	Asp	Glu	Asp	Leu	Ala	Thr	Met	Leu	Ala	Gly		
			55				60						65				
ctt	gat	cag	ctg	ggc	aag	gat	gtc	gcc	gac	gga	acc	ttc	ggg	ccg	ctg	355	
Leu	Asp	Gln	Leu	Gly	Lys	Asp	Val	Ala	Asp	Gly	Thr	Phe	Gly	Pro	Leu		
			70				75						80	85			
cct	tct	gat	gag	gat	gtg	cac	ggc	gcg	atg	gaa	cgc	ggg	gtg	att	gac	403	
Pro	Ser	Asp	Glu	Asp	Val	His	Gly	Ala	Met	Glu	Arg	Gly	Val	Ile	Asp		
			90						95						100		
cgc	gtt	ggg	cct	gag	gtg	ggc	ggc	cgt	ctg	cgc	gct	ggg	cgt	tcc	cgc	451	
Arg	Val	Gly	Pro	Glu	Val	Gly	Gly	Arg	Leu	Arg	Ala	Gly	Arg	Ser	Arg		
			105				110						115				
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Asn	Asp	Gln	Val	Ala	Thr	Leu	Phe	Arg	Met	Trp	Val	Arg	Asp	Ala	Val		
			120				125						130				
cgc	gac	atc	gcg	ctg	gga	aca	acc	gag	ctt	gtc	gac	gcc	ctc	agc	gcc	547	
Arg	Asp	Ile	Ala	Leu	Gly	Thr	Thr	Glu	Leu	Val	Asp	Ala	Leu	Ser	Ala		
			135				140						145				
caa	gct	aag	gca	cat	gca	ggc	gcg	atc	atg	cca	ggc	aag	acc	cac	ttc	595	
Gln	Ala	Lys	Ala	His	Ala	Gly	Ala	Ile	Met	Pro	Gly	Lys	Thr	His	Phe		
150			155			160			165								
cag	gca	gct	cag	ccg	gtc	ctt	ctg	gca	cac	cag	ctg	ctg	gca	cac	gca	643	
Gln	Ala	Ala	Gln	Pro	Val	Leu	Leu	Ala	His	Gln	Leu	Leu	Ala	His	Ala		
			170			175						180					
cag	cct	ttg	ctg	cgc	gat	att	gat	cgt	atc	cgt	gac	ctg	gac	aag	cgt	691	
Gln	Pro	Leu	Leu	Arg	Asp	Ile	Asp	Arg	Ile	Arg	Asp	Leu	Asp	Lys	Arg		
			185			190						195					
ctt	gcg	gtg	tct	cct	tac	ggg	tcc	ggc	gca	ctt	gct	ggg	tcc	tct	ttg	739	
Leu	Ala	Val	Ser	Pro	Tyr	Gly	Ser	Gly	Ala	Leu	Ala	Gly	Ser	Ser	Leu		
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aag	ctc	aac	cct	gaa	gca	atc	gct	gaa	gaa	ctc	ggc	ttt	gat	tcc	gca	787	
Lys	Leu	Asn	Pro	Glu	Ala	Ile	Ala	Glu	Glu	Leu	Gly	Phe	Asp	Ser	Ala		
			215			220						225					
gca	gat	aac	tcc	att	gat	gcc	acc	agc	tcc	cgc	gat	ttc	gca	tct	gaa	835	
Ala	Asp	Asn	Ser	Ile	Asp	Ala	Thr	Ser	Ser	Arg	Asp	Phe	Ala	Ser	Glu		
230			235			240			245								
acc	gcc	ttc	gtg	ctg	gcg	cag	ctt	gca	ngt	gga	tat	gtc	ccg	ctt	ggc	883	
Thr	Ala	Phe	Val	Leu	Ala	Gln	Leu	Ala	Xaa	Gly	Tyr	Val	Pro	Leu	Gly		
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906

&lt;210&gt; 340

&lt;211&gt; 261

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 340

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			20					25					30		

Phe	Asp	Trp	Val	Leu	Ala	Pro	Tyr	Asp	Val	Leu	Ala	Ser	Lys	Ala	His
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Ala	Lys	Val	Leu	His	Gln	Ala	Asp	Leu	Leu	Ser	Asp	Glu	Asp	Leu	Ala
	50					55					60				

Thr	Met	Leu	Ala	Gly	Leu	Asp	Gln	Leu	Gly	Lys	Asp	Val	Ala	Asp	Gly
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Thr	Phe	Gly	Pro	Leu	Pro	Ser	Asp	Glu	Asp	Val	His	Gly	Ala	Met	Glu
				85					90					95	

Arg	Gly	Val	Ile	Asp	Arg	Val	Gly	Pro	Glu	Val	Gly	Gly	Arg	Leu	Arg
			100					105					110		

Ala	Gly	Arg	Ser	Arg	Asn	Asp	Gln	Val	Ala	Thr	Leu	Phe	Arg	Met	Trp
		115					120					125			

Val	Arg	Asp	Ala	Val	Arg	Asp	Ile	Ala	Leu	Gly	Thr	Thr	Glu	Leu	Val
	130					135					140				

Asp	Ala	Leu	Ser	Ala	Gln	Ala	Lys	Ala	His	Ala	Gly	Ala	Ile	Met	Pro
145					150					155					160

Gly	Lys	Thr	His	Phe	Gln	Ala	Ala	Gln	Pro	Val	Leu	Leu	Ala	His	Gln
				165					170					175	

Leu	Leu	Ala	His	Ala	Gln	Pro	Leu	Leu	Arg	Asp	Ile	Asp	Arg	Ile	Arg
			180					185					190		

Asp	Leu	Asp	Lys	Arg	Leu	Ala	Val	Ser	Pro	Tyr	Gly	Ser	Gly	Ala	Leu
		195					200					205			

Ala	Gly	Ser	Ser	Leu	Lys	Leu	Asn	Pro	Glu	Ala	Ile	Ala	Glu	Glu	Leu
	210					215					220				

Gly	Phe	Asp	Ser	Ala	Ala	Asp	Asn	Ser	Ile	Asp	Ala	Thr	Ser	Ser	Arg
225					230					235					240

Asp	Phe	Ala	Ser	Glu	Thr	Ala	Phe	Val	Leu	Ala	Gln	Leu	Ala	Xaa	Gly
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Tyr	Val	Pro	Leu	Gly
			260	

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 <222> (101)..(763)  
 <223> FRXA02162

<400> 341

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Met Ser Arg Leu Ala
1 5

gaa gaa atc atc gca tgg tgc acc cca gaa ttt ggt tac atc acc ttg 163
Glu Glu Ile Ile Ala Trp Cys Thr Pro Glu Phe Gly Tyr Ile Thr Leu
10 15 20

tct gat tcc tgg tcc aca ggc agc tca atc atg ccg cag aag aag aac 211
Ser Asp Ser Trp Ser Thr Gly Ser Ser Ile Met Pro Gln Lys Lys Asn
25 30 35

cct gac gtg gca gag ctg acc cgt ggc aag tct ggt cgc ttg atc ggt 259
Pro Asp Val Ala Glu Leu Thr Arg Gly Lys Ser Gly Arg Leu Ile Gly
40 45 50

aac ctc acc ggt ctg ctg gct acc ctg aag gca cag cct tta gcg tac 307
Asn Leu Thr Gly Leu Leu Ala Thr Leu Lys Ala Gln Pro Leu Ala Tyr
55 60 65

aac cgc gac ctg cag gaa gat aag gaa cca atc gta gat tcc gtg gcg 355
Asn Arg Asp Leu Gln Glu Asp Lys Glu Pro Ile Val Asp Ser Val Ala
70 75 80 85

cag ctc aac ctg ctg ctc cct gca atg act ggt ttg gtt tcc acc ttg 403
Gln Leu Asn Leu Leu Leu Pro Ala Met Thr Gly Leu Val Ser Thr Leu
90 95 100

acc ttc aac acc gag cgc atg cgt gaa ctt gca cca gca ggt ttc acc 451
Thr Phe Asn Thr Glu Arg Met Arg Glu Leu Ala Pro Ala Gly Phe Thr
105 110 115

ctt gcc acc gac ttg gct gag tgg atg gtg cgc cag ggc gtt cca ttc 499
Leu Ala Thr Asp Leu Ala Glu Trp Met Val Arg Gln Gly Val Pro Phe
120 125 130

cgt gag gca cac gaa gca tcc ggc gct tgc gtg cgg atc gcg gag tcc 547
Arg Glu Ala His Glu Ala Ser Gly Ala Cys Val Arg Ile Ala Glu Ser
135 140 145

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Arg Gly Val Asp Leu Ile Asp Leu Thr Asp Glu Glu Leu Ser Gly Val
150 155 160 165

gat gca cgt ctg acc cca gag gta cgg gaa gtg ctc acc att gat ggt 643
Asp Ala Arg Leu Thr Pro Glu Val Arg Glu Val Leu Thr Ile Asp Gly
170 175 180
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 Ala Val Ala Ser Arg Ala Thr Arg Gly Gly Thr Ala Gly Val Arg Val  
                   185                                  190                                  195

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 Ala Glu Gln Arg Ala Arg Val Asp Ala Ala Ser Thr Ala His Ala Glu  
                   200                                  205                                  210

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<212> PRT

<213> Corynebacterium glutamicum

<400> 342

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Gly Tyr Ile Thr Leu Ser Asp Ser Trp Ser Thr Gly Ser Ser Ile Met  
                   20                                  25                                  30

Pro Gln Lys Lys Asn Pro Asp Val Ala Glu Leu Thr Arg Gly Lys Ser  
                   35                                  40                                  45

Gly Arg Leu Ile Gly Asn Leu Thr Gly Leu Leu Ala Thr Leu Lys Ala  
                   50                                  55                                  60

Gln Pro Leu Ala Tyr Asn Arg Asp Leu Gln Glu Asp Lys Glu Pro Ile  
                   65                                  70                                  75                                  80

Val Asp Ser Val Ala Gln Leu Asn Leu Leu Leu Pro Ala Met Thr Gly  
                   85                                  90                                  95

Leu Val Ser Thr Leu Thr Phe Asn Thr Glu Arg Met Arg Glu Leu Ala  
                   100                                  105                                  110

Pro Ala Gly Phe Thr Leu Ala Thr Asp Leu Ala Glu Trp Met Val Arg  
                   115                                  120                                  125

Gln Gly Val Pro Phe Arg Glu Ala His Glu Ala Ser Gly Ala Cys Val  
                   130                                  135                                  140

Arg Ile Ala Glu Ser Arg Gly Val Asp Leu Ile Asp Leu Thr Asp Glu  
                   145                                  150                                  155                                  160

Glu Leu Ser Gly Val Asp Ala Arg Leu Thr Pro Glu Val Arg Glu Val  
                   165                                  170                                  175

Leu Thr Ile Asp Gly Ala Val Ala Ser Arg Ala Thr Arg Gly Gly Thr  
                   180                                  185                                  190

Ala Gly Val Arg Val Ala Glu Gln Arg Ala Arg Val Asp Ala Ala Ser  
                   195                                  200                                  205

Thr Ala His Ala Glu Trp Ala Arg Ala Gly Val Arg Arg  
                   210                                  215                                  220



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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1246)  
 <223> RXA02262

<400> 343

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Met Thr Ala Thr Tyr
1 5

acc act gaa acc gcc atc aat ttc ttg ttc ttg agc gaa ccg gac atg 163
Thr Thr Glu Thr Ala Ile Asn Phe Leu Phe Leu Ser Glu Pro Asp Met
10 15 20

atc gcg gcc gga gtc aaa gac gtc gcg caa tgc gtc gat gtc atg gag 211
Ile Ala Ala Gly Val Lys Asp Val Ala Gln Cys Val Asp Val Met Glu
25 30 35

gaa acg ctc gtg ctc ttg gcg cag ggc gac tac aaa atg gcc ggt ttg 259
Glu Thr Leu Val Leu Leu Ala Gln Gly Asp Tyr Lys Met Ala Gly Leu
40 45 50

aac tcc aac tcg cat ggc gcg atg atc acc ttc ccg gaa aac cca gaa 307
Asn Ser Asn Ser His Gly Ala Met Ile Thr Phe Pro Glu Asn Pro Glu
55 60 65

ttt gaa ggc atg ccc aag gac ggc ccc gac cgc cga ttc atg gcg atg 355
Phe Glu Gly Met Pro Lys Asp Gly Pro Asp Arg Arg Phe Met Ala Met
70 75 80 85

ccc gca tac ctc ggc ggg cga ttc aaa aac acc ggc gtg aag tgg tac 403
Pro Ala Tyr Leu Gly Gly Arg Phe Lys Asn Thr Gly Val Lys Trp Tyr
90 95 100

gga tcc aac gcg gaa aac aag gcc tca ggc ttg cct cgc tcg atc cac 451
Gly Ser Asn Ala Glu Asn Lys Ala Ser Gly Leu Pro Arg Ser Ile His
105 110 115

acc ttc gtc ctc aac gac acg gtc acc ggt gca ccg aag gcc atc atg 499
Thr Phe Val Leu Asn Asp Thr Val Thr Gly Ala Pro Lys Ala Ile Met
120 125 130

tcc gcg aac ctg ctg tcc gcc tac cgc acc ggc gcg gtt ccc ggc gtg 547
Ser Ala Asn Leu Leu Ser Ala Tyr Arg Thr Gly Ala Val Pro Gly Val
135 140 145

ggc gtg aag cac tta gcg gtc gcc gac gcg aca acc ttg gct gtc gtc 595
Gly Val Lys His Leu Ala Val Ala Asp Ala Thr Thr Leu Ala Val Val
150 155 160 165

gga cct ggt gtc atg gcg aaa acc atc acc gaa gcg tgc atc gca gag 643
Gly Pro Gly Val Met Ala Lys Thr Ile Thr Glu Ala Cys Ile Ala Glu
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170								175				180				
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Arg Pro Gly Ile Thr Thr Ile Lys Ile Lys Gly Arg Ser Glu Arg Gly																
185 190 195																
atc aac gcc ttt gca aca tgg gcg ttg gaa aaa ttc ccc gag atc gaa	739															
Ile Asn Ala Phe Ala Thr Trp Ala Leu Glu Lys Phe Pro Glu Ile Glu																
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Val Val Ala Val Gly Ser Glu Glu Asp Val Val Lys Asp Ala Asp Ile																
215 220 225																
gtc atc gcc gcc acc acc acg gac gcc gcc ggc tcc tcc gcc ttc cca	835															
Val Ile Ala Ala Thr Thr Thr Asp Ala Ala Gly Ser Ser Ala Phe Pro																
230 235 240 245																
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Tyr Phe Lys Lys Glu Trp Leu Lys Pro Gly Ala Leu Leu Leu Leu Pro																
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265 270 275																
gtt gtt gac tac atg ggg ctc tac gaa gcc tgg gca gaa gaa tac ggc	979															
Val Val Asp Tyr Met Gly Leu Tyr Glu Ala Trp Ala Glu Glu Tyr Gly																
280 285 290																
cca cag gcc tac caa cta ctc ggc att cca gga acc cac tgg tac gac																
1027																
Pro Gln Ala Tyr Gln Leu Leu Gly Ile Pro Gly Thr His Trp Tyr Asp																
295 300 305																
ctg gcg ctg caa gga aaa ctc gac ctt gca aag att tcc cag att ggc																
1075																
Leu Ala Leu Gln Gly Lys Leu Asp Leu Ala Lys Ile Ser Gln Ile Gly																
310 315 320 325																
gat atc tgc tcc ggc aag cta ccc gga cgc acc aac gat gag gaa atc																
1123																
Asp Ile Cys Ser Gly Lys Leu Pro Gly Arg Thr Asn Asp Glu Glu Ile																
330 335 340																
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1171																
Ile Leu Tyr Ser Val Gly Gly Met Pro Val Glu Asp Val Ala Trp Ala																
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1219																
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360 365 370																
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375 380																

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1269

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<400> 344

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Val	Asp	Val	Met	Glu	Glu	Thr	Leu	Val	Leu	Leu	Ala	Gln	Gly	Asp	Tyr
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Lys	Met	Ala	Gly	Leu	Asn	Ser	Asn	Ser	His	Gly	Ala	Met	Ile	Thr	Phe
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Pro	Glu	Asn	Pro	Glu	Phe	Glu	Gly	Met	Pro	Lys	Asp	Gly	Pro	Asp	Arg
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Arg	Phe	Met	Ala	Met	Pro	Ala	Tyr	Leu	Gly	Gly	Arg	Phe	Lys	Asn	Thr
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Gly	Val	Lys	Trp	Tyr	Gly	Ser	Asn	Ala	Glu	Asn	Lys	Ala	Ser	Gly	Leu
			100					105					110		
Pro	Arg	Ser	Ile	His	Thr	Phe	Val	Leu	Asn	Asp	Thr	Val	Thr	Gly	Ala
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Pro	Lys	Ala	Ile	Met	Ser	Ala	Asn	Leu	Leu	Ser	Ala	Tyr	Arg	Thr	Gly
	130					135					140				
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Thr	Leu	Ala	Val	Val	Gly	Pro	Gly	Val	Met	Ala	Lys	Thr	Ile	Thr	Glu
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			180					185					190		
Arg	Ser	Glu	Arg	Gly	Ile	Asn	Ala	Phe	Ala	Thr	Trp	Ala	Leu	Glu	Lys
		195					200					205			
Phe	Pro	Glu	Ile	Glu	Val	Val	Ala	Val	Gly	Ser	Glu	Glu	Asp	Val	Val
	210					215					220				
Lys	Asp	Ala	Asp	Ile	Val	Ile	Ala	Ala	Thr	Thr	Thr	Asp	Ala	Ala	Gly
	225				230					235					240
Ser	Ser	Ala	Phe	Pro	Tyr	Phe	Lys	Lys	Glu	Trp	Leu	Lys	Pro	Gly	Ala
				245					250					255	
Leu	Leu	Leu	Leu	Pro	Ala	Ala	Gly	Arg	Phe	Asp	Asp	Ala	Tyr	Leu	Leu
			260					265					270		

Asp Asp Ala Arg Leu Val Val Asp Tyr Met Gly Leu Tyr Glu Ala Trp  
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 Ala Glu Glu Tyr Gly Pro Gln Ala Tyr Gln Leu Leu Gly Ile Pro Gly  
 290 295 300  
 Thr His Trp Tyr Asp Leu Ala Leu Gln Gly Lys Leu Asp Leu Ala Lys  
 305 310 315 320  
 Ile Ser Gln Ile Gly Asp Ile Cys Ser Gly Lys Leu Pro Gly Arg Thr  
 325 330 335  
 Asn Asp Glu Glu Ile Ile Leu Tyr Ser Val Gly Gly Met Pro Val Glu  
 340 345 350  
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 Val Gly Thr Thr Leu Asn Leu Trp Glu Ser Pro Ala Leu Ala  
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&lt;210&gt; 345

&lt;211&gt; 1065

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1042)

&lt;223&gt; RXA00219

&lt;400&gt; 345

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 Val Ala Arg Lys Lys  
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 Asn Thr Ser Asp Gln Ser Arg Ser Gln Ala Ala Asn Thr Pro Ile Ala  
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 Gly Thr Tyr Glu Gly Glu Tyr Ser Val Ile Glu Leu Glu Ala Asp Ser  
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 Tyr Thr Thr Asp Gly Trp Leu Ile Ser Ile Asn Gly Val Pro Ser Ser  
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 cat att gtc ctg ggg caa ccg cag gca ctg gaa ttt gag tac atg cgg 307  
 His Ile Val Leu Gly Gln Pro Gln Ala Leu Glu Phe Glu Tyr Met Arg  
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 Trp Ile Ala Thr Gly Ala Arg Ala Phe Ile Asp Ala His Gln Asp Ala  
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Arg	Tyr	Phe	Ala	Asp	Val	Tyr	Pro	Gln	Ser	Arg	Asn	Thr	Val	Val	Glu			
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Leu	Asp	Ala	Glu	Leu	Ala	Arg	Leu	Ser	Arg	Glu	Trp	Phe	Asp	Ile	Pro			
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cgc	gcg	cca	cgg	gta	aag	att	cgt	gtg	gat	gat	gcc	cga	atg	gtg	gca	547		
Arg	Ala	Pro	Arg	Val	Lys	Ile	Arg	Val	Asp	Asp	Ala	Arg	Met	Val	Ala			
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gaa	tct	ttc	act	ccc	gca	agc	cgc	gat	gtg	atc	atc	cgt	gac	gtt	ttt	595		
Glu	Ser	Phe	Thr	Pro	Ala	Ser	Arg	Asp	Val	Ile	Ile	Arg	Asp	Val	Phe			
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Ala	Gly	Ala	Ile	Thr	Pro	Gln	Asn	Phe	Thr	Thr	Val	Glu	Phe	Phe	Glu			
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cac	tgt	cac	cgt	ggc	ctt	gct	ccc	ggc	gga	ttg	tac	gtt	gcc	aac	tgt	691		
His	Cys	His	Arg	Gly	Leu	Ala	Pro	Gly	Gly	Leu	Tyr	Val	Ala	Asn	Cys			
			185					190					195					
ggc	gat	cat	tcg	gat	ctg	cgc	gga	gct	aaa	tct	gag	ctc	gcg	gga	atg	739		
Gly	Asp	His	Ser	Asp	Leu	Arg	Gly	Ala	Lys	Ser	Glu	Leu	Ala	Gly	Met			
		200					205					210						
atg	gag	gtg	ttc	gag	cac	gtc	gcg	gtc	atc	gcc	gat	ccc	ccg	atg	ctt	787		
Met	Glu	Val	Phe	Glu	His	Val	Ala	Val	Ile	Ala	Asp	Pro	Pro	Met	Leu			
	215					220					225							
aaa	ggg	cgc	cgt	tac	ggc	aac	atc	att	ttg	atg	ggg	tca	gac	acc	gag	835		
Lys	Gly	Arg	Arg	Tyr	Gly	Asn	Ile	Ile	Leu	Met	Gly	Ser	Asp	Thr	Glu			
230					235				240						245			
ttc	ttt	agc	tcc	aac	agc	acg	gaa	gcg	tcc	gcg	att	acc	cgt	gag	ctt	883		
Phe	Phe	Ser	Ser	Asn	Ser	Thr	Glu	Ala	Ser	Ala	Ile	Thr	Arg	Glu	Leu			
				250					255					260				
ctt	ggc	ggc	ggc	gtt	cca	gcg	cag	tac	aag	gat	gaa	tcc	tgg	gtg	cgg	931		
Leu	Gly	Gly	Gly	Val	Pro	Ala	Gln	Tyr	Lys	Asp	Glu	Ser	Trp	Val	Arg			
			265					270					275					
aaa	ttc	gcc	tcg	gga	gcc	cag	gcc	cgc	cac	gat	ggg	gtc	tct	acc	ctc	979		
Lys	Phe	Ala	Ser	Gly	Ala	Gln	Ala	Arg	His	Asp	Gly	Val	Ser	Thr	Leu			
		280					285					290						
caa	atg	ccg	agt	gat	act	cca	caa	cac	cct	gcg	gaa	acg	ccg	gag	cat			
1027																		
Gln	Met	Pro	Ser	Asp	Thr	Pro	Gln	His	Pro	Ala	Glu	Thr	Pro	Glu	His			
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Ser	Asn	Thr	Gln	Pro														
310																		

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 <211> 314  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 346

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Leu	Glu	Ala	Asp	Ser	Tyr	Thr	Thr	Asp	Gly	Trp	Leu	Ile	Ser	Ile	Asn
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Gly	Val	Pro	Ser	Ser	His	Ile	Val	Leu	Gly	Gln	Pro	Gln	Ala	Leu	Glu
	50					55					60				
Phe	Glu	Tyr	Met	Arg	Trp	Ile	Ala	Thr	Gly	Ala	Arg	Ala	Phe	Ile	Asp
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Ala	His	Gln	Asp	Ala	Ser	Lys	Leu	Arg	Ile	Thr	His	Leu	Gly	Gly	Gly
				85					90					95	
Ala	Cys	Thr	Met	Ala	Arg	Tyr	Phe	Ala	Asp	Val	Tyr	Pro	Gln	Ser	Arg
			100					105					110		
Asn	Thr	Val	Val	Glu	Leu	Asp	Ala	Glu	Leu	Ala	Arg	Leu	Ser	Arg	Glu
		115					120					125			
Trp	Phe	Asp	Ile	Pro	Arg	Ala	Pro	Arg	Val	Lys	Ile	Arg	Val	Asp	Asp
	130					135					140				
Ala	Arg	Met	Val	Ala	Glu	Ser	Phe	Thr	Pro	Ala	Ser	Arg	Asp	Val	Ile
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Ile	Arg	Asp	Val	Phe	Ala	Gly	Ala	Ile	Thr	Pro	Gln	Asn	Phe	Thr	Thr
				165					170					175	
Val	Glu	Phe	Phe	Glu	His	Cys	His	Arg	Gly	Leu	Ala	Pro	Gly	Gly	Leu
			180					185					190		
Tyr	Val	Ala	Asn	Cys	Gly	Asp	His	Ser	Asp	Leu	Arg	Gly	Ala	Lys	Ser
		195					200					205			
Glu	Leu	Ala	Gly	Met	Met	Glu	Val	Phe	Glu	His	Val	Ala	Val	Ile	Ala
	210					215					220				
Asp	Pro	Pro	Met	Leu	Lys	Gly	Arg	Arg	Tyr	Gly	Asn	Ile	Ile	Leu	Met
225					230					235					240
Gly	Ser	Asp	Thr	Glu	Phe	Phe	Ser	Ser	Asn	Ser	Thr	Glu	Ala	Ser	Ala
				245					250					255	
Ile	Thr	Arg	Glu	Leu	Leu	Gly	Gly	Gly	Val	Pro	Ala	Gln	Tyr	Lys	Asp
			260				265						270		
Glu	Ser	Trp	Val	Arg	Lys	Phe	Ala	Ser	Gly	Ala	Gln	Ala	Arg	His	Asp
		275					280					285			
Gly	Val	Ser	Thr	Leu	Gln	Met	Pro	Ser	Asp	Thr	Pro	Gln	His	Pro	Ala

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<223> RXA01508

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Met Ser Asp Leu Gly  
1 5  
ccc atc tgg cgc tgg ctg tta tta gtt tcc gtc tcc att tgt gcg gca 163  
Pro Ile Trp Arg Trp Leu Leu Leu Val Ser Val Ser Ile Cys Ala Ala  
10 15 20  
tcg ggg ctg gtc tat gag cta gcc ctg gta tcc ctt tcc acc agc ttg 211  
Ser Gly Leu Val Tyr Glu Leu Ala Leu Val Ser Leu Ser Thr Ser Leu  
25 30 35  
aac ggt ggc gga att gta gaa acc tcc ctc atc gtc gca ggt tat gta 259  
Asn Gly Gly Gly Ile Val Glu Thr Ser Leu Ile Val Ala Gly Tyr Val  
40 45 50  
gct gcc ctt gga ctt ggt gca ctg ctg gtc aag ccg ttt ctc aac tgg 307  
Ala Ala Leu Gly Leu Gly Ala Leu Leu Val Lys Pro Phe Leu Asn Trp  
55 60 65  
cct gcg caa acc ttc ctc ggt gtg gaa acc ctc ctt gga ctt att ggt 355  
Pro Ala Gln Thr Phe Leu Gly Val Glu Thr Leu Leu Gly Leu Ile Gly  
70 75 80 85  
ggt tgt tcc gcg ctg gtg ctg tat ttc acc ttc gcg acc atc ggc caa 403  
Gly Cys Ser Ala Leu Val Leu Tyr Phe Thr Phe Ala Thr Ile Gly Gln  
90 95 100  
tcc ctg tgg att ctg gtg att gcc acc gct gca att ggc atc ctg gtc 451  
Ser Leu Trp Ile Leu Val Ile Ala Thr Ala Ala Ile Gly Ile Leu Val  
105 110 115  
ggc gct gaa ctt cca ctg ctg atg acc atg atc cag caa ggc cgc ctc 499  
Gly Ala Glu Leu Pro Leu Leu Met Thr Met Ile Gln Gln Gly Arg Leu  
120 125 130  
gcc gac gcc aaa acc aca gga tct ctg gtt gcc acc ttg aat gct gct 547  
Ala Asp Ala Lys Thr Thr Gly Ser Leu Val Ala Thr Leu Asn Ala Ala  
135 140 145  
gat tac ctt ggc gca ctt tta ggt ggc ctg gcc tgg cct ttt gtg ttg 595  
Asp Tyr Leu Gly Ala Leu Leu Gly Gly Leu Ala Trp Pro Phe Val Leu

150	155	160	165	
ctg ccg tgg ctt ggc atg atg cgc ggt gcc gca gca gcc gga atg atc				643
Leu Pro Trp Leu Gly Met Met Arg Gly Ala Ala Ala Gly Met Ile				
	170	175	180	
aac ctc gtt gca gca cta ttc gtg ggc tgt gtg ctg ctg cga cat ttg				691
Asn Leu Val Ala Ala Leu Phe Val Gly Cys Val Leu Leu Arg His Leu				
	185	190	195	
ctt ccg cgc acc cac ttc ttc gta tcc gtg gtg gcg ctt ctt ctc gcg				739
Leu Pro Arg Thr His Phe Phe Val Ser Val Val Ala Leu Leu Leu Ala				
	200	205	210	
atc gca gcg cta gcc acc gtg ttg gtg aaa tcc gac ggg atc gtt gcc				787
Ile Ala Ala Leu Ala Thr Val Leu Val Lys Ser Asp Gly Ile Val Ala				
	215	220	225	
acc gcc cgc gca cag ctc tac cgc gac ccc gtg atc tat tca cac caa				835
Thr Ala Arg Ala Gln Leu Tyr Arg Asp Pro Val Ile Tyr Ser His Gln				
	230	235	240	245
tct gac tac caa gac atc gta gtg aca gaa cga ggc aaa gac cga cgc				883
Ser Asp Tyr Gln Asp Ile Val Val Thr Glu Arg Gly Lys Asp Arg Arg				
	250	255	260	
ctc tac ctc aat ggc ggt ttg cag tat tcc act cgt gac cag cat aga				931
Leu Tyr Leu Asn Gly Gly Leu Gln Tyr Ser Thr Arg Asp Gln His Arg				
	265	270	275	
tat aca gaa tca ctg gtg tat cca agc ctt aat cca gag gca gaa tcg				979
Tyr Thr Glu Ser Leu Val Tyr Pro Ser Leu Asn Pro Glu Ala Glu Ser				
	280	285	290	
gtg tta atc atc ggc ggt ggc gat ggc ctc gca gca cgg gaa ctc ctc				
1027				
Val Leu Ile Ile Gly Gly Gly Asp Gly Leu Ala Ala Arg Glu Leu Leu				
	295	300	305	
cga ttc cca tca atg cag atc acc caa gtt gaa tta gac cca gaa gtc				
1075				
Arg Phe Pro Ser Met Gln Ile Thr Gln Val Glu Leu Asp Pro Glu Val				
	310	315	320	325
atc gaa gta gcc aac aca gtg ctg cgc tct gac aat ggg gga gcg atg				
1123				
Ile Glu Val Ala Asn Thr Val Leu Arg Ser Asp Asn Gly Gly Ala Met				
	330	335	340	
gaa gat ccc cgc gtc tcc atc atc gtt gac gac gct ttc acc tgg ctg				
1171				
Glu Asp Pro Arg Val Ser Ile Ile Val Asp Asp Ala Phe Thr Trp Leu				
	345	350	355	
cgc tcc ggc gga aat aat ggc gaa act tac gat tcc atc atc atc gat				
1219				
Arg Ser Gly Gly Asn Asn Gly Glu Thr Tyr Asp Ser Ile Ile Ile Asp				
	360	365	370	
ctt ccc gac cca aac aac gac acc atg gcc agg ctg tat tca gaa gag				
1267				



Leu Pro Asp Pro Asn Asn Asp Thr Met Ala Arg Leu Tyr Ser Glu Glu  
 375 380 385  
 ttc tac acc ttg gcc cga gca cga ctg aac gaa caa ggc cgc atg gtg  
 1315  
 Phe Tyr Thr Leu Ala Arg Ala Arg Leu Asn Glu Gln Gly Arg Met Val  
 390 395 400 405  
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 1363  
 Val Gln Ser Ser Ser Ala Tyr Thr Thr Pro Asp Val Phe Trp Arg Val  
 410 415 420  
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 1411  
 Gly Ala Thr Leu Lys Ser Ala Gly Cys Glu Gln Val Ile Pro Tyr His  
 425 430 435  
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 1459  
 Val His Val Pro Thr Phe Gly Asp Trp Gly Phe Gln Leu Cys Gly Pro  
 440 445 450  
 gcc gac atg gaa tta gag ctt cgg gaa gac acc ccg cca ctg act ttc  
 1507  
 Ala Asp Met Glu Leu Glu Leu Arg Glu Asp Thr Pro Pro Leu Thr Phe  
 455 460 465  
 ctt aat gat gaa gtt ctg gtg gct gct ggg gtg ttt ggg ttg gat aat  
 1555  
 Leu Asn Asp Glu Val Leu Val Ala Ala Gly Val Phe Gly Leu Asp Asn  
 470 475 480 485  
 cag cct cgt gaa ttg gaa cct tcc acg ctg gat cat ccc cgc gtg gtg  
 1603  
 Gln Pro Arg Glu Leu Glu Pro Ser Thr Leu Asp His Pro Arg Val Val  
 490 495 500  
 gag gat ctg cgc aag gga tac cgc gaa tca ggc gac tagctgcaac  
 1649  
 Glu Asp Leu Arg Lys Gly Tyr Arg Glu Ser Gly Asp  
 505 510  
 gatgcgctgt gtg  
 1662

&lt;210&gt; 348

&lt;211&gt; 513

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 348

Met Ser Asp Leu Gly Pro Ile Trp Arg Trp Leu Leu Leu Val Ser Val  
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Ser Ile Cys Ala Ala Ser Gly Leu Val Tyr Glu Leu Ala Leu Val Ser  
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Leu Ser Thr Ser Leu Asn Gly Gly Gly Ile Val Glu Thr Ser Leu Ile  
 35 40 45

Val	Ala	Gly	Tyr	Val	Ala	Ala	Leu	Gly	Leu	Gly	Ala	Leu	Leu	Val	Lys
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Pro	Phe	Leu	Asn	Trp	Pro	Ala	Gln	Thr	Phe	Leu	Gly	Val	Glu	Thr	Leu
65					70					75					80
Leu	Gly	Leu	Ile	Gly	Gly	Cys	Ser	Ala	Leu	Val	Leu	Tyr	Phe	Thr	Phe
				85					90					95	
Ala	Thr	Ile	Gly	Gln	Ser	Leu	Trp	Ile	Leu	Val	Ile	Ala	Thr	Ala	Ala
			100					105					110		
Ile	Gly	Ile	Leu	Val	Gly	Ala	Glu	Leu	Pro	Leu	Leu	Met	Thr	Met	Ile
	115						120					125			
Gln	Gln	Gly	Arg	Leu	Ala	Asp	Ala	Lys	Thr	Thr	Gly	Ser	Leu	Val	Ala
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Thr	Leu	Asn	Ala	Ala	Asp	Tyr	Leu	Gly	Ala	Leu	Leu	Gly	Gly	Leu	Ala
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Trp	Pro	Phe	Val	Leu	Leu	Pro	Trp	Leu	Gly	Met	Met	Arg	Gly	Ala	Ala
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Ala	Ala	Gly	Met	Ile	Asn	Leu	Val	Ala	Ala	Leu	Phe	Val	Gly	Cys	Val
			180					185					190		
Leu	Leu	Arg	His	Leu	Leu	Pro	Arg	Thr	His	Phe	Phe	Val	Ser	Val	Val
		195					200					205			
Ala	Leu	Leu	Leu	Ala	Ile	Ala	Ala	Leu	Ala	Thr	Val	Leu	Val	Lys	Ser
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Asp	Gly	Ile	Val	Ala	Thr	Ala	Arg	Ala	Gln	Leu	Tyr	Arg	Asp	Pro	Val
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Ile	Tyr	Ser	His	Gln	Ser	Asp	Tyr	Gln	Asp	Ile	Val	Val	Thr	Glu	Arg
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Gly	Lys	Asp	Arg	Arg	Leu	Tyr	Leu	Asn	Gly	Gly	Leu	Gln	Tyr	Ser	Thr
			260					265					270		
Arg	Asp	Gln	His	Arg	Tyr	Thr	Glu	Ser	Leu	Val	Tyr	Pro	Ser	Leu	Asn
		275					280					285			
Pro	Glu	Ala	Glu	Ser	Val	Leu	Ile	Ile	Gly	Gly	Gly	Asp	Gly	Leu	Ala
	290					295					300				
Ala	Arg	Glu	Leu	Leu	Arg	Phe	Pro	Ser	Met	Gln	Ile	Thr	Gln	Val	Glu
305					310					315					320
Leu	Asp	Pro	Glu	Val	Ile	Glu	Val	Ala	Asn	Thr	Val	Leu	Arg	Ser	Asp
				325					330					335	
Asn	Gly	Gly	Ala	Met	Glu	Asp	Pro	Arg	Val	Ser	Ile	Ile	Val	Asp	Asp
			340					345					350		
Ala	Phe	Thr	Trp	Leu	Arg	Ser	Gly	Gly	Asn	Asn	Gly	Glu	Thr	Tyr	Asp
			355				360					365			

Ser Ile Ile Ile Asp Leu Pro Asp Pro Asn Asn Asp Thr Met Ala Arg  
 370 375 380

Leu Tyr Ser Glu Glu Phe Tyr Thr Leu Ala Arg Ala Arg Leu Asn Glu  
 385 390 395 400

Gln Gly Arg Met Val Val Gln Ser Ser Ser Ala Tyr Thr Thr Pro Asp  
 405 410 415

Val Phe Trp Arg Val Gly Ala Thr Leu Lys Ser Ala Gly Cys Glu Gln  
 420 425 430

Val Ile Pro Tyr His Val His Val Pro Thr Phe Gly Asp Trp Gly Phe  
 435 440 445

Gln Leu Cys Gly Pro Ala Asp Met Glu Leu Glu Leu Arg Glu Asp Thr  
 450 455 460

Pro Pro Leu Thr Phe Leu Asn Asp Glu Val Leu Val Ala Ala Gly Val  
 465 470 475 480

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His Pro Arg Val Val Glu Asp Leu Arg Lys Gly Tyr Arg Glu Ser Gly  
 500 505 510

Asp

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<220>  
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 <223> RXA01757

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 Met Pro Thr Ala Ser  
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cca att tat gat gtc gtt gtc gtc gga gcc ggc att tct ggc ctc atc 163  
 Pro Ile Tyr Asp Val Val Val Val Gly Ala Gly Ile Ser Gly Leu Ile  
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gcc acg caa ctg ttg gac cgc gca ggt cta aac atc aaa tgc ttc gaa 211  
 Ala Thr Gln Leu Leu Asp Arg Ala Gly Leu Asn Ile Lys Cys Phe Glu  
 25 30 35

gcc tgc tca aga gtt ggc ggc cga gca gtg tct gtc caa cag tcc gat 259  
 Ala Cys Ser Arg Val Gly Gly Arg Ala Val Ser Val Gln Gln Ser Asp  
 40 45 50

ttg ttc ctg gac ctc ggc gca aca tgg ttc tgg ctc aac gaa cca ctt 307

Leu	Phe	Leu	Asp	Leu	Gly	Ala	Thr	Trp	Phe	Trp	Leu	Asn	Glu	Pro	Leu	
55						60					65					
gtg	cag	caa	ctc	gtc	aat	aat	ctc	ggc	ctc	ggc	aca	ttc	cct	cag	gcc	355
Val	Gln	Gln	Leu	Val	Asn	Asn	Leu	Gly	Leu	Gly	Thr	Phe	Pro	Gln	Ala	
70					75					80					85	
atc	gag	ggt	gat	gcg	ctt	ttt	gag	acg	ctt	gtc	gac	gcc	ccg	agc	cgc	403
Ile	Glu	Gly	Asp	Ala	Leu	Phe	Glu	Thr	Leu	Val	Asp	Ala	Pro	Ser	Arg	
				90					95					100		
ctg	cgg	ggt	aac	ccc	ata	gac	gct	gct	tca	ggc	agg	ttc	caa	gca	ggg	451
Leu	Arg	Gly	Asn	Pro	Ile	Asp	Ala	Ala	Ser	Gly	Arg	Phe	Gln	Ala	Gly	
			105					110					115			
gcc	tcc	tcg	ctt	gcg	ctc	ggg	ctt	gca	gcc	cag	ctc	aag	cca	gga	gtt	499
Ala	Ser	Ser	Leu	Ala	Leu	Gly	Leu	Ala	Ala	Gln	Leu	Lys	Pro	Gly	Val	
		120					125					130				
tta	gaa	ctc	ggg	gac	ccc	gtc	cat	tct	ctc	agt	gag	gaa	gat	ggg	gaa	547
Leu	Glu	Leu	Gly	Asp	Pro	Val	His	Ser	Leu	Ser	Glu	Glu	Asp	Gly	Glu	
	135					140					145					
atc	gtt	gtg	aag	tct	tcc	aaa	cag	att	gtg	agg	gca	aag	cac	gtc	atc	595
Ile	Val	Val	Lys	Ser	Ser	Lys	Gln	Ile	Val	Arg	Ala	Lys	His	Val	Ile	
150						155				160					165	
att	gcg	gtt	cca	ccg	gca	ctc	gct	gcc	gag	ttg	att	ggt	ttc	acc	cta	643
Ile	Ala	Val	Pro	Pro	Ala	Leu	Ala	Ala	Glu	Leu	Ile	Gly	Phe	Thr	Leu	
				170					175					180		
gat	tta	cca	gct	gac	gtg	cga	aaa	gca	gcg	cat	cca	caa	cat	ata	gct	691
Asp	Leu	Pro	Ala	Asp	Val	Arg	Lys	Ala	Ala	His	Pro	Gln	His	Ile	Ala	
			185					190					195			
gtg	atg	aat	tgg	gca	aag	gag	aaa	tac	acc	tta	ccc	aca	caa	gcc	gca	739
Val	Met	Asn	Trp	Ala	Lys	Glu	Lys	Tyr	Thr	Leu	Pro	Thr	Gln	Ala	Ala	
		200					205					210				
tcg	gct	ggg	ggt	ttt	ggg	cat	gag	ctg	ttc	caa	caa	cca	ctc	gga	cat	787
Ser	Ala	Gly	Gly	Phe	Gly	His	Glu	Leu	Phe	Gln	Gln	Pro	Leu	Gly	His	
	215					220					225					
ggg	cga	att	cat	tgg	gca	tca	acg	gaa	gtt	gcc	act	gag	ttt	ggt	gga	835
Gly	Arg	Ile	His	Trp	Ala	Ser	Thr	Glu	Val	Ala	Thr	Glu	Phe	Gly	Gly	
230					235					240				245		
cac	ctt	gaa	ggc	gca	gtt	cgt	gca	gga	att	cag	gct	gcg	ctt	caa	aca	883
His	Leu	Glu	Gly	Ala	Val	Arg	Ala	Gly	Ile	Gln	Ala	Ala	Leu	Gln	Thr	
				250					255					260		
gga	ttt	aat	cta	aaa	tct	taaacctcgt attttccctg ata										924
Gly	Phe	Asn	Leu	Lys	Ser											
			265													

&lt;210&gt; 350

&lt;211&gt; 267

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 350

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Met Pro Thr Ala Ser Pro Ile Tyr Asp Val Val Val Val Gly Ala Gly
 1           5           10           15

Ile Ser Gly Leu Ile Ala Thr Gln Leu Leu Asp Arg Ala Gly Leu Asn
      20           25           30

Ile Lys Cys Phe Glu Ala Cys Ser Arg Val Gly Gly Arg Ala Val Ser
      35           40           45

Val Gln Gln Ser Asp Leu Phe Leu Asp Leu Gly Ala Thr Trp Phe Trp
      50           55           60

Leu Asn Glu Pro Leu Val Gln Gln Leu Val Asn Asn Leu Gly Leu Gly
      65           70           75           80

Thr Phe Pro Gln Ala Ile Glu Gly Asp Ala Leu Phe Glu Thr Leu Val
      85           90           95

Asp Ala Pro Ser Arg Leu Arg Gly Asn Pro Ile Asp Ala Ala Ser Gly
      100          105          110

Arg Phe Gln Ala Gly Ala Ser Ser Leu Ala Leu Gly Leu Ala Ala Gln
      115          120          125

Leu Lys Pro Gly Val Leu Glu Leu Gly Asp Pro Val His Ser Leu Ser
      130          135          140

Glu Glu Asp Gly Glu Ile Val Val Lys Ser Ser Lys Gln Ile Val Arg
      145          150          155          160

Ala Lys His Val Ile Ile Ala Val Pro Pro Ala Leu Ala Ala Glu Leu
      165          170          175

Ile Gly Phe Thr Leu Asp Leu Pro Ala Asp Val Arg Lys Ala Ala His
      180          185          190

Pro Gln His Ile Ala Val Met Asn Trp Ala Lys Glu Lys Tyr Thr Leu
      195          200          205

Pro Thr Gln Ala Ala Ser Ala Gly Gly Phe Gly His Glu Leu Phe Gln
      210          215          220

Gln Pro Leu Gly His Gly Arg Ile His Trp Ala Ser Thr Glu Val Ala
      225          230          235          240

Thr Glu Phe Gly Gly His Leu Glu Gly Ala Val Arg Ala Gly Ile Gln
      245          250          255

Ala Ala Leu Gln Thr Gly Phe Asn Leu Lys Ser
      260          265

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&lt;210&gt; 351

&lt;211&gt; 636

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(613)

&lt;223&gt; RXA02159

&lt;400&gt; 351

tgatggacca gcgtccaaag ttttcgatga agcagaaaac cgcctccacg ctcagaaagc 60

actgctggtg tggctgctgg ccaaccagcc gaggtaagac atg tcc ctt ggc tca 115  
 Met Ser Leu Gly Ser  
 1 5

acc ccg tca aca ccg gaa aac tta aat ccc gtg act cgc act gca cgc 163  
 Thr Pro Ser Thr Pro Glu Asn Leu Asn Pro Val Thr Arg Thr Ala Arg  
 10 15 20

caa gct ctc att ttg cag att ttg gac aaa caa aaa gtc acc agc cag 211  
 Gln Ala Leu Ile Leu Gln Ile Leu Asp Lys Gln Lys Val Thr Ser Gln  
 25 30 35

gta caa ctg tct gaa ttg ctg ctg gat gaa ggc atc gat atc acc cag 259  
 Val Gln Leu Ser Glu Leu Leu Leu Asp Glu Gly Ile Asp Ile Thr Gln  
 40 45 50

gcc acc ttg tcc cga gat ctc gat gaa ctc ggt gca cgc aag gtt cgc 307  
 Ala Thr Leu Ser Arg Asp Leu Asp Glu Leu Gly Ala Arg Lys Val Arg  
 55 60 65

ccc gat ggg gga cgc gcc tac tac gcg gtc ggc cca gta gat agc atc 355  
 Pro Asp Gly Gly Arg Ala Tyr Tyr Ala Val Gly Pro Val Asp Ser Ile  
 70 75 80 85

gcc cgc gaa gat ctc cgg ggt ccg tcg gag aag ctg cgc cgc atg ctt 403  
 Ala Arg Glu Asp Leu Arg Gly Pro Ser Glu Lys Leu Arg Arg Met Leu  
 90 95 100

gat gaa ctg ctg gtt tct aca gat cat tcc ggc aac atc gcg atg ctg 451  
 Asp Glu Leu Leu Val Ser Thr Asp His Ser Gly Asn Ile Ala Met Leu  
 105 110 115

cgc acc ccg ccg gga gct gcc cag tac ctg gca agt ttc atc gat agg 499  
 Arg Thr Pro Pro Gly Ala Ala Gln Tyr Leu Ala Ser Phe Ile Asp Arg  
 120 125 130

gtg ggg ctg aaa gaa gtc gtt ggc acc atc gct ggt gat gac acc gtt 547  
 Val Gly Leu Lys Glu Val Val Gly Thr Ile Ala Gly Asp Asp Thr Val  
 135 140 145

ttc gtt ctc gcc cgt gat ccg ctc aca ggt aaa gaa cta ggt gaa tta 595  
 Phe Val Leu Ala Arg Asp Pro Leu Thr Gly Lys Glu Leu Gly Glu Leu  
 150 155 160 165

ctc agc ggg cgc acc act taaagcgccc ctagttcaag gct 636  
 Leu Ser Gly Arg Thr Thr  
 170

&lt;210&gt; 352

&lt;211&gt; 171

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 352

Met Ser Leu Gly Ser Thr Pro Ser Thr Pro Glu Asn Leu Asn Pro Val

1	5	10	15
Thr Arg Thr	Ala Arg Gln Ala	Leu Ile Leu Gln Ile Leu	Asp Lys Gln
	20	25	30
Lys Val Thr	Ser Gln Val Gln	Leu Ser Glu Leu Leu Leu	Asp Glu Gly
	35	40	45
Ile Asp Ile	Thr Gln Ala Thr	Leu Ser Arg Asp Leu	Asp Glu Leu Gly
	50	55	60
Ala Arg Lys	Val Arg Pro Asp	Gly Gly Arg Ala Tyr Tyr	Ala Val Gly
	65	70	75
Pro Val Asp	Ser Ile Ala Arg	Glu Asp Leu Arg Gly	Pro Ser Glu Lys
	85	90	95
Leu Arg Arg	Met Leu Asp Glu	Leu Leu Val Ser Thr	Asp His Ser Gly
	100	105	110
Asn Ile Ala	Met Leu Arg Thr	Pro Pro Gly Ala Ala	Gln Tyr Leu Ala
	115	120	125
Ser Phe Ile	Asp Arg Val Gly	Leu Lys Glu Val Val	Gly Thr Ile Ala
	130	135	140
Gly Asp Asp	Thr Val Phe Val	Leu Ala Arg Asp	Pro Leu Thr Gly Lys
	145	150	155
Glu Leu Gly	Glu Leu Leu Ser	Gly Arg Thr Thr	
	165	170	

&lt;210&gt; 353

&lt;211&gt; 414

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(391)

&lt;223&gt; RXN02154

&lt;400&gt; 353

cccagaacct cggcgaagtc agcgacaagc cagtcaaggt gagcttcacc ccagtgcttg 60

caccgttacc tcgcgaattc tcaccactgc aaccgcacct ttg aaa gaa ggc gtt 115  
 Leu Lys Glu Gly Val  
 1 5

acc gca gaa cag gct cgc gca gta tat gaa gag ttc tat gca cag gaa 163  
 Thr Ala Glu Gln Ala Arg Ala Val Tyr Glu Glu Phe Tyr Ala Gln Glu  
 10 15 20

acc ttc gtg cat gtt ctt cca gaa ggt gca cag cca caa acc caa gca 211  
 Thr Phe Val His Val Leu Pro Glu Gly Ala Gln Pro Gln Thr Gln Ala  
 25 30 35

gtt ctt ggc tcc aac atg tgc cac gtg cag gta gaa att gat gag gaa 259  
 Val Leu Gly Ser Asn Met Cys His Val Gln Val Glu Ile Asp Glu Glu  
 40 45 50

gca ggc aaa gtc ctt gtt acc tcc gca atc gat aac ctc acc aag gga 307  
Ala Gly Lys Val Leu Val Thr Ser Ala Ile Asp Asn Leu Thr Lys Gly  
55 60 65

act gcc ggc gcc gct gtt cag tgc atg aac tta agc gtt ggt ttt gat 355  
Thr Ala Gly Ala Ala Val Gln Cys Met Asn Leu Ser Val Gly Phe Asp  
70 75 80 85

gag gca gca ggc ctg cca cag gtc ggc gtc gca cct taaagtagcg 401  
Glu Ala Ala Gly Leu Pro Gln Val Gly Val Ala Pro  
90 95

ccttaaagcg gcg 414

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<210> 354
<211> 97
<212> PRT
<213> Corynebacterium glutamicum
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<400> 354
Leu Lys Glu Gly Val Thr Ala Glu Gln Ala Arg Ala Val Tyr Glu Glu
  1                      5                      10                      15
Phe Tyr Ala Gln Glu Thr Phe Val His Val Leu Pro Glu Gly Ala Gln
                20                      25                      30
Pro Gln Thr Gln Ala Val Leu Gly Ser Asn Met Cys His Val Gln Val
          35                      40                      45
Glu Ile Asp Glu Glu Ala Gly Lys Val Leu Val Thr Ser Ala Ile Asp
      50                      55                      60
Asn Leu Thr Lys Gly Thr Ala Gly Ala Ala Val Gln Cys Met Asn Leu
  65                      70                      75                      80
Ser Val Gly Phe Asp Glu Ala Ala Gly Leu Pro Gln Val Gly Val Ala
          85                      90                      95
Pro

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<210> 355
<211> 1302
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1279)
<223> RXS00147
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<400> 355  
attgcatata atgcaatgaa ttgaataaac tacattcagg gttatcaacc agccaatttc 60  
  
ttttaaaaag gcagacacac gaaaggcgac aacagtcacc gtg agt aaa gac acc 115  
Val Ser Lys Asp Thr  
1 5
```



acc	acc	tac	cag	gga	gtc	acc	gag	atc	gga	tcc	gtt	ccg	gca	tac	ctg	163
Thr	Thr	Tyr	Gln	Gly	Val	Thr	Glu	Ile	Gly	Ser	Val	Pro	Ala	Tyr	Leu	
				10					15					20		
gtt	ctt	gca	gac	gga	cgt	acc	ttc	acc	gga	ttt	ggc	ttt	gga	gct	atc	211
Val	Leu	Ala	Asp	Gly	Arg	Thr	Phe	Thr	Gly	Phe	Gly	Phe	Gly	Ala	Ile	
			25				30						35			
ggc	acc	acc	ctt	ggg	gag	gca	gtg	ttc	act	acc	gcc	atg	acc	ggg	tac	259
Gly	Thr	Thr	Leu	Gly	Glu	Ala	Val	Phe	Thr	Thr	Ala	Met	Thr	Gly	Tyr	
		40					45					50				
caa	gaa	acc	atg	acc	gat	cct	tcc	tat	cac	cgc	cag	att	gtt	gtg	gct	307
Gln	Glu	Thr	Met	Thr	Asp	Pro	Ser	Tyr	His	Arg	Gln	Ile	Val	Val	Ala	
	55					60					65					
acc	gca	cca	cag	atc	ggc	aac	acc	ggc	tgg	aac	gat	gag	gac	aac	gag	355
Thr	Ala	Pro	Gln	Ile	Gly	Asn	Thr	Gly	Trp	Asn	Asp	Glu	Asp	Asn	Glu	
70					75				80						85	
tcc	cgc	gac	ggc	aag	att	tgg	gtt	gca	ggc	ctt	gtt	atc	cgc	gac	ctc	403
Ser	Arg	Asp	Gly	Lys	Ile	Trp	Val	Ala	Gly	Leu	Val	Ile	Arg	Asp	Leu	
				90					95					100		
gca	gca	cgt	gtg	tcc	aac	tgg	cgc	gcc	acc	acc	tcc	ttg	cag	cag	gaa	451
Ala	Ala	Arg	Val	Ser	Asn	Trp	Arg	Ala	Thr	Thr	Ser	Leu	Gln	Gln	Glu	
			105					110					115			
atg	gca	ggc	cag	ggc	atc	gtc	ggc	atc	ggc	gga	atc	gac	acc	cgc	gca	499
Met	Ala	Gly	Gln	Gly	Ile	Val	Gly	Ile	Gly	Gly	Ile	Asp	Thr	Arg	Ala	
		120					125					130				
ctg	gtt	cgc	cac	ctg	cgc	aat	gaa	ggg	tcc	att	gca	gcg	ggc	atc	ttc	547
Leu	Val	Arg	His	Leu	Arg	Asn	Glu	Gly	Ser	Ile	Ala	Ala	Gly	Ile	Phe	
	135					140					145					
tcc	ggc	gct	gac	gca	cag	cgc	cca	gtt	gaa	gaa	ctc	gta	gag	atc	gtc	595
Ser	Gly	Ala	Asp	Ala	Gln	Arg	Pro	Val	Glu	Glu	Leu	Val	Glu	Ile	Val	
150					155				160						165	
aag	aat	cag	cca	gca	atg	acc	ggc	gca	aac	ctc	tcc	gtt	gag	gtc	tct	643
Lys	Asn	Gln	Pro	Ala	Met	Thr	Gly	Ala	Asn	Leu	Ser	Val	Glu	Val	Ser	
			170						175					180		
gct	gat	gaa	acc	tac	gtc	atc	gaa	gct	gaa	ggc	gaa	gag	cgc	cac	acc	691
Ala	Asp	Glu	Thr	Tyr	Val	Ile	Glu	Ala	Glu	Gly	Glu	Glu	Arg	His	Thr	
			185					190					195			
gtc	gtg	gcc	tac	gac	ctg	ggc	att	aag	caa	aac	acc	cca	cgt	cgt	ttc	739
Val	Val	Ala	Tyr	Asp	Leu	Gly	Ile	Lys	Gln	Asn	Thr	Pro	Arg	Arg	Phe	
		200				205						210				
tct	gca	cgc	ggg	gtt	cgc	acc	gtc	atc	gtg	cct	gct	gaa	acc	cca	ttc	787
Ser	Ala	Arg	Gly	Val	Arg	Thr	Val	Ile	Val	Pro	Ala	Glu	Thr	Pro	Phe	
	215					220					225					
gag	gat	atc	aag	cag	tac	aac	cca	tca	ggc	gtg	ttc	atc	tcc	aac	ggc	835
Glu	Asp	Ile	Lys	Gln	Tyr	Asn	Pro	Ser	Gly	Val	Phe	Ile	Ser	Asn	Gly	
230				235					240						245	
cct	ggc	gat	cct	gca	gca	gca	gac	gtc	atg	gtt	gat	atc	gtc	cgc	gaa	883

Pro Gly Asp Pro Ala Ala Ala Asp Val Met Val Asp Ile Val Arg Glu  
 250 255 260

gtt ctt gaa gcc gac att cca ttc ttt ggc atc tgc ttc ggc aac cag 931  
 Val Leu Glu Ala Asp Ile Pro Phe Phe Gly Ile Cys Phe Gly Asn Gln  
 265 270 275

att ctt ggc cgc gca ttc ggc atg gag acc tac aag ctg aag ttc ggc 979  
 Ile Leu Gly Arg Ala Phe Gly Met Glu Thr Tyr Lys Leu Lys Phe Gly  
 280 285 290

cac cgc ggc atc aac gtt cca gtg aag aac cac atc acc ggc aag atc  
 1027  
 His Arg Gly Ile Asn Val Pro Val Lys Asn His Ile Thr Gly Lys Ile  
 295 300 305

gac atc acc gcc cag aac cac ggc ttc gca ctc aag ggt gaa gca ggc  
 1075  
 Asp Ile Thr Ala Gln Asn His Gly Phe Ala Leu Lys Gly Glu Ala Gly  
 310 315 320 325

cag gaa ttc gag acc gat ttc ggc act gca att gtc acc cac acc tgc  
 1123  
 Gln Glu Phe Glu Thr Asp Phe Gly Thr Ala Ile Val Thr His Thr Cys  
 330 335 340

ctc aac gac ggc gtc gtt gaa ggt att gcg ctg aag tcc gga cgc gca  
 1171  
 Leu Asn Asp Gly Val Val Glu Gly Ile Ala Leu Lys Ser Gly Arg Ala  
 345 350 355

tac tcc gtt cag tac cac cca gag gcc gct gcc ggc cca aat gat gca  
 1219  
 Tyr Ser Val Gln Tyr His Pro Glu Ala Ala Ala Gly Pro Asn Asp Ala  
 360 365 370

agc ccc ctg ttt gac cag ttt gtt gag ctg atg gat gca gac gct cag  
 1267  
 Ser Pro Leu Phe Asp Gln Phe Val Glu Leu Met Asp Ala Asp Ala Gln  
 375 380 385

aag aaa ggc gca taaataacat gccaaagcgt tca  
 1302  
 Lys Lys Gly Ala  
 390

&lt;210&gt; 356

&lt;211&gt; 393

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 356

Val Ser Lys Asp Thr Thr Thr Tyr Gln Gly Val Thr Glu Ile Gly Ser  
 1 5 10 15

Val Pro Ala Tyr Leu Val Leu Ala Asp Gly Arg Thr Phe Thr Gly Phe  
 20 25 30

Gly Phe Gly Ala Ile Gly Thr Thr Leu Gly Glu Ala Val Phe Thr Thr  
 35 40 45

Ala Met Thr Gly Tyr Gln Glu Thr Met Thr Asp Pro Ser Tyr His Arg  
 50 55 60  
 Gln Ile Val Val Ala Thr Ala Pro Gln Ile Gly Asn Thr Gly Trp Asn  
 65 70 75 80  
 Asp Glu Asp Asn Glu Ser Arg Asp Gly Lys Ile Trp Val Ala Gly Leu  
 85 90 95  
 Val Ile Arg Asp Leu Ala Ala Arg Val Ser Asn Trp Arg Ala Thr Thr  
 100 105 110  
 Ser Leu Gln Gln Glu Met Ala Gly Gln Gly Ile Val Gly Ile Gly Gly  
 115 120 125  
 Ile Asp Thr Arg Ala Leu Val Arg His Leu Arg Asn Glu Gly Ser Ile  
 130 135 140  
 Ala Ala Gly Ile Phe Ser Gly Ala Asp Ala Gln Arg Pro Val Glu Glu  
 145 150 155 160  
 Leu Val Glu Ile Val Lys Asn Gln Pro Ala Met Thr Gly Ala Asn Leu  
 165 170 175  
 Ser Val Glu Val Ser Ala Asp Glu Thr Tyr Val Ile Glu Ala Glu Gly  
 180 185 190  
 Glu Glu Arg His Thr Val Val Ala Tyr Asp Leu Gly Ile Lys Gln Asn  
 195 200 205  
 Thr Pro Arg Arg Phe Ser Ala Arg Gly Val Arg Thr Val Ile Val Pro  
 210 215 220  
 Ala Glu Thr Pro Phe Glu Asp Ile Lys Gln Tyr Asn Pro Ser Gly Val  
 225 230 235 240  
 Phe Ile Ser Asn Gly Pro Gly Asp Pro Ala Ala Ala Asp Val Met Val  
 245 250 255  
 Asp Ile Val Arg Glu Val Leu Glu Ala Asp Ile Pro Phe Phe Gly Ile  
 260 265 270  
 Cys Phe Gly Asn Gln Ile Leu Gly Arg Ala Phe Gly Met Glu Thr Tyr  
 275 280 285  
 Lys Leu Lys Phe Gly His Arg Gly Ile Asn Val Pro Val Lys Asn His  
 290 295 300  
 Ile Thr Gly Lys Ile Asp Ile Thr Ala Gln Asn His Gly Phe Ala Leu  
 305 310 315 320  
 Lys Gly Glu Ala Gly Gln Glu Phe Glu Thr Asp Phe Gly Thr Ala Ile  
 325 330 335  
 Val Thr His Thr Cys Leu Asn Asp Gly Val Val Glu Gly Ile Ala Leu  
 340 345 350  
 Lys Ser Gly Arg Ala Tyr Ser Val Gln Tyr His Pro Glu Ala Ala Ala  
 355 360 365

Gly Pro Asn Asp Ala Ser Pro Leu Phe Asp Gln Phe Val Glu Leu Met  
 370 375 380

Asp Ala Asp Ala Gln Lys Lys Gly Ala  
 385 390

<210> 357

<211> 924

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(901)

<223> RXS00905

<400> 357

cgctgccct ctatgctgct cctagttacc cctgcacaaa tagcgggtttt tctcacgcat 60

tctgcatcga gtcgggtcga cgtatataag gtggaaaggc atg acc caa ttc gaa 115  
 Met Thr Gln Phe Glu  
 1 5

aac gcg caa gta ctt aaa gag aac atc gaa aac caa cgc gag cag atc 163  
 Asn Ala Gln Val Leu Lys Glu Asn Ile Glu Asn Gln Arg Glu Gln Ile  
 10 15 20

ttt acc cag ttg aaa gaa att gtg tct ttc aac tcc gtg cac agc gat 211  
 Phe Thr Gln Leu Lys Glu Ile Val Ser Phe Asn Ser Val His Ser Asp  
 25 30 35

cca aac cta ctg gag gac tac gcc ggc gcg aaa gaa tgg gta aaa gaa 259  
 Pro Asn Leu Leu Glu Asp Tyr Ala Gly Ala Lys Glu Trp Val Lys Glu  
 40 45 50

aca ctg acc aac gca ggt ctc acc gtc agc gaa ttc gct gcc gaa gat 307  
 Thr Leu Thr Asn Ala Gly Leu Thr Val Ser Glu Phe Ala Ala Glu Asp  
 55 60 65

gga acc acc aac ttc atc ggc acc cgc aag ggc tcc gaa ggt gca cca 355  
 Gly Thr Thr Asn Phe Ile Gly Thr Arg Lys Gly Ser Glu Gly Ala Pro  
 70 75 80 85

aag gta ctg ctg tac agc cac ttc gac gtt gtc cca tcc ggc cct ttg 403  
 Lys Val Leu Leu Tyr Ser His Phe Asp Val Val Pro Ser Gly Pro Leu  
 90 95 100

gat ctc tgg gac acc aat cct ttt gaa ctc acc gag cgc gac gct ggc 451  
 Asp Leu Trp Asp Thr Asn Pro Phe Glu Leu Thr Glu Arg Asp Ala Gly  
 105 110 115

cac ggc acc cgc tgg tac ggc cgc ggc gcc gct gac tgc aag ggc aac 499  
 His Gly Thr Arg Trp Tyr Gly Arg Gly Ala Ala Asp Cys Lys Gly Asn  
 120 125 130

ctg gtc atg cac ctc gca gca ctg cgc gcc gtc gaa gcc agc ggc gac 547  
 Leu Val Met His Leu Ala Ala Leu Arg Ala Val Glu Ala Ser Gly Asp  
 135 140 145

acc aca ctc aac ctc acc tac gtg gtc gag ggc tcc gag gaa atg gga 595

Thr 150	Thr	Leu	Asn	Leu	Thr 155	Tyr	Val	Val	Glu	Gly 160	Ser	Glu	Glu	Met	Gly 165	
ggc	gga	gcg	ctc	agc	gcg	ctc	atc	aag	gac	aag	cct	gag	ctt	ttc	gac	643
Gly	Gly	Ala	Leu	Ser 170	Ala	Leu	Ile	Lys	Asp 175	Lys	Pro	Glu	Leu	Phe	Asp 180	
gca	gat	gtc	atc	ttg	att	gca	gac	agc	gga	aac	gct	tcc	gtg	ggc	acc	691
Ala	Asp	Val	Ile 185	Leu	Ile	Ala	Asp	Ser 190	Gly	Asn	Ala	Ser	Val	Gly	Thr 195	
cca	acc	ttg	acc	act	acc	ctg	cgc	ggc	ggc	gga	cag	gtc	acc	gtc	acc	739
Pro	Thr	Leu 200	Thr	Thr	Thr	Leu	Arg 205	Gly	Gly	Gly	Gln	Val	Thr	Val	Thr 210	
gtg	gac	acc	ctt	gaa	ggc	gct	gtt	cac	tcc	ggc	cag	aac	ggc	ggc	gct	787
Val	Asp 215	Thr	Leu	Glu	Gly	Ala 220	Val	His	Ser	Gly	Gln	Asn	Gly	Gly	Ala 225	
gcc	cca	gat	gct	gtt	gct	gct	ctc	gtg	cgc	gtt	ctg	gat	act	ttg	cgc	835
Ala	Pro	Asp	Ala	Val	Ala 235	Ala	Leu	Val	Arg	Val 240	Leu	Asp	Thr	Leu	Arg 245	
gat	gaa	cac	gga	cgc	acc	gtt	atc	gac	ggc	tgt	caa	cac	cac	cgc	aaa	883
Asp	Glu	His	Gly	Arg 250	Thr	Val	Ile	Asp	Gly 255	Cys	Gln	His	His	Arg	Lys 260	
ctg	gaa	ggg	cga	gcc	tta	tgatccagag	actttccgca	gcg								924
Leu	Glu	Gly	Arg 265	Ala	Leu											

&lt;210&gt; 358

&lt;211&gt; 267

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 358

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Gln	Arg	Glu	Gln	Ile	Phe	Thr	Gln	Leu 25	Lys	Glu	Ile	Val	Ser	Phe	Asn 30
Ser	Val	His	Ser	Asp	Pro	Asn	Leu 40	Leu	Glu	Asp	Tyr	Ala	Gly	Ala	Lys 45
Glu	Trp	Val	Lys	Glu	Thr	Leu	Thr 55	Asn	Ala	Gly	Leu	Thr	Val	Ser	Glu 60
Phe 65	Ala	Ala	Glu	Asp	Gly	Thr	Thr	Asn	Phe	Ile	Gly	Thr	Arg	Lys	Gly 80
Ser	Glu	Gly	Ala	Pro	Lys	Val	Leu	Leu	Tyr 90	Ser	His	Phe	Asp	Val	Val 95
Pro	Ser	Gly	Pro	Leu	Asp	Leu	Trp	Asp	Thr 105	Asn	Pro	Phe	Glu	Leu	Thr 110
Glu	Arg	Asp	Ala	Gly	His	Gly	Thr	Arg	Trp	Tyr	Gly	Arg	Gly	Ala	Ala 125

Asp Cys Lys Gly Asn Leu Val Met His Leu Ala Ala Leu Arg Ala Val  
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 Glu Ala Ser Gly Asp Thr Thr Leu Asn Leu Thr Tyr Val Val Glu Gly  
 145 150 155 160  
 Ser Glu Glu Met Gly Gly Gly Ala Leu Ser Ala Leu Ile Lys Asp Lys  
 165 170 175  
 Pro Glu Leu Phe Asp Ala Asp Val Ile Leu Ile Ala Asp Ser Gly Asn  
 180 185 190  
 Ala Ser Val Gly Thr Pro Thr Leu Thr Thr Thr Leu Arg Gly Gly Gly  
 195 200 205  
 Gln Val Thr Val Thr Val Asp Thr Leu Glu Gly Ala Val His Ser Gly  
 210 215 220  
 Gln Asn Gly Gly Ala Ala Pro Asp Ala Val Ala Ala Leu Val Arg Val  
 225 230 235 240  
 Leu Asp Thr Leu Arg Asp Glu His Gly Arg Thr Val Ile Asp Gly Cys  
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 Gln His His Arg Lys Leu Glu Gly Arg Ala Leu  
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&lt;210&gt; 359

&lt;211&gt; 627

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

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&lt;222&gt; (101)..(604)

&lt;223&gt; RXS00906

&lt;400&gt; 359

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 Met Asn Thr Asp Ala  
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ccg tta tcg acg gct gtc aac acc acc gca aac tgg aag ggc gag cct 163  
 Pro Leu Ser Thr Ala Val Asn Thr Thr Ala Asn Trp Lys Gly Glu Pro  
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 Tyr Asp Pro Glu Thr Phe Arg Ser Asp Ala Gly Ile Leu Asp Gly Val  
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gac atc atg ggc gac ggc gac aac cca gca agc atg ctg tgg tcc agg 259  
 Asp Ile Met Gly Asp Gly Asp Asn Pro Ala Ser Met Leu Trp Ser Arg  
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 Pro Ala Ile Ser Ile Thr Gly Phe Thr Ser Thr Pro Val Ala Glu Ala  
 55 60 65

ctc aac gca gtg ccc gca acg gcg tcc gcc aag cta aac ctt cgc gtg 355  
 Leu Asn Ala Val Pro Ala Thr Ala Ser Ala Lys Leu Asn Leu Arg Val  
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 cca gca ggc ctg gaa gca aac gat gtg gcc gag aag ctg aag cag cac 403  
 Pro Ala Gly Leu Glu Ala Asn Asp Val Ala Glu Lys Leu Lys Gln His  
 90 95 100  
 ctg atc aat cac aca cct tgg ggc gca aag atc acg gtg gag atc gat 451  
 Leu Ile Asn His Thr Pro Trp Gly Ala Lys Ile Thr Val Glu Ile Asp  
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 Asp Ile Asn Gln Pro Phe Ser Thr Asp Ile Thr Gly Pro Ala Met Ser  
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 Thr Leu Ala Ser Cys Leu Ser Ala Ala Tyr Glu Gly Lys Asp Leu Val  
 135 140 145  
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 Val Asn Pro

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 <212> PRT  
 <213> *Corynebacterium glutamicum*

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 35 40 45  
 Met Leu Trp Ser Arg Pro Ala Ile Ser Ile Thr Gly Phe Thr Ser Thr  
 50 55 60  
 Pro Val Ala Glu Ala Leu Asn Ala Val Pro Ala Thr Ala Ser Ala Lys  
 65 70 75 80  
 Leu Asn Leu Arg Val Pro Ala Gly Leu Glu Ala Asn Asp Val Ala Glu  
 85 90 95  
 Lys Leu Lys Gln His Leu Ile Asn His Thr Pro Trp Gly Ala Lys Ile  
 100 105 110  
 Thr Val Glu Ile Asp Asp Ile Asn Gln Pro Phe Ser Thr Asp Ile Thr  
 115 120 125  
 Gly Pro Ala Met Ser Thr Leu Ala Ser Cys Leu Ser Ala Ala Tyr Glu

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 <212> DNA  
 <213> Corynebacterium glutamicum

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 Leu Ala Leu Tyr Gly  
 1 5

gtg gaa gaa ccc ctc acc gtt atc cac tcc gct aat gaa tct gtt gac 163  
 Val Glu Glu Pro Leu Thr Val Ile His Ser Ala Asn Glu Ser Val Asp  
 10 15 20

ccc aat gag att cgc gat atc gcc acc gca gaa gca ttg ttc ctg ctc 211  
 Pro Asn Glu Ile Arg Asp Ile Ala Thr Ala Glu Ala Leu Phe Leu Leu  
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aac tac acc aag tagaccctaaa agcaggcggtt aac 246  
 Asn Tyr Thr Lys  
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 <212> DNA  
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&lt;222&gt; (101) .. (1258)

&lt;223&gt; RXS02001

&lt;400&gt; 363

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Met Pro Val Ile Asn
1 5

agt atc gcc agt ttt tcc gac gag atg acc cgc tgg cgg cgt cac ctg 163
Ser Ile Ala Ser Phe Ser Asp Glu Met Thr Arg Trp Arg Arg His Leu
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cat caa aac ccc gaa atc agc ttt gat tgt gtg gaa act gcg gcc ttc 211
His Gln Asn Pro Glu Ile Ser Phe Asp Cys Val Glu Thr Ala Ala Phe
25 30 35

gtg gcc gag cag ctg cgc agc ttc ggg gtg gat gaa att cac acc ggc 259
Val Ala Glu Gln Leu Arg Ser Phe Gly Val Asp Glu Ile His Thr Gly
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atc gcg aaa acc ggt atc atc gcc ctg att cac ggg cgc gag gct ggc 307
Ile Ala Lys Thr Gly Ile Ile Ala Leu Ile His Gly Arg Glu Ala Gly
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ccc gtc gtc ggc ctg cgc gcc gat atg gac gcg ctg ccg ctg acc gag 355
Pro Val Val Gly Leu Arg Ala Asp Met Asp Ala Leu Pro Leu Thr Glu
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Ile Thr Gly Val Asp Tyr Ala Ser Thr Thr Pro Gly Lys Met His Ala
90 95 100

tgc ggc cac gac ggc cac acg acc atg ctg ctg ggc gcc gcc aaa tat 451
Cys Gly His Asp Gly His Thr Thr Met Leu Leu Gly Ala Ala Lys Tyr
105 110 115

ctg gcc gag acg cgc aat ttc gca ggt acc gtc gcg ctg atc ttc cag 499
Leu Ala Glu Thr Arg Asn Phe Ala Gly Thr Val Ala Leu Ile Phe Gln
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Pro Ala Glu Glu Asn Gly Gly Gly Ala Gly Val Met Val Asp Glu Gly
135 140 145

gtc ctc gac cgc ttt gcc atc gcc gaa gtc tac gcc ctg cac aac cag 595
Val Leu Asp Arg Phe Ala Ile Ala Glu Val Tyr Ala Leu His Asn Gln
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ccc ggc ctg ccg ctt ggc cat ttt atg acg aca gcc ggc ccg atc atg 643
Pro Gly Leu Pro Leu Gly His Phe Met Thr Thr Ala Gly Pro Ile Met
170 175 180

gcc gct gtc gac acg ttc gac atc aac att acc gga cgc ggc ggc cac 691
Ala Ala Val Asp Thr Phe Asp Ile Asn Ile Thr Gly Arg Gly Gly His
185 190 195

ggt gcc aaa ccg cac caa acc cgc gac ccc atc gtc gca gcc gtc gga 739
Gly Ala Lys Pro His Gln Thr Arg Asp Pro Ile Val Ala Ala Val Gly

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Ile Val Gln Ala Phe Gln Thr Ile Val Ser Arg Asn His Asn Pro Val																		
215 220 225																		
gag gac ctt gtc gtg tcg gtc acg caa atc cac acc ggc agc gcc gat	835																	
Glu Asp Leu Val Val Ser Val Thr Gln Ile His Thr Gly Ser Ala Asp																		
230 235 240 245																		
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Asn Ile Ile Pro Glu Thr Ala Tyr Ile Asn Gly Thr Val Arg Thr Phe																		
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265 270 275																		
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Arg Asn Tyr Pro Ala Thr Ile Asn Asp Ala Ala Lys Ala Ala Ile Ala																		
295 300 305																		
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1123																		
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330 335 340																		
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345 350 355																		
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1219																		
Pro Ala Tyr Asn Phe Asn Asp Glu Ala Ala Pro Tyr Gly Ala Ser Phe																		
360 365 370																		
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1281																		

&lt;210&gt; 364

&lt;211&gt; 386

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 364

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Glu	Thr	Ala	Ala	Phe	Val	Ala	Glu	Gln	Leu	Arg	Ser	Phe	Gly	Val	Asp
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Glu	Ile	His	Thr	Gly	Ile	Ala	Lys	Thr	Gly	Ile	Ile	Ala	Leu	Ile	His
	50					55					60				
Gly	Arg	Glu	Ala	Gly	Pro	Val	Val	Gly	Leu	Arg	Ala	Asp	Met	Asp	Ala
65					70					75					80
Leu	Pro	Leu	Thr	Glu	Ile	Thr	Gly	Val	Asp	Tyr	Ala	Ser	Thr	Thr	Pro
				85					90					95	
Gly	Lys	Met	His	Ala	Cys	Gly	His	Asp	Gly	His	Thr	Thr	Met	Leu	Leu
			100					105					110		
Gly	Ala	Ala	Lys	Tyr	Leu	Ala	Glu	Thr	Arg	Asn	Phe	Ala	Gly	Thr	Val
		115					120					125			
Ala	Leu	Ile	Phe	Gln	Pro	Ala	Glu	Glu	Asn	Gly	Gly	Gly	Ala	Gly	Val
	130					135					140				
Met	Val	Asp	Glu	Gly	Val	Leu	Asp	Arg	Phe	Ala	Ile	Ala	Glu	Val	Tyr
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Ala	Leu	His	Asn	Gln	Pro	Gly	Leu	Pro	Leu	Gly	His	Phe	Met	Thr	Thr
				165				170						175	
Ala	Gly	Pro	Ile	Met	Ala	Ala	Val	Asp	Thr	Phe	Asp	Ile	Asn	Ile	Thr
			180					185					190		
Gly	Arg	Gly	Gly	His	Gly	Ala	Lys	Pro	His	Gln	Thr	Arg	Asp	Pro	Ile
		195					200					205			
Val	Ala	Ala	Val	Gly	Ile	Val	Gln	Ala	Phe	Gln	Thr	Ile	Val	Ser	Arg
	210					215					220				
Asn	His	Asn	Pro	Val	Glu	Asp	Leu	Val	Val	Ser	Val	Thr	Gln	Ile	His
225					230					235				240	
Thr	Gly	Ser	Ala	Asp	Asn	Ile	Ile	Pro	Glu	Thr	Ala	Tyr	Ile	Asn	Gly
				245				250						255	
Thr	Val	Arg	Thr	Phe	Asn	Lys	Asp	Val	Gln	Ala	Met	Val	Ile	Thr	Arg
			260					265					270		
Met	Glu	Glu	Ile	Val	Ala	Gly	Gln	Ala	Ala	Ala	Tyr	Gly	Val	Glu	Ala
		275					280					285			
Thr	Leu	Thr	Tyr	Asn	Arg	Asn	Tyr	Pro	Ala	Thr	Ile	Asn	Asp	Ala	Ala
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<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(1363)  
<223> RXS02101
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Glu Leu Leu Asn Asn His Gly Val Asp Leu Ser Trp Gln Glu Ala Ala  
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Tyr Gln Asp Phe His Glu His Pro Glu Leu Ser Gly Phe Glu Ser Glu  
25 30 35

acc gca gat cgc att cag aaa tac ctc gag cgt ttt gat tgt gag gtg 259  
Thr Ala Asp Arg Ile Gln Lys Tyr Leu Glu Arg Phe Asp Cys Glu Val  
40 45 50

att cca aat gtt ggc ggt tac ggc att ctg gcc gtg ttc cga aat ggg 307  
Ile Pro Asn Val Gly Gly Tyr Gly Ile Leu Ala Val Phe Arg Asn Gly  
55 60 65

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Ser	Thr	Asp	Pro	Gly	Ala	Pro	Val	Ala	Leu	Met	Arg	Ala	Asp	Phe	Asp	
70					75					80					85	

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90 95 100

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Met Arg Pro His Asp Gly Ala Asn Val His Val Met His Ala Cys Gly  
105 110 115

cac gat gtc cac gtc acc gcg ctg ctt ggt gcg tgt gcc att tta gat	499
His Asp Val His Val Thr Ala Leu Leu Gly Ala Cys Ala Ile Leu Asp	
120 125 130	
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Glu Arg Arg Asp Ala Trp Glu Gly Thr Phe Ile Ala Leu Phe Gln Pro	
135 140 145	
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Ser Glu Glu Asn Ser Gln Gly Ala Asn Lys Met Val Ala Gly Gly Leu	
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Val Asp Leu Ile Pro Arg Pro Asp Val Cys Phe Gly Gln His Val Val	
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Pro Gly Ala Ala Gly Thr Val Met Ser Met Pro Gly Gly Ala Leu Ala	
185 190 195	
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Ala Cys Asp Ser Ile Glu Ile Arg Ile Gln Gly Arg Ser Ala His Gly	
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Ser Met Pro His Asn Ser Ile Asp Pro Thr Tyr Val Ala Ala Met Ile	
215 220 225	
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Val Val Arg Leu Gln Gly Ile Val Gly Arg Glu Val Ser Pro Glu Asp	
230 235 240 245	
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Phe Ala Val Ile Ser Val Gly Thr Leu Gln Ser Gly Asn Thr Asn Asn	
250 255 260	
acc att cca gca agt gct cgt ttg gtg ttg aac tgc cgt ttc tac aac	931
Thr Ile Pro Ala Ser Ala Arg Leu Val Leu Asn Cys Arg Phe Tyr Asn	
265 270 275	
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Asp Lys Val Lys His Lys Val Tyr Arg Ala Ile Glu Arg Val Val Arg	
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1171	

Tyr Arg Trp Thr Ala Ser Glu Asp Phe Pro Ser Ile Pro Lys Ala Phe  
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Asn Ser Pro Tyr Leu Tyr Trp Thr Ile Gly Val Thr Pro Arg Asp Gln  
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Trp Thr Glu Ala Val Glu Arg Asp Arg Val Ala Ser Asp Val Pro Ala  
 375 380 385

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 1315

Asn His Met Gly Asp Phe Leu Pro Asp Tyr Ala Pro Thr Met Ser Ala  
 390 395 400 405

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<211> 421

<212> PRT

<213> Corynebacterium glutamicum

<400> 366

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Gly Phe Glu Ser Glu Thr Ala Asp Arg Ile Gln Lys Tyr Leu Glu Arg  
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Phe Asp Cys Glu Val Ile Pro Asn Val Gly Gly Tyr Gly Ile Leu Ala  
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Val Phe Arg Asn Gly Ser Thr Asp Pro Gly Ala Pro Val Ala Leu Met  
 65 70 75 80

Arg Ala Asp Phe Asp Gly Leu Pro Val Lys Glu Ile Thr Gly Val Pro  
 85 90 95

Phe Ala Ser Thr Arg Met Arg Pro His Asp Gly Ala Asn Val His Val  
 100 105 110

Met His Ala Cys Gly His Asp Val His Val Thr Ala Leu Leu Gly Ala  
 115 120 125

Cys Ala Ile Leu Asp Glu Arg Arg Asp Ala Trp Glu Gly Thr Phe Ile  
 130 135 140

Ala Leu Phe Gln Pro Ser Glu Glu Asn Ser Gln Gly Ala Asn Lys Met

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Gly	Gly	Ala	Leu	Ala	Ala	Cys	Asp	Ser	Ile	Glu	Ile	Arg	Ile	Gln	Gly
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Val	Ala	Ala	Met	Ile	Val	Val	Arg	Leu	Gln	Gly	Ile	Val	Gly	Arg	Glu
225					230					235					240
Val	Ser	Pro	Glu	Asp	Phe	Ala	Val	Ile	Ser	Val	Gly	Thr	Leu	Gln	Ser
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Cys	Arg	Phe	Tyr	Asn	Asp	Lys	Val	Lys	His	Lys	Val	Tyr	Arg	Ala	Ile
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Pro	Val	Ile	Glu	Tyr	Phe	Ala	His	Gly	Asp	Leu	Thr	Asn	Asn	Thr	Pro
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Asp	Ser	Ile	Asp	Ala	Tyr	Arg	Trp	Thr	Ala	Ser	Glu	Asp	Phe	Pro	Ser
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Pro	Thr	Met	Ser	Ala	Ala	Thr	Arg	Ala	Ala	Ala	Ala	Ala	Leu	Leu	Thr
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&lt;210&gt; 367

&lt;211&gt; 3462

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(3439)

&lt;223&gt; RXS02234

&lt;400&gt; 367

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gat	att	aac	cac	gtc	ctc	gtc	atc	ggc	tcc	ggc	ccc	atc	gtc	att	ggc	163
Asp	Ile	Asn	His	Val	Leu	Val	Ile	Gly	Ser	Gly	Pro	Ile	Val	Ile	Gly	
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cag	gca	tgt	gaa	ttc	gac	tac	tcc	ggc	acc	cag	gct	tgc	cgc	gtg	ctg	211
Gln	Ala	Cys	Glu	Phe	Asp	Tyr	Ser	Gly	Thr	Gln	Ala	Cys	Arg	Val	Leu	
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aag	gaa	gag	gga	ctg	cgc	gtc	acc	ctc	atc	aac	tcc	aac	cca	gca	acg	259
Lys	Glu	Glu	Gly	Leu	Arg	Val	Thr	Leu	Ile	Asn	Ser	Asn	Pro	Ala	Thr	
			40				45					50				

atc	atg	acc	gac	cca	gaa	atg	gct	gac	cac	acc	tac	gtg	gag	cca	atc	307
Ile	Met	Thr	Asp	Pro	Glu	Met	Ala	Asp	His	Thr	Tyr	Val	Glu	Pro	Ile	
	55					60					65					

gag	ccg	gaa	tac	atc	gac	aag	att	ttc	gct	aag	gaa	atc	gag	cag	ggc	355
Glu	Pro	Glu	Tyr	Ile	Asp	Lys	Ile	Phe	Ala	Lys	Glu	Ile	Glu	Gln	Gly	
	70				75					80					85	

cac	cca	atc	gac	gcc	gtc	ctg	gca	acc	ctt	ggc	ggc	cag	act	gca	ctt	403
His	Pro	Ile	Asp	Ala	Val	Leu	Ala	Thr	Leu	Gly	Gly	Gln	Thr	Ala	Leu	
				90					95					100		

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Asn	Ala	Ala	Ile	Gln	Leu	Asp	Arg	Leu	Gly	Ile	Leu	Glu	Lys	Tyr	Gly	
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gtt	gaa	ctc	atc	ggc	gca	gac	atc	gat	gcc	att	gag	cgc	ggc	gaa	gat	499
Val	Glu	Leu	Ile	Gly	Ala	Asp	Ile	Asp	Ala	Ile	Glu	Arg	Gly	Glu	Asp	
		120					125					130				

cgc	cag	aag	ttc	aag	gat	att	gtc	acc	acc	atc	ggc	ggc	gaa	tcc	gcg	547
Arg	Gln	Lys	Phe	Lys	Asp	Ile	Val	Thr	Thr	Ile	Gly	Gly	Glu	Ser	Ala	
	135					140					145					

cgt	tcc	cgc	gtc	tgc	cac	aac	atg	gaa	gaa	gtc	cac	gag	act	gtc	gca	595
Arg	Ser	Arg	Val	Cys	His	Asn	Met	Glu	Glu	Val	His	Glu	Thr	Val	Ala	
	150				155					160					165	

gaa	ctc	ggc	ctt	cca	gta	gtc	gtg	cgt	cca	tcc	ttc	act	atg	ggc	ggc	643
Glu	Leu	Gly	Leu	Pro	Val	Val	Val	Arg	Pro	Ser	Phe	Thr	Met	Gly	Gly	
				170				175						180		

ctg	ggc	tcc	ggc	ctt	gca	tac	aac	acc	gaa	gac	ctt	gag	cgc	atc	gct	691
Leu	Gly	Ser	Gly	Leu	Ala	Tyr	Asn	Thr	Glu	Asp	Leu	Glu	Arg	Ile	Ala	
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ggc	ggc	gga	ctt	gct	gca	tct	cct	gaa	gca	aac	gtc	ttg	atc	gaa	gaa	739
Gly	Gly	Gly	Leu	Ala	Ala	Ser	Pro	Glu	Ala	Asn	Val	Leu	Ile	Glu	Glu	
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Ala Asp Asn Val Val Val Ile Cys Ser Ile Glu Asn Val Asp Ala Leu	
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Gly Val His Thr Gly Asp Ser Val Thr Val Ala Pro Ala Leu Thr Leu	
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Thr Asp Arg Glu Phe Gln Lys Met Arg Asp Gln Gly Ile Ala Ile Ile	
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1075	
Ser Arg Ser Ser Ala Leu Ala Ser Lys Ala Thr Gly Phe Pro Ile Ala	
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1123	
Lys Met Ala Ala Lys Leu Ala Ile Gly Tyr Thr Leu Asp Glu Ile Thr	
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1171	
Asn Asp Ile Thr Gly Glu Thr Pro Ala Ala Phe Glu Pro Thr Ile Asp	
345 350 355	
tac gtc gtg gtc aag gcc cca cgc ttt gct ttc gag aag ttt gtc ggc	
1219	
Tyr Val Val Val Lys Ala Pro Arg Phe Ala Phe Glu Lys Phe Val Gly	
360 365 370	
gct gat gac act ttg acc acc acc atg aag tcc gtc ggt gag gtc atg	
1267	
Ala Asp Asp Thr Leu Thr Thr Thr Met Lys Ser Val Gly Glu Val Met	
375 380 385	
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 425 430 435

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 1459  
 Arg Pro Thr Glu Gly Arg Leu Tyr Asp Val Glu Leu Ala Met Arg Leu  
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 1699  
 Glu Asp Gly Val Arg Thr Leu Arg Leu Ser Leu Gly Ile Arg Pro Val  
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 1747  
 Phe Lys Thr Val Asp Thr Cys Ala Ala Glu Phe Glu Ala Lys Thr Pro  
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tac cac tac tcc gca tac gag ctg gat cca gca gct gag tct gag gtc  
 1795  
 Tyr His Tyr Ser Ala Tyr Glu Leu Asp Pro Ala Ala Glu Ser Glu Val  
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 1843  
 Ala Pro Gln Thr Glu Arg Glu Lys Val Leu Ile Leu Gly Ser Gly Pro  
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 1891  
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 585 590 595

gct ctt gag ctc tcc cgc gtc ggc tac gaa act gtc atg gtc aac tgc  
 1939  
 Ala Leu Glu Leu Ser Arg Val Gly Tyr Glu Thr Val Met Val Asn Cys  
 600 605 610

aac cca gag acc gtg tcc acc gac tac gac acc gct gac cgc ctg tac  
 1987  
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 Thr Glu Leu Ser Ser Asp His Pro Val Leu Val Asp Arg Phe Leu Asp  
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 Glu Tyr Asp Gly Gly Ser Leu Pro Leu Asp Ala Pro Ile Ala Val Lys  
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 Glu Ala Val Leu Pro Phe Asn Arg Phe Arg Arg Pro Asp Gly Lys Thr  
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 935 940 945

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 Asn Arg Asp Lys Arg Thr Leu Ile Leu Pro Ile Gln Arg Leu Ala Leu  
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3139

Met Gly Tyr Lys Ile Leu Ala Thr Glu Gly Thr Ala Gly Met Leu Arg  
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3235

Glu Gly Val Glu Gly Lys Ser Ile Val Asp Arg Ile Arg Glu Gly Glu  
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3283

Val Asp Leu Ile Leu Asn Thr Pro Ala Gly Ser Ala Gly Ala Arg His  
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3379

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3427

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3462

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35 40 45

Ser Asn Pro Ala Thr Ile Met Thr Asp Pro Glu Met Ala Asp His Thr  
50 55 60

Tyr Val Glu Pro Ile Glu Pro Glu Tyr Ile Asp Lys Ile Phe Ala Lys  
65 70 75 80

Glu Ile Glu Gln Gly His Pro Ile Asp Ala Val Leu Ala Thr Leu Gly  
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 Gly Gln Thr Ala Leu Asn Ala Ala Ile Gln Leu Asp Arg Leu Gly Ile  
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 Leu Glu Lys Tyr Gly Val Glu Leu Ile Gly Ala Asp Ile Asp Ala Ile  
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 Gly Phe Pro Ile Ala Lys Met Ala Ala Lys Leu Ala Ile Gly Tyr Thr  
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 Leu Asp Glu Ile Thr Asn Asp Ile Thr Gly Glu Thr Pro Ala Ala Phe  
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 Glu Pro Thr Ile Asp Tyr Val Val Val Lys Ala Pro Arg Phe Ala Phe  
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 Glu Lys Phe Val Gly Ala Asp Asp Thr Leu Thr Thr Thr Met Lys Ser  
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 Val Gly Glu Val Met Ser Leu Gly Arg Asn Tyr Ile Ala Ala Leu Asn  
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Lys Ala Leu Arg Ser Leu Glu Thr Lys Gln Gln Gly Phe Trp Thr Lys  
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 Pro Asp Glu Phe Phe Ala Gly Glu Arg Ala Thr Asp Lys Ala Ala Val  
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 435 440 445  
 Leu Ala Met Arg Leu Gly Ala Ser Val Glu Glu Leu Tyr Glu Ala Ser  
 450 455 460  
 Ser Ile Asp Pro Trp Phe Leu Ala Glu Leu Glu Ala Leu Val Gln Phe  
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 Arg Gln Lys Leu Val Asp Ala Pro Phe Leu Asn Glu Asp Leu Leu Arg  
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 Val Tyr His Ala Glu Ala Gln Ser Gly Thr Val Ala Gly Val Ile Val  
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 Ala Gly Val Pro Val Ile Gly Thr Ser Pro Glu Ala Ile Asp Met Ala  
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 705 710 715 720  
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725								730				735			
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	770					775					780				
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785					790					795					800
Ala	Gly	Ile	His	Ser	Gly	Asp	Ser	Ala	Cys	Ala	Leu	Pro	Pro	Met	Thr
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	850					855					860				
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Ala	Ser	Arg	Ile	Ala	Val	Gly	Ala	Thr	Ile	Lys	Asp	Leu	Gln	Asp	Glu
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Lys	Ala	Glu	Ala	Gly	Ala	Phe	Gly	Ala	Leu	Pro	Thr	Glu	Gly	Thr	Val
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 Val His Glu Thr Val Ala Glu Leu Gly Leu Pro Val Val Val Arg Pro  
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Gln Gly Ile Ala Ile Ile Arg Glu Val Gly Val Asp Thr Gly Gly Cys	
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2256																							
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2304																							
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3024

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                                   105 110 115

ctg aca ttc gtt ggc gtt gct gat gag gaa gcc cgc ggc gga ctc gga 499
Leu Thr Phe Val Gly Val Ala Asp Glu Glu Ala Arg Gly Gly Leu Gly
                                   120 125 130

gcg aag tgg ctt tcc gaa gaa cac caa aac ctc ttc agc tgg aaa aac 547
Ala Lys Trp Leu Ser Glu Glu His Gln Asn Leu Phe Ser Trp Lys Asn
                                   135 140 145

tgc ctc tcc gaa tcc ggt gga tcg cac ctt cca gtc cac gac ggc agc 595
Cys Leu Ser Glu Ser Gly Gly Ser His Leu Pro Val His Asp Gly Ser
150 155 160 165

gac gca gta gta att aac gtt gga gaa aaa ggt gca gct caa cgt cgt 643

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Asp	Ala	Val	Val	Ile	Asn	Val	Gly	Glu	Lys	Gly	Ala	Ala	Gln	Arg	Arg	
				170					175					180		
att	cac	gtc	aat	ggc	gat	gct	ggg	cat	ggg	tcc	att	cct	ttc	gac	cgt	691
Ile	His	Val	Asn	Gly	Asp	Ala	Gly	His	Gly	Ser	Ile	Pro	Phe	Asp	Arg	
			185					190					195			
gac	agc	gct	att	gtc	aag	atc	ggg	gaa	gtc	gcc	cgc	cga	atc	gct	gcc	739
Asp	Ser	Ala	Ile	Val	Lys	Ile	Gly	Glu	Val	Ala	Arg	Arg	Ile	Ala	Ala	
		200					205					210				
gcc	gat	ctg	aag	gta	gcc	aag	gac	gat	atc	tgg	caa	ggc	ttc	gtc	caa	787
Ala	Asp	Leu	Lys	Val	Ala	Lys	Asp	Asp	Ile	Trp	Gln	Gly	Phe	Val	Gln	
	215					220					225					
gcg	cac	cgt	ttc	gac	cca	gaa	acg	gag	cag	gcg	ctt	ctt	agc	ggg	acc	835
Ala	His	Arg	Phe	Asp	Pro	Glu	Thr	Glu	Gln	Ala	Leu	Leu	Ser	Gly	Thr	
	230				235					240					245	
tcc	cct	gag	gcc	tac	gca	gag	ttc	ggc	gga	ctc	tcc	cgc	ttc	gcc	cac	883
Ser	Pro	Glu	Ala	Tyr	Ala	Glu	Phe	Gly	Gly	Leu	Ser	Arg	Phe	Ala	His	
				250				255						260		
gcg	gtg	tct	cat	ctc	acg	atc	gcc	caa	act	gtg	gtt	cgt	gca	ggg	caa	931
Ala	Val	Ser	His	Leu	Thr	Ile	Ala	Gln	Thr	Val	Val	Arg	Ala	Gly	Gln	
			265					270					275			
gcc	atc	aat	gta	ttg	cca	tcg	cat	gcg	tac	ttg	gaa	ctg	gat	atc	cgt	979
Ala	Ile	Asn	Val	Leu	Pro	Ser	His	Ala	Tyr	Leu	Glu	Leu	Asp	Ile	Arg	
		280					285					290				
acc	ctt	cca	ggc	caa	acc	aat	gac	tat	gtt	gat	gac	acc	ctg	cgt	gct	
1027																
Thr	Leu	Pro	Gly	Gln	Thr	Asn	Asp	Tyr	Val	Asp	Asp	Thr	Leu	Arg	Ala	
	295					300					305					
gct	ctg	ggc	gat	ctt	gcc	gat	gaa	gta	gaa	atc	gaa	cac	ctc	atc	tct	
1075																
Ala	Leu	Gly	Asp	Leu	Ala	Asp	Glu	Val	Glu	Ile	Glu	His	Leu	Ile	Ser	
	310				315				320					325		
gaa	gaa	gca	acg	gtg	agc	cca	act	gat	tcc	agg	ttg	tat	aac	acc	ttg	
1123																
Glu	Glu	Ala	Thr	Val	Ser	Pro	Thr	Asp	Ser	Arg	Leu	Tyr	Asn	Thr	Leu	
				330					335					340		
gaa	aaa	gtt	ctt	ggg	gat	ttc	ttc	ccc	gat	gcg	cct	gtg	gtc	cca	att	
1171																
Glu	Lys	Val	Leu	Gly	Asp	Phe	Phe	Pro	Asp	Ala	Pro	Val	Val	Pro	Ile	
			345					350					355			
att	tcc	tct	ggg	ggc	tct	gac	ctg	cgc	ttt	ggg	cgt	cga	cta	ggc	ggg	
1219																
Ile	Ser	Ser	Gly	Gly	Ser	Asp	Leu	Arg	Phe	Gly	Arg	Arg	Leu	Gly	Gly	
		360					365					370				
gtt	ggg	tat	ggg	ttt	gca	gtt	cat	gca	cgt	gaa	cga	act	ttg	gcg	gaa	
1267																
Val	Gly	Tyr	Gly	Phe	Ala	Val	His	Ala	Arg	Glu	Arg	Thr	Leu	Ala	Glu	
	375					380					385					

gca atg ggg caa ctt cac tcc cat gac gag gcg ctg tac ctg gaa gat  
 1315  
 Ala Met Gly Gln Leu His Ser His Asp Glu Ala Leu Tyr Leu Glu Asp  
 390 395 400 405

ctt gaa ctg act gtt cgg ggt tat gac tcc gtc gtg cgt gaa ttc cta  
 1363  
 Leu Glu Leu Thr Val Arg Gly Tyr Asp Ser Val Val Arg Glu Phe Leu  
 410 415 420

ggc taaaaacatg aagcaggagt ctt  
 1389  
 Gly

<210> 372  
 <211> 422  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 372  
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 Ser Leu Glu Arg Phe Phe Glu Gly Thr Pro Asn Val Lys Ile Thr Lys  
 20 25 30  
 Leu Glu Pro His Pro Gly Arg Thr Ser Ile Ile Val Thr Val Pro Gly  
 35 40 45  
 Ser Asp Pro Asp Ala Glu Pro Leu Thr Leu Leu Gly His Thr Asp Val  
 50 55 60  
 Val Pro Val Asp Leu Pro Lys Trp Thr Lys Asp Pro Phe Gly Ala Glu  
 65 70 75 80  
 Ile Ser Asp Gly Gln Ile Trp Gly Arg Gly Ser Val Asp Met Leu Phe  
 85 90 95  
 Ile Thr Ala Thr Gln Ala Ala Val Thr Arg Gln Val Ala Arg Glu Gly  
 100 105 110  
 Gly Leu Arg Gly Thr Leu Thr Phe Val Gly Val Ala Asp Glu Glu Ala  
 115 120 125  
 Arg Gly Gly Leu Gly Ala Lys Trp Leu Ser Glu Glu His Gln Asn Leu  
 130 135 140  
 Phe Ser Trp Lys Asn Cys Leu Ser Glu Ser Gly Gly Ser His Leu Pro  
 145 150 155 160  
 Val His Asp Gly Ser Asp Ala Val Val Ile Asn Val Gly Glu Lys Gly  
 165 170 175  
 Ala Ala Gln Arg Arg Ile His Val Asn Gly Asp Ala Gly His Gly Ser  
 180 185 190  
 Ile Pro Phe Asp Arg Asp Ser Ala Ile Val Lys Ile Gly Glu Val Ala  
 195 200 205

Arg Arg Ile Ala Ala Ala Asp Leu Lys Val Ala Lys Asp Asp Ile Trp  
 210 215 220  
 Gln Gly Phe Val Gln Ala His Arg Phe Asp Pro Glu Thr Glu Gln Ala  
 225 230 235 240  
 Leu Leu Ser Gly Thr Ser Pro Glu Ala Tyr Ala Glu Phe Gly Gly Leu  
 245 250 255  
 Ser Arg Phe Ala His Ala Val Ser His Leu Thr Ile Ala Gln Thr Val  
 260 265 270  
 Val Arg Ala Gly Gln Ala Ile Asn Val Leu Pro Ser His Ala Tyr Leu  
 275 280 285  
 Glu Leu Asp Ile Arg Thr Leu Pro Gly Gln Thr Asn Asp Tyr Val Asp  
 290 295 300  
 Asp Thr Leu Arg Ala Ala Leu Gly Asp Leu Ala Asp Glu Val Glu Ile  
 305 310 315 320  
 Glu His Leu Ile Ser Glu Glu Ala Thr Val Ser Pro Thr Asp Ser Arg  
 325 330 335  
 Leu Tyr Asn Thr Leu Glu Lys Val Leu Gly Asp Phe Phe Pro Asp Ala  
 340 345 350  
 Pro Val Val Pro Ile Ile Ser Ser Gly Gly Ser Asp Leu Arg Phe Gly  
 355 360 365  
 Arg Arg Leu Gly Gly Val Gly Tyr Gly Phe Ala Val His Ala Arg Glu  
 370 375 380  
 Arg Thr Leu Ala Glu Ala Met Gly Gln Leu His Ser His Asp Glu Ala  
 385 390 395 400  
 Leu Tyr Leu Glu Asp Leu Glu Leu Thr Val Arg Gly Tyr Asp Ser Val  
 405 410 415  
 Val Arg Glu Phe Leu Gly  
 420

<210> 373  
 <211> 525  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(502)  
 <223> RXS02937

<400> 373  
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tcgaaacatc caacgcattg gtgacaccgg tggtgtcgcg gtg atc agc aat ggg 115  
 Val Ile Ser Asn Gly  
 1 5

gaa ggt ccg gtt gtt gcg ctt cgt ggc gac att gat gcg ttg ccc atg 163

Glu Gly Pro Val Val Ala Leu Arg Gly Asp Ile Asp Ala Leu Pro Met  
                           10                          15                          20  
 gcg gag cga tcc ggc aaa gaa tac gca gca acc gga gtg aca cag gtg 211  
 Ala Glu Arg Ser Gly Lys Glu Tyr Ala Ala Thr Gly Val Thr Gln Val  
                           25                          30                          35  
 gat aac acc acc ggt caa gaa act ccg gtg gcg cat acc tgt ggc cac 259  
 Asp Asn Thr Thr Gly Gln Glu Thr Pro Val Ala His Thr Cys Gly His  
                           40                          45                          50  
 gat gtg cat att tca tca ctg ttg ggt gcg gtg cag gcg ttc aat tct 307  
 Asp Val His Ile Ser Ser Leu Leu Gly Ala Val Gln Ala Phe Asn Ser  
                           55                          60                          65  
 cat cgg gaa ttg tgg aac gga acg ttg atg gcc gtt ttc cag cca gcg 355  
 His Arg Glu Leu Trp Asn Gly Thr Leu Met Ala Val Phe Gln Pro Ala  
                           70                          75                          80                          85  
 gaa gag acg gca gct ggt gcg agg atg atg gcg gat cag gac aac gcg 403  
 Glu Glu Thr Ala Ala Gly Ala Arg Met Met Ala Asp Gln Asp Asn Ala  
                           90                          95                          100  
 ccg gga aat cac tct cca gcg ttc gcg cca gat atg cag cca act ctt 451  
 Pro Gly Asn His Ser Pro Ala Phe Ala Pro Asp Met Gln Pro Thr Leu  
                           105                          110                          115  
 gat cgt ggt gtg gaa gcg ctg gtt gta gct gct tct gcg tgg cta gta 499  
 Asp Arg Gly Val Glu Ala Leu Val Val Ala Ala Ser Ala Trp Leu Val  
                           120                          125                          130  
 aaa taattggcta atgaatcctt ttc 525  
 Lys

<210> 374  
 <211> 134  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 374  
 Val Ile Ser Asn Gly Glu Gly Pro Val Val Ala Leu Arg Gly Asp Ile  
   1                          5                          10                          15  
 Asp Ala Leu Pro Met Ala Glu Arg Ser Gly Lys Glu Tyr Ala Ala Thr  
                           20                          25                          30  
 Gly Val Thr Gln Val Asp Asn Thr Thr Gly Gln Glu Thr Pro Val Ala  
                           35                          40                          45  
 His Thr Cys Gly His Asp Val His Ile Ser Ser Leu Leu Gly Ala Val  
                           50                          55                          60  
 Gln Ala Phe Asn Ser His Arg Glu Leu Trp Asn Gly Thr Leu Met Ala  
   65                          70                          75                          80  
 Val Phe Gln Pro Ala Glu Glu Thr Ala Ala Gly Ala Arg Met Met Ala  
                           85                          90                          95  
 Asp Gln Asp Asn Ala Pro Gly Asn His Ser Pro Ala Phe Ala Pro Asp

100	105	110	
Met Gln Pro Thr Leu Asp Arg Gly Val Glu Ala Leu Val Val Ala Ala			
115	120	125	
Ser Ala Trp Leu Val Lys			
130			
<210> 375			
<211> 966			
<212> DNA			
<213> Corynebacterium glutamicum			
<220>			
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<222> (101)..(943)			
<223> RXA02194			
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gaagatatct acaagaacct gtaggagttt taaagcaatc atg ttg aaa atc gct 115			
		Met Leu Lys Ile Ala	1 5
gtc cca aac aaa ggc tcg ctg tcc gag cgc gcc atg gaa atc ctc gcc 163			
Val Pro Asn Lys Gly Ser Leu Ser Glu Arg Ala Met Glu Ile Leu Ala	10	15	20
gaa gca ggc tac gca ggc cgt gga gat tcc aaa tcc ctc aac gtt ttt 211			
Glu Ala Gly Tyr Ala Gly Arg Gly Asp Ser Lys Ser Leu Asn Val Phe	25	30	35
gat gaa gca aac aac gtt gaa ttc ttc ttc ctt cgc cct aaa gat atc 259			
Asp Glu Ala Asn Asn Val Glu Phe Phe Phe Leu Arg Pro Lys Asp Ile	40	45	50
gcc atc tac gtt gct ggt ggc cag ctc gat ttg ggt atc acc ggc cgc 307			
Ala Ile Tyr Val Ala Gly Gly Gln Leu Asp Leu Gly Ile Thr Gly Arg	55	60	65
gac ctt gct cgc gat tcc cag gct gat gtc cac gaa gtt ctt tcc ctc 355			
Asp Leu Ala Arg Asp Ser Gln Ala Asp Val His Glu Val Leu Ser Leu	70	75	80 85
ggc ttc ggt tcc tcc act ttc cgt tac gca gca cca gct gat gaa gag 403			
Gly Phe Gly Ser Ser Thr Phe Arg Tyr Ala Ala Pro Ala Asp Glu Glu	90	95	100
tgg agc atc gaa aag ctc gac ggc aag cgc atc gct acc tct tac ccc 451			
Trp Ser Ile Glu Lys Leu Asp Gly Lys Arg Ile Ala Thr Ser Tyr Pro	105	110	115
aac ctt gtt cgc gat gac ctc gca gca cgt ggg ctt tcc gct gag gtg 499			
Asn Leu Val Arg Asp Asp Leu Ala Ala Arg Gly Leu Ser Ala Glu Val	120	125	130
ctc cgc ctc gac ggt gca gta gag gta tcc atc aag ctt ggt gtc gca 547			
Leu Arg Leu Asp Gly Ala Val Glu Val Ser Ile Lys Leu Gly Val Ala	135	140	145

gat gcc atc gcc gat gtt gta tcc acc ggc cgc acg ctg cgt cag caa 595  
 Asp Ala Ile Ala Asp Val Val Ser Thr Gly Arg Thr Leu Arg Gln Gln  
 150 155 160 165  
 ggt ctt gca cct ttc ggc gag gtt ctg tgc acc tct gag gct gtc att 643  
 Gly Leu Ala Pro Phe Gly Glu Val Leu Cys Thr Ser Glu Ala Val Ile  
 170 175 180  
 gtt ggc cgc aag gat gaa aag gtc acc cca gag cag cag atc ctg ctt 691  
 Val Gly Arg Lys Asp Glu Lys Val Thr Pro Glu Gln Gln Ile Leu Leu  
 185 190 195  
 cgc cgc atc cag gga att ttg cac gcg cag aac ttc ctc atg ctg gat 739  
 Arg Arg Ile Gln Gly Ile Leu His Ala Gln Asn Phe Leu Met Leu Asp  
 200 205 210  
 tac aac gtc gac cgc gac aac ctg gac gct gcc act gca gta acc cca 787  
 Tyr Asn Val Asp Arg Asp Asn Leu Asp Ala Ala Thr Ala Val Thr Pro  
 215 220 225  
 ggc tta tcc ggc cca acg gta tcc cca ctg gca cgc gac aac tgg gtt 835  
 Gly Leu Ser Gly Pro Thr Val Ser Pro Leu Ala Arg Asp Asn Trp Val  
 230 235 240 245  
 gct gta cgc gcc atg gtg cca cgc agg tca gct aac gcc atc atg gat 883  
 Ala Val Arg Ala Met Val Pro Arg Arg Ser Ala Asn Ala Ile Met Asp  
 250 255 260  
 aag ctt gct gga ctc ggc gct gaa gcc atc ctg gct tct gaa atc cgc 931  
 Lys Leu Ala Gly Leu Gly Ala Glu Ala Ile Leu Ala Ser Glu Ile Arg  
 265 270 275  
 atc gcc cgc atc tagttttaac taccctcgaa aat 966  
 Ile Ala Arg Ile  
 280

&lt;210&gt; 376

&lt;211&gt; 281

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 376

Met Leu Lys Ile Ala Val Pro Asn Lys Gly Ser Leu Ser Glu Arg Ala  
 1 5 10 15  
 Met Glu Ile Leu Ala Glu Ala Gly Tyr Ala Gly Arg Gly Asp Ser Lys  
 20 25 30  
 Ser Leu Asn Val Phe Asp Glu Ala Asn Asn Val Glu Phe Phe Phe Leu  
 35 40 45  
 Arg Pro Lys Asp Ile Ala Ile Tyr Val Ala Gly Gly Gln Leu Asp Leu  
 50 55 60  
 Gly Ile Thr Gly Arg Asp Leu Ala Arg Asp Ser Gln Ala Asp Val His  
 65 70 75 80  
 Glu Val Leu Ser Leu Gly Phe Gly Ser Ser Thr Phe Arg Tyr Ala Ala  
 85 90 95



Pro Ala Asp Glu Glu Trp Ser Ile Glu Lys Leu Asp Gly Lys Arg Ile  
 100 105 110

Ala Thr Ser Tyr Pro Asn Leu Val Arg Asp Asp Leu Ala Ala Arg Gly  
 115 120 125

Leu Ser Ala Glu Val Leu Arg Leu Asp Gly Ala Val Glu Val Ser Ile  
 130 135 140

Lys Leu Gly Val Ala Asp Ala Ile Ala Asp Val Val Ser Thr Gly Arg  
 145 150 155 160

Thr Leu Arg Gln Gln Gly Leu Ala Pro Phe Gly Glu Val Leu Cys Thr  
 165 170 175

Ser Glu Ala Val Ile Val Gly Arg Lys Asp Glu Lys Val Thr Pro Glu  
 180 185 190

Gln Gln Ile Leu Leu Arg Arg Ile Gln Gly Ile Leu His Ala Gln Asn  
 195 200 205

Phe Leu Met Leu Asp Tyr Asn Val Asp Arg Asp Asn Leu Asp Ala Ala  
 210 215 220

Thr Ala Val Thr Pro Gly Leu Ser Gly Pro Thr Val Ser Pro Leu Ala  
 225 230 235 240

Arg Asp Asn Trp Val Ala Val Arg Ala Met Val Pro Arg Arg Ser Ala  
 245 250 255

Asn Ala Ile Met Asp Lys Leu Ala Gly Leu Gly Ala Glu Ala Ile Leu  
 260 265 270

Ala Ser Glu Ile Arg Ile Ala Arg Ile  
 275 280

&lt;210&gt; 377

&lt;211&gt; 393

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(370)

&lt;223&gt; RXA02195

&lt;400&gt; 377

tcgagccggc aggtgtcgca aaataaaacc aggtggggga gtgaaattat tcgactaata 60

tcctccccca aacacacatt gataactgtt gtgtggaaga atg tac cga gtg aag 115  
 Met Tyr Arg Val Lys  
 1 5

aca ttt gac tcg ctg tac gaa gaa ctt ctt aac cgt gct cag acc cgc 163  
 Thr Phe Asp Ser Leu Tyr Glu Glu Leu Leu Asn Arg Ala Gln Thr Arg  
 10 15 20

cct gaa ggg tct gga acc gtg gcc gcc ttg gat aaa ggc atc cat cat 211  
 Pro Glu Gly Ser Gly Thr Val Ala Ala Leu Asp Lys Gly Ile His His

25	30	35	
cta ggt aag aag gtc atc gaa gaa gcc gga gag gtc tgg att gca gcc			259
Leu Gly Lys Lys Val Ile Glu Glu Ala Gly Glu Val Trp Ile Ala Ala			
40	45	50	
gag tat gag acc gat gaa gag cta gcc gga gaa atc tcc cag ctc att			307
Glu Tyr Glu Thr Asp Glu Glu Leu Ala Gly Glu Ile Ser Gln Leu Ile			
55	60	65	
tat tgg acc cag gtc atc atg gtt gct cgc ggc ctg aag cca gaa gat			355
Tyr Trp Thr Gln Val Ile Met Val Ala Arg Gly Leu Lys Pro Glu Asp			
70	75	80	85
atc tac aag aac ctg taggagtttt aaagcaatca tgt			393
Ile Tyr Lys Asn Leu			
90			

<210> 378  
 <211> 90  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 378  
 Met Tyr Arg Val Lys Thr Phe Asp Ser Leu Tyr Glu Glu Leu Leu Asn  
 1 5 10 15  
 Arg Ala Gln Thr Arg Pro Glu Gly Ser Gly Thr Val Ala Ala Leu Asp  
 20 25 30  
 Lys Gly Ile His His Leu Gly Lys Lys Val Ile Glu Glu Ala Gly Glu  
 35 40 45  
 Val Trp Ile Ala Ala Glu Tyr Glu Thr Asp Glu Glu Leu Ala Gly Glu  
 50 55 60  
 Ile Ser Gln Leu Ile Tyr Trp Thr Gln Val Ile Met Val Ala Arg Gly  
 65 70 75 80  
 Leu Lys Pro Glu Asp Ile Tyr Lys Asn Leu  
 85 90

<210> 379  
 <211> 477  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(454)  
 <223> RXA01097

<400> 379  
 gcgccaacgc agtgcttgcc gcgaccattt tccacttccg cgaagtaacc atcgccgaag 60  
 taaagggagc cattaaagat gcaggatttg aggtgcggaa atg agt gac aat cca 115  
 Met Ser Asp Asn Pro  
 1 5

caa gag tat gag ctg gat tgg gac gtc gaa aag cga tta aag ctt aac 163  
 Gln Glu Tyr Glu Leu Asp Trp Asp Val Glu Lys Arg Leu Lys Leu Asn  
                   10                  15                  20

gac gcc ggc ctg gtg ccg gca atc gtc cag gcc gac ggg acc aac gag 211  
 Asp Ala Gly Leu Val Pro Ala Ile Val Gln Ala Asp Gly Thr Asn Glu  
                   25                  30                  35

gtc ctc atg atg gcc tgg atg gat acc cac gcg cta gcc tat act ttg 259  
 Val Leu Met Met Ala Trp Met Asp Thr His Ala Leu Ala Tyr Thr Leu  
                   40                  45                  50

gcg acc cgc cgt gga acc tat ttt tct agg tcc cgc aac gag tac tgg 307  
 Ala Thr Arg Arg Gly Thr Tyr Phe Ser Arg Ser Arg Asn Glu Tyr Trp  
                   55                  60                  65

atc aag ggc ctg acc tct gga aac gtc caa gaa gtc acc gga ctt gcc 355  
 Ile Lys Gly Leu Thr Ser Gly Asn Val Gln Glu Val Thr Gly Leu Ala  
                   70                  75                  80                  85

ctc gac tgc gac ggc gac acc gtc ctt ctg acc gtg aaa caa acc ggc 403  
 Leu Asp Cys Asp Gly Asp Thr Val Leu Leu Thr Val Lys Gln Thr Gly  
                   90                  95                  100

ggt gcg tgc cac act ggt gcc cac aca tgt ttc gac aat gac gtt ttg 451  
 Gly Ala Cys His Thr Gly Ala His Thr Cys Phe Asp Asn Asp Val Leu  
                   105                  110                  115

ctg taaaagcaac aacgattaag gaa 477  
 Leu

&lt;210&gt; 380

&lt;211&gt; 118

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 380

Met Ser Asp Asn Pro Gln Glu Tyr Glu Leu Asp Trp Asp Val Glu Lys  
   1                  5                  10                  15

Arg Leu Lys Leu Asn Asp Ala Gly Leu Val Pro Ala Ile Val Gln Ala  
                   20                  25                  30

Asp Gly Thr Asn Glu Val Leu Met Met Ala Trp Met Asp Thr His Ala  
                   35                  40                  45

Leu Ala Tyr Thr Leu Ala Thr Arg Arg Gly Thr Tyr Phe Ser Arg Ser  
                   50                  55                  60

Arg Asn Glu Tyr Trp Ile Lys Gly Leu Thr Ser Gly Asn Val Gln Glu  
                   65                  70                  75                  80

Val Thr Gly Leu Ala Leu Asp Cys Asp Gly Asp Thr Val Leu Leu Thr  
                   85                  90                  95

Val Lys Gln Thr Gly Gly Ala Cys His Thr Gly Ala His Thr Cys Phe  
                   100                  105                  110

Asp Asn Asp Val Leu Leu

115

<210> 381  
 <211> 861  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(838)  
 <223> RXA01100

&lt;400&gt; 381

gctgtgggct actcaattcc acccagaaaa atcaggtgac gcaggcgcac agctactgcg 60

aaactggatc aactacatct aacagatagg atcaatatcc atg acc ttc act att 115  
 Met Thr Phe Thr Ile  
 1 5

ctt cct gca gtc gat gta gtt aac gga caa gca gtt cgc cta gat cag 163  
 Leu Pro Ala Val Asp Val Val Asn Gly Gln Ala Val Arg Leu Asp Gln  
 10 15 20

ggc gag gcc ggc act gaa aag tct tat ggc acc cct ttg gaa tcc gca 211  
 Gly Glu Ala Gly Thr Glu Lys Ser Tyr Gly Thr Pro Leu Glu Ser Ala  
 25 30 35

ctg aag tgg cag gag cag ggt gca aag tgg ttg cac ttt gtg gac ctg 259  
 Leu Lys Trp Gln Glu Gln Gly Ala Lys Trp Leu His Phe Val Asp Leu  
 40 45 50

gac gca gcg ttc aac cgt ggt tcc aac cat gag atg atg gcg gaa att 307  
 Asp Ala Ala Phe Asn Arg Gly Ser Asn His Glu Met Met Ala Glu Ile  
 55 60 65

gtc ggc aag ctc gat gtt gat gtg gag ctc act ggc ggt atc cgt gat 355  
 Val Gly Lys Leu Asp Val Asp Val Glu Leu Thr Gly Gly Ile Arg Asp  
 70 75 80 85

gat gag tct ctg gag cgc gcg ctg gca acc ggt gca cgt cgt gta aac 403  
 Asp Glu Ser Leu Glu Arg Ala Leu Ala Thr Gly Ala Arg Arg Val Asn  
 90 95 100

att ggt acc gct gct ctg gag aag cca gag tgg att gct tct gcg att 451  
 Ile Gly Thr Ala Ala Leu Glu Lys Pro Glu Trp Ile Ala Ser Ala Ile  
 105 110 115

caa cgc tat ggc gag aag att gct gtc gat atc gct gtg cgt ttg gaa 499  
 Gln Arg Tyr Gly Glu Lys Ile Ala Val Asp Ile Ala Val Arg Leu Glu  
 120 125 130

gat ggt gaa tgg cgc acc cgt gga aac ggt tgg gtc tcc gat ggt ggc 547  
 Asp Gly Glu Trp Arg Thr Arg Gly Asn Gly Trp Val Ser Asp Gly Gly  
 135 140 145

gat ctg tgg gaa gtt ctc gag cgt ttg gat tcc caa ggt tgt gca cgt 595  
 Asp Leu Trp Glu Val Leu Glu Arg Leu Asp Ser Gln Gly Cys Ala Arg  
 150 155 160 165

ttc gtg gtt acc gat gtg tcc aag gac ggc acc ttg agt ggt cca aat 643

Phe Val Val Thr Asp Val Ser Lys Asp Gly Thr Leu Ser Gly Pro Asn  
 170 175 180  
 gtt gag ctg ctg cgt gag gtt gct gca gct aca gac gca cct atc gtg 691  
 Val Glu Leu Leu Arg Glu Val Ala Ala Ala Thr Asp Ala Pro Ile Val  
 185 190 195  
 gca tct ggt gga att tct gtt ttg gaa gat gtt ttg gaa cta gcc aag 739  
 Ala Ser Gly Gly Ile Ser Val Leu Glu Asp Val Leu Glu Leu Ala Lys  
 200 205 210  
 tac cag gat gag ggc att gat tcc gtc atc att ggc aag gca ctt tat 787  
 Tyr Gln Asp Glu Gly Ile Asp Ser Val Ile Ile Gly Lys Ala Leu Tyr  
 215 220 225  
 gag cac aag ttc acc ctc gaa gag gct ttg gct gca gta gaa aag ctc 835  
 Glu His Lys Phe Thr Leu Glu Glu Ala Leu Ala Ala Val Glu Lys Leu  
 230 235 240 245  
 ggt taatacatgg atgctcgtgg gat 861  
 Gly

<210> 382  
 <211> 246  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

<400> 382  
 Met Thr Phe Thr Ile Leu Pro Ala Val Asp Val Val Asn Gly Gln Ala  
 1 5 10 15  
 Val Arg Leu Asp Gln Gly Glu Ala Gly Thr Glu Lys Ser Tyr Gly Thr  
 20 25 30  
 Pro Leu Glu Ser Ala Leu Lys Trp Gln Glu Gln Gly Ala Lys Trp Leu  
 35 40 45  
 His Phe Val Asp Leu Asp Ala Ala Phe Asn Arg Gly Ser Asn His Glu  
 50 55 60  
 Met Met Ala Glu Ile Val Gly Lys Leu Asp Val Asp Val Glu Leu Thr  
 65 70 75 80  
 Gly Gly Ile Arg Asp Asp Glu Ser Leu Glu Arg Ala Leu Ala Thr Gly  
 85 90 95  
 Ala Arg Arg Val Asn Ile Gly Thr Ala Ala Leu Glu Lys Pro Glu Trp  
 100 105 110  
 Ile Ala Ser Ala Ile Gln Arg Tyr Gly Glu Lys Ile Ala Val Asp Ile  
 115 120 125  
 Ala Val Arg Leu Glu Asp Gly Glu Trp Arg Thr Arg Gly Asn Gly Trp  
 130 135 140  
 Val Ser Asp Gly Gly Asp Leu Trp Glu Val Leu Glu Arg Leu Asp Ser  
 145 150 155 160  
 Gln Gly Cys Ala Arg Phe Val Val Thr Asp Val Ser Lys Asp Gly Thr

				165					170					175			
Leu	Ser	Gly	Pro	Asn	Val	Glu	Leu	Leu	Arg	Glu	Val	Ala	Ala	Ala	Thr		
			180					185					190				
Asp	Ala	Pro	Ile	Val	Ala	Ser	Gly	Gly	Ile	Ser	Val	Leu	Glu	Asp	Val		
		195					200					205					
Leu	Glu	Leu	Ala	Lys	Tyr	Gln	Asp	Glu	Gly	Ile	Asp	Ser	Val	Ile	Ile		
	210					215					220						
Gly	Lys	Ala	Leu	Tyr	Glu	His	Lys	Phe	Thr	Leu	Glu	Glu	Ala	Leu	Ala		
225					230					235					240		
Ala	Val	Glu	Lys	Leu	Gly												
				245													

&lt;210&gt; 383

&lt;211&gt; 756

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(733)

&lt;223&gt; RXA01101

&lt;400&gt; 383

atcgcagcta ggccagtgtg gtggatataa aacccttttg gggagaaaga aactcgactg 60

cggttcttga tcctgaaagc acgtgacata aactatcggc atg acc aaa act gtc 115  
 Met Thr Lys Thr Val  
 1 5

gcc ctt ctc gac tac gga tct gga aac ctt cgt tct gct caa cgc gca 163  
 Ala Leu Leu Asp Tyr Gly Ser Gly Asn Leu Arg Ser Ala Gln Arg Ala  
 10 15 20

cta gag cgt gcc ggt gca gaa gtt atc gtg agc tcc gat cca gaa gtt 211  
 Leu Glu Arg Ala Gly Ala Glu Val Ile Val Ser Ser Asp Pro Glu Val  
 25 30 35

tgc acc aac gct gat ggc ctc cta gtt cct gga gtg ggc gca ttt gat 259  
 Cys Thr Asn Ala Asp Gly Leu Leu Val Pro Gly Val Gly Ala Phe Asp  
 40 45 50

gcc tgc atg aag ggt ttg aaa aac gtc ttc gga cat cgc att atc gga 307  
 Ala Cys Met Lys Gly Leu Lys Asn Val Phe Gly His Arg Ile Ile Gly  
 55 60 65

cag cgt ctt gct ggt gga cgt cca gtg atg ggt att tgt gtg ggc atg 355  
 Gln Arg Leu Ala Gly Gly Arg Pro Val Met Gly Ile Cys Val Gly Met  
 70 75 80 85

cag atc ctg ttc gat gaa ggc gat gag cac ggc att aag tca gct ggt 403  
 Gln Ile Leu Phe Asp Glu Gly Asp Glu His Gly Ile Lys Ser Ala Gly  
 90 95 100

tgc ggc gag tgg cct ggc aaa gtg gaa cgc ctc caa gcg gag atc ctg 451  
 Cys Gly Glu Trp Pro Gly Lys Val Glu Arg Leu Gln Ala Glu Ile Leu

105							110							115							
cct	cac	atg	ggg	tgg	aac	aca	ctt	gaa	atg	cct	acc	aac	tca	cca	atg	499					
Pro	His	Met	Gly	Trp	Asn	Thr	Leu	Glu	Met	Pro	Thr	Asn	Ser	Pro	Met						
		120						125				130									
ttt	gag	gga	att	tca	cct	gat	gag	cgt	ttc	tac	ttc	gtg	cac	tcc	tat	547					
Phe	Glu	Gly	Ile	Ser	Pro	Asp	Glu	Arg	Phe	Tyr	Phe	Val	His	Ser	Tyr						
	135					140					145										
ggt	gtg	cgc	aag	tgg	acg	ttg	gaa	acc	gac	gat	ctg	acc	acg	cct	cca	595					
Gly	Val	Arg	Lys	Trp	Thr	Leu	Glu	Thr	Asp	Asp	Leu	Thr	Thr	Pro	Pro						
150					155				160						165						
gag	gtt	gtg	tgg	gcg	aag	cac	gaa	aat	gat	cgt	ttt	gtg	gca	gct	gtg	643					
Glu	Val	Val	Trp	Ala	Lys	His	Glu	Asn	Asp	Arg	Phe	Val	Ala	Ala	Val						
			170						175					180							
gaa	aac	ggc	acg	ctg	tgg	gct	act	caa	ttc	cac	cca	gaa	aaa	tca	ggt	691					
Glu	Asn	Gly	Thr	Leu	Trp	Ala	Thr	Gln	Phe	His	Pro	Glu	Lys	Ser	Gly						
		185						190					195								
gac	gca	ggc	gca	cag	cta	ctg	cga	aac	tgg	atc	aac	tac	atc			733					
Asp	Ala	Gly	Ala	Gln	Leu	Leu	Arg	Asn	Trp	Ile	Asn	Tyr	Ile								
		200					205					210									
taacagatag gatcaatatt cat															756						

&lt;210&gt; 384

&lt;211&gt; 211

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 384

Met	Thr	Lys	Thr	Val	Ala	Leu	Leu	Asp	Tyr	Gly	Ser	Gly	Asn	Leu	Arg
1				5					10					15	

Ser	Ala	Gln	Arg	Ala	Leu	Glu	Arg	Ala	Gly	Ala	Glu	Val	Ile	Val	Ser
		20						25					30		

Ser	Asp	Pro	Glu	Val	Cys	Thr	Asn	Ala	Asp	Gly	Leu	Leu	Val	Pro	Gly
		35					40					45			

Val	Gly	Ala	Phe	Asp	Ala	Cys	Met	Lys	Gly	Leu	Lys	Asn	Val	Phe	Gly
	50					55					60				

His	Arg	Ile	Ile	Gly	Gln	Arg	Leu	Ala	Gly	Gly	Arg	Pro	Val	Met	Gly
65					70					75					80

Ile	Cys	Val	Gly	Met	Gln	Ile	Leu	Phe	Asp	Glu	Gly	Asp	Glu	His	Gly
				85					90					95	

Ile	Lys	Ser	Ala	Gly	Cys	Gly	Glu	Trp	Pro	Gly	Lys	Val	Glu	Arg	Leu
			100					105					110		

Gln	Ala	Glu	Ile	Leu	Pro	His	Met	Gly	Trp	Asn	Thr	Leu	Glu	Met	Pro
		115					120					125			

Thr	Asn	Ser	Pro	Met	Phe	Glu	Gly	Ile	Ser	Pro	Asp	Glu	Arg	Phe	Tyr
	130					135					140				

Phe Val His Ser Tyr Gly Val Arg Lys Trp Thr Leu Glu Thr Asp Asp  
 145 150 155 160  
 Leu Thr Thr Pro Pro Glu Val Val Trp Ala Lys His Glu Asn Asp Arg  
 165 170 175  
 Phe Val Ala Ala Val Glu Asn Gly Thr Leu Trp Ala Thr Gln Phe His  
 180 185 190  
 Pro Glu Lys Ser Gly Asp Ala Gly Ala Gln Leu Leu Arg Asn Trp Ile  
 195 200 205  
 Asn Tyr Ile  
 210

<210> 385  
 <211> 723  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(700)  
 <223> RXN01657

<400> 385  
 cctccgtcat tgccgacgta tcccgcggcc tgggtgaagc catggtgggc atcaacgtat 60

ccgacgttcc agcaccacac cgactcgccg agcgcggctg gtg atc gtt gga gtt 115  
 Val Ile Val Gly Val  
 1 5

tta gct ctc cag ggc ggg gtg gaa gaa cac ctc acc gcc ttg gaa gct 163  
 Leu Ala Leu Gln Gly Gly Val Glu Glu His Leu Thr Ala Leu Glu Ala  
 10 15 20

ctc gga gcg acg acc cga aaa gta cgt gtg cca aag gac ctt gat ggt 211  
 Leu Gly Ala Thr Thr Arg Lys Val Arg Val Pro Lys Asp Leu Asp Gly  
 25 30 35

ctc gaa ggc atc gtc atc ccc ggc ggg gaa tcc acc gtg ttg gac aaa 259  
 Leu Glu Gly Ile Val Ile Pro Gly Gly Glu Ser Thr Val Leu Asp Lys  
 40 45 50

ctg gct cgg aca ttc gac gtg gta gaa cct cta gcg aat ctc att cgc 307  
 Leu Ala Arg Thr Phe Asp Val Val Glu Pro Leu Ala Asn Leu Ile Arg  
 55 60 65

gac ggc cta ccc gtt ttc gct acc tgc gct ggc ctg atc tat ctg gcg 355  
 Asp Gly Leu Pro Val Phe Ala Thr Cys Ala Gly Leu Ile Tyr Leu Ala  
 70 75 80 85

aaa cac ctc gac aac cca gca agg gga caa caa acc ttg gcg gta gtg 403  
 Lys His Leu Asp Asn Pro Ala Arg Gly Gln Gln Thr Leu Ala Val Val  
 90 95 100

gac gtg gtg gtg cgt cga aac gca ttt ggc gcc caa cgc gaa tcc ttc 451  
 Asp Val Val Val Arg Arg Asn Ala Phe Gly Ala Gln Arg Glu Ser Phe  
 105 110 115



gac acc acc gtg gat gtt tcc ttc gac ggt gca aca ttc ccc gga gtg 499  
 Asp Thr Thr Val Asp Val Ser Phe Asp Gly Ala Thr Phe Pro Gly Val  
 120 125 130  
 cag gcc tcg ttt atc cga gct ccc atc gtc act gct ttt ggt cct acg 547  
 Gln Ala Ser Phe Ile Arg Ala Pro Ile Val Thr Ala Phe Gly Pro Thr  
 135 140 145  
 gta gaa gcg atc gct gct ctc aac ggt ggg gag gtg gtt ggt gta cgc 595  
 Val Glu Ala Ile Ala Ala Leu Asn Gly Gly Glu Val Val Gly Val Arg  
 150 155 160 165  
 caa ggc aac atc atc gcg ctg tct ttc cat ccc gaa gaa acc ggc gat 643  
 Gln Gly Asn Ile Ile Ala Leu Ser Phe His Pro Glu Glu Thr Gly Asp  
 170 175 180  
 tac cgc atc cac caa gcc tgg ctg gac ctg gtg aga aaa cac gct gaa 691  
 Tyr Arg Ile His Gln Ala Trp Leu Asp Leu Val Arg Lys His Ala Glu  
 185 190 195  
 ctg gcg att tgatgttttc ggtagcgctc tgt 723  
 Leu Ala Ile  
 200

&lt;210&gt; 386

&lt;211&gt; 200

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 386

Val Ile Val Gly Val Leu Ala Leu Gln Gly Gly Val Glu Glu His Leu  
 1 5 10 15  
 Thr Ala Leu Glu Ala Leu Gly Ala Thr Thr Arg Lys Val Arg Val Pro  
 20 25 30  
 Lys Asp Leu Asp Gly Leu Glu Gly Ile Val Ile Pro Gly Gly Glu Ser  
 35 40 45  
 Thr Val Leu Asp Lys Leu Ala Arg Thr Phe Asp Val Val Glu Pro Leu  
 50 55 60  
 Ala Asn Leu Ile Arg Asp Gly Leu Pro Val Phe Ala Thr Cys Ala Gly  
 65 70 75 80  
 Leu Ile Tyr Leu Ala Lys His Leu Asp Asn Pro Ala Arg Gly Gln Gln  
 85 90 95  
 Thr Leu Ala Val Val Asp Val Val Val Arg Arg Asn Ala Phe Gly Ala  
 100 105 110  
 Gln Arg Glu Ser Phe Asp Thr Thr Val Asp Val Ser Phe Asp Gly Ala  
 115 120 125  
 Thr Phe Pro Gly Val Gln Ala Ser Phe Ile Arg Ala Pro Ile Val Thr  
 130 135 140  
 Ala Phe Gly Pro Thr Val Glu Ala Ile Ala Ala Leu Asn Gly Gly Glu  
 145 150 155 160

Val Val Gly Val Arg Gln Gly Asn Ile Ile Ala Leu Ser Phe His Pro  
 165 170 175

Glu Glu Thr Gly Asp Tyr Arg Ile His Gln Ala Trp Leu Asp Leu Val  
 180 185 190

Arg Lys His Ala Glu Leu Ala Ile  
 195 200

<210> 387

<211> 601

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(601)

<223> FRXA01657

<400> 387

cctccgcatc tgccgacgta tcccgcggcc tgggtgaagc catggtgggc atcaacgtat 60

ccgacgttcc agcaccacac cgactcgccg agcgcggctg gtg atc gtt gga gtt 115  
 Val Ile Val Gly Val  
 1 5

tta gct ctc cag ggc ggg gtg gaa gaa cac ctc acc gcc ttg gaa gct 163  
 Leu Ala Leu Gln Gly Gly Val Glu Glu His Leu Thr Ala Leu Glu Ala  
 10 15 20

ctc gga gcg acg acc cga aaa gta cgt gtg cca aag gac ctt gat ggt 211  
 Leu Gly Ala Thr Thr Arg Lys Val Arg Val Pro Lys Asp Leu Asp Gly  
 25 30 35

ctc gaa ggc atc gtc atc ccc ggc ggg gaa tcc acc gtg ttg gac aaa 259  
 Leu Glu Gly Ile Val Ile Pro Gly Gly Glu Ser Thr Val Leu Asp Lys  
 40 45 50

ctg gct cgg aca ttc gac gtg gta gaa cct cta gcg aat ctc att cgc 307  
 Leu Ala Arg Thr Phe Asp Val Val Glu Pro Leu Ala Asn Leu Ile Arg  
 55 60 65

gac ggc cta ccc gtt ttc gct acc tgc gct ggc ctg atc tat ctg gcg 355  
 Asp Gly Leu Pro Val Phe Ala Thr Cys Ala Gly Leu Ile Tyr Leu Ala  
 70 75 80 85

aaa cac ctc gac aac cca gca agg gga caa caa acc ttg gcg gta gtg 403  
 Lys His Leu Asp Asn Pro Ala Arg Gly Gln Gln Thr Leu Ala Val Val  
 90 95 100

gac gtg gtg gtg cgt cga aac gca ttt ggc gcc caa cgc gaa tcc ttc 451  
 Asp Val Val Val Arg Arg Asn Ala Phe Gly Ala Gln Arg Glu Ser Phe  
 105 110 115

gac acc acc gtg gat gtt tcc ttc gac ggt gca aca ttc ccc gga gtg 499  
 Asp Thr Thr Val Asp Val Ser Phe Asp Gly Ala Thr Phe Pro Gly Val  
 120 125 130

cag gcc tcg ttt atc cga gct ccc atc gtc act gct ttt ggt cct acg 547

Gln Ala Ser Phe Ile Arg Ala Pro Ile Val Thr Ala Phe Gly Pro Thr  
 135 140 145

gta gaa gcg atc gct gct ctc aac ggt ggg gag gtg gtt ggt gta cgc 595  
 Val Glu Ala Ile Ala Ala Leu Asn Gly Gly Glu Val Val Gly Val Arg  
 150 155 160 165

caa ggc 601  
 Gln Gly

<210> 388  
 <211> 167  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 388  
 Val Ile Val Gly Val Leu Ala Leu Gln Gly Gly Val Glu Glu His Leu  
 1 5 10 15

Thr Ala Leu Glu Ala Leu Gly Ala Thr Thr Arg Lys Val Arg Val Pro  
 20 25 30

Lys Asp Leu Asp Gly Leu Glu Gly Ile Val Ile Pro Gly Gly Glu Ser  
 35 40 45

Thr Val Leu Asp Lys Leu Ala Arg Thr Phe Asp Val Val Glu Pro Leu  
 50 55 60

Ala Asn Leu Ile Arg Asp Gly Leu Pro Val Phe Ala Thr Cys Ala Gly  
 65 70 75 80

Leu Ile Tyr Leu Ala Lys His Leu Asp Asn Pro Ala Arg Gly Gln Gln  
 85 90 95

Thr Leu Ala Val Val Asp Val Val Val Arg Arg Asn Ala Phe Gly Ala  
 100 105 110

Gln Arg Glu Ser Phe Asp Thr Thr Val Asp Val Ser Phe Asp Gly Ala  
 115 120 125

Thr Phe Pro Gly Val Gln Ala Ser Phe Ile Arg Ala Pro Ile Val Thr  
 130 135 140

Ala Phe Gly Pro Thr Val Glu Ala Ile Ala Ala Leu Asn Gly Gly Glu  
 145 150 155 160

Val Val Gly Val Arg Gln Gly  
 165

<210> 389  
 <211> 897  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(874)  
 <223> RXA01098

&lt;400&gt; 389

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aaaagggctc acgatgtgct gttaagtaag attgaaaaag ttcggttgat gcatgcagat 60

gcaggtaatg accagtcggtt aaatgaggag tacaagtaaa atg ggc gtg gca att 115
                                         Met Gly Val Ala Ile
                                         1                               5

cga gtt att cct tgc ctg gac gtg gac aac ggc cgg gtt gtt aaa ggc 163
Arg Val Ile Pro Cys Leu Asp Val Asp Asn Gly Arg Val Val Lys Gly
                        10                               15                               20

gtg aac ttt gaa aac ctc cgc gat gct ggc gat cct gtg gag ttg gca 211
Val Asn Phe Glu Asn Leu Arg Asp Ala Gly Asp Pro Val Glu Leu Ala
                        25                               30                               35

aag cgc tat gac gag gaa ggg gca gat gag ctg acc ttc ctg gat gtc 259
Lys Arg Tyr Asp Glu Glu Gly Ala Asp Glu Leu Thr Phe Leu Asp Val
                        40                               45                               50

acc gcc tcg aag cat ggt cgc ggc acc atg ctg gat gtt gtt cga cgc 307
Thr Ala Ser Lys His Gly Arg Gly Thr Met Leu Asp Val Val Arg Arg
                        55                               60                               65

acc gct gat cag gtg ttc atc cct ctg act gtc ggt ggc ggc gtg cgc 355
Thr Ala Asp Gln Val Phe Ile Pro Leu Thr Val Gly Gly Gly Val Arg
                        70                               75                               80                               85

agc gaa gaa gat gtt gat caa ttg ctg cgc gct ggc gcc gac aag gtt 403
Ser Glu Glu Asp Val Asp Gln Leu Leu Arg Ala Gly Ala Asp Lys Val
                        90                               95                               100

tcg gtg aac acg tct gcg att gcc cgt cca gaa ctg ctg tca gag ctg 451
Ser Val Asn Thr Ser Ala Ile Ala Arg Pro Glu Leu Leu Ser Glu Leu
                        105                               110                               115

tcc aag cgt ttt ggt gct cag tgc atc gtg ttg tct gtg gat gcc agg 499
Ser Lys Arg Phe Gly Ala Gln Cys Ile Val Leu Ser Val Asp Ala Arg
                        120                               125                               130

cgc gtt cct gaa ggt gga act cct cag cca tct ggt ttt gaa gtc acc 547
Arg Val Pro Glu Gly Gly Thr Pro Gln Pro Ser Gly Phe Glu Val Thr
                        135                               140                               145

acc cac ggc ggt tcc aag tcc gca gaa ctt gat gca atc gag tgg gca 595
Thr His Gly Gly Ser Lys Ser Ala Glu Leu Asp Ala Ile Glu Trp Ala
                        150                               155                               160                               165

aag cgc ggc gaa gag ctg ggc gtt ggc gaa att ctg ctc aac tcc atg 643
Lys Arg Gly Glu Glu Leu Gly Val Gly Glu Ile Leu Leu Asn Ser Met
                        170                               175                               180

gac ggc gac ggc acc aaa aac ggc ttt gac cta gag ctg ctg gaa aaa 691
Asp Gly Asp Gly Thr Lys Asn Gly Phe Asp Leu Glu Leu Leu Glu Lys
                        185                               190                               195

gtt cgc gca gcc gta tcc att cct gta atc gcc tcc ggc ggc gct ggc 739
Val Arg Ala Ala Val Ser Ile Pro Val Ile Ala Ser Gly Gly Ala Gly
                        200                               205                               210

aag gcg gag cat ttc cca cca gct gtt gca gct ggc gcc aac gca gtg 787

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Lys Ala Glu His Phe Pro Pro Ala Val Ala Ala Gly Ala Asn Ala Val  
 215 220 225  
 ctt gcc gcg acc att ttc cac ttc cgc gaa gta acc atc gcc gaa gta 835  
 Leu Ala Ala Thr Ile Phe His Phe Arg Glu Val Thr Ile Ala Glu Val  
 230 235 240 245  
 aag gga gcc att aaa gat gca gga ttt gag gtg cgg aaa tgagtgacaa 884  
 Lys Gly Ala Ile Lys Asp Ala Gly Phe Glu Val Arg Lys  
 250 255  
 tccacaagag tat 897

<210> 390  
 <211> 258  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 390

Met Gly Val Ala Ile Arg Val Ile Pro Cys Leu Asp Val Asp Asn Gly  
 1 5 10 15  
 Arg Val Val Lys Gly Val Asn Phe Glu Asn Leu Arg Asp Ala Gly Asp  
 20 25 30  
 Pro Val Glu Leu Ala Lys Arg Tyr Asp Glu Glu Gly Ala Asp Glu Leu  
 35 40 45  
 Thr Phe Leu Asp Val Thr Ala Ser Lys His Gly Arg Gly Thr Met Leu  
 50 55 60  
 Asp Val Val Arg Arg Thr Ala Asp Gln Val Phe Ile Pro Leu Thr Val  
 65 70 75 80  
 Gly Gly Gly Val Arg Ser Glu Glu Asp Val Asp Gln Leu Leu Arg Ala  
 85 90 95  
 Gly Ala Asp Lys Val Ser Val Asn Thr Ser Ala Ile Ala Arg Pro Glu  
 100 105 110  
 Leu Leu Ser Glu Leu Ser Lys Arg Phe Gly Ala Gln Cys Ile Val Leu  
 115 120 125  
 Ser Val Asp Ala Arg Arg Val Pro Glu Gly Gly Thr Pro Gln Pro Ser  
 130 135 140  
 Gly Phe Glu Val Thr Thr His Gly Gly Ser Lys Ser Ala Glu Leu Asp  
 145 150 155 160  
 Ala Ile Glu Trp Ala Lys Arg Gly Glu Glu Leu Gly Val Gly Glu Ile  
 165 170 175  
 Leu Leu Asn Ser Met Asp Gly Asp Gly Thr Lys Asn Gly Phe Asp Leu  
 180 185 190  
 Glu Leu Leu Glu Lys Val Arg Ala Ala Val Ser Ile Pro Val Ile Ala  
 195 200 205  
 Ser Gly Gly Ala Gly Lys Ala Glu His Phe Pro Pro Ala Val Ala Ala  
 210 215 220

Gly Ala Asn Ala Val Leu Ala Ala Thr Ile Phe His Phe Arg Glu Val  
 225 230 235 240

Thr Ile Ala Glu Val Lys Gly Ala Ile Lys Asp Ala Gly Phe Glu Val  
 245 250 255

Arg Lys

<210> 391

<211> 729

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101) .. (706)

<223> RXN01104

<400> 391

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gagatcatca agctgaacct gtaagagaga agaattttttc atg act gtc gca cca 115  
 Met Thr Val Ala Pro  
 1 5

aga att ggt acc gca acc cgc acc acc agc gaa tcc gac atc acc gtc 163  
 Arg Ile Gly Thr Ala Thr Arg Thr Thr Ser Glu Ser Asp Ile Thr Val  
 10 15 20

gag atc aac ctg gac ggc acc ggc aaa gta gat atc gat acc ggc ctg 211  
 Glu Ile Asn Leu Asp Gly Thr Gly Lys Val Asp Ile Asp Thr Gly Leu  
 25 30 35

cca ttt ttc gac cac atg ctc act gca ttc ggc gtg cac ggc agt ttt 259  
 Pro Phe Phe Asp His Met Leu Thr Ala Phe Gly Val His Gly Ser Phe  
 40 45 50

gat ctg aaa gtc cat gcc aag ggc gac atc gag atc gac gca cac cac 307  
 Asp Leu Lys Val His Ala Lys Gly Asp Ile Glu Ile Asp Ala His His  
 55 60 65

acc gtg gaa gat acc gcc atc gtg ctc ggc caa gca ctc ctt gac gct 355  
 Thr Val Glu Asp Thr Ala Ile Val Leu Gly Gln Ala Leu Leu Asp Ala  
 70 75 80 85

att ggc gac aag aaa ggc atc cgc cgt ttc gca tcc tgc cag ctg ccc 403  
 Ile Gly Asp Lys Lys Gly Ile Arg Arg Phe Ala Ser Cys Gln Leu Pro  
 90 95 100

atg gat gag gca tta gtg gag tcc gtg gtg gat atc tcc ggt cgc cca 451  
 Met Asp Glu Ala Leu Val Glu Ser Val Val Asp Ile Ser Gly Arg Pro  
 105 110 115

tac ttc gtg atc tcc ggc gaa cca gac cac atg atc acc tcc gtg atc 499  
 Tyr Phe Val Ile Ser Gly Glu Pro Asp His Met Ile Thr Ser Val Ile  
 120 125 130

ggt gga cac tac gca acc gtg atc aac gag cac ttc ttt gaa acc ctc 547

Gly Gly His Tyr Ala Thr Val Ile Asn Glu His Phe Phe Glu Thr Leu  
 135 140 145  
 gcg ctc aac tcc cga atc acc ctc cac gtg atc tgc cac tac ggc cgc 595  
 Ala Leu Asn Ser Arg Ile Thr Leu His Val Ile Cys His Tyr Gly Arg  
 150 155 160 165  
 gac cct cac cac atc acc gaa gca gag tac aag gct gtt gcc cgt gcg 643  
 Asp Pro His His Ile Thr Glu Ala Glu Tyr Lys Ala Val Ala Arg Ala  
 170 175 180  
 ctg cgc ggt gcc gta gag atg gat cct cgt caa aca gga atc cca tcc 691  
 Leu Arg Gly Ala Val Glu Met Asp Pro Arg Gln Thr Gly Ile Pro Ser  
 185 190 195  
 act aag gga gcg ctc tagacatgaa ctcttctccc atc 729  
 Thr Lys Gly Ala Leu  
 200

&lt;210&gt; 392

&lt;211&gt; 202

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 392

Met Thr Val Ala Pro Arg Ile Gly Thr Ala Thr Arg Thr Thr Ser Glu  
 1 5 10 15  
 Ser Asp Ile Thr Val Glu Ile Asn Leu Asp Gly Thr Gly Lys Val Asp  
 20 25 30  
 Ile Asp Thr Gly Leu Pro Phe Phe Asp His Met Leu Thr Ala Phe Gly  
 35 40 45  
 Val His Gly Ser Phe Asp Leu Lys Val His Ala Lys Gly Asp Ile Glu  
 50 55 60  
 Ile Asp Ala His His Thr Val Glu Asp Thr Ala Ile Val Leu Gly Gln  
 65 70 75 80  
 Ala Leu Leu Asp Ala Ile Gly Asp Lys Lys Gly Ile Arg Arg Phe Ala  
 85 90 95  
 Ser Cys Gln Leu Pro Met Asp Glu Ala Leu Val Glu Ser Val Val Asp  
 100 105 110  
 Ile Ser Gly Arg Pro Tyr Phe Val Ile Ser Gly Glu Pro Asp His Met  
 115 120 125  
 Ile Thr Ser Val Ile Gly Gly His Tyr Ala Thr Val Ile Asn Glu His  
 130 135 140  
 Phe Phe Glu Thr Leu Ala Leu Asn Ser Arg Ile Thr Leu His Val Ile  
 145 150 155 160  
 Cys His Tyr Gly Arg Asp Pro His His Ile Thr Glu Ala Glu Tyr Lys  
 165 170 175  
 Ala Val Ala Arg Ala Leu Arg Gly Ala Val Glu Met Asp Pro Arg Gln  
 180 185 190

Thr Gly Ile Pro Ser Thr Lys Gly Ala Leu  
195 200

<210> 393

<211> 729

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(706)

<223> FRXA01104

<400> 393

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gagatcatca agctgaacct gtaagagaga agaatttttc atg act gtc gca cca 115  
Met Thr Val Ala Pro  
1 5

aga att ggt acc gca acc cgc acc acc agc gaa tcc gac atc acc gtc 163  
Arg Ile Gly Thr Ala Thr Arg Thr Thr Ser Glu Ser Asp Ile Thr Val  
10 15 20

gag atc aac ctg gac ggc acc ggc aaa gta gat atc gat acc ggc ctg 211  
Glu Ile Asn Leu Asp Gly Thr Gly Lys Val Asp Ile Asp Thr Gly Leu  
25 30 35

cca ttt ttc gac cac atg ctc act gca ttc ggc gtg cac ggc agt ttt 259  
Pro Phe Phe Asp His Met Leu Thr Ala Phe Gly Val His Gly Ser Phe  
40 45 50

gat ctg aaa gtc cat gcc aag ggc gac atc gag atc gac gca cac cac 307  
Asp Leu Lys Val His Ala Lys Gly Asp Ile Glu Ile Asp Ala His His  
55 60 65

acc gtg gaa gat acc gcc atc gtg ctc ggc caa gca ctc ctt gac gct 355  
Thr Val Glu Asp Thr Ala Ile Val Leu Gly Gln Ala Leu Leu Asp Ala  
70 75 80 85

att ggc gac aag aaa ggc atc cgc cgt ttc gca tcc tgc cag ctg ccc 403  
Ile Gly Asp Lys Lys Gly Ile Arg Arg Phe Ala Ser Cys Gln Leu Pro  
90 95 100

atg gat gag gca tta gtg gag tcc gtg gtg gat atc tcc ggt cgc cca 451  
Met Asp Glu Ala Leu Val Glu Ser Val Val Asp Ile Ser Gly Arg Pro  
105 110 115

tac ttc gtg atc tcc ggc gaa cca gac cac atg atc acc tcc gtg atc 499  
Tyr Phe Val Ile Ser Gly Glu Pro Asp His Met Ile Thr Ser Val Ile  
120 125 130

ggt gga cac tac gca acc gtg atc aac gag cac ttc ttt gaa acc ctc 547  
Gly Gly His Tyr Ala Thr Val Ile Asn Glu His Phe Phe Glu Thr Leu  
135 140 145

gcg ctc aac tcc cga atc acc ctc cac gtg atc tgc cac tac ggc cgc 595  
Ala Leu Asn Ser Arg Ile Thr Leu His Val Ile Cys His Tyr Gly Arg  
150 155 160 165



gac cct cac cac atc acc gaa gca gag tac aag gct gtt gcc cgt gcg 643  
 Asp Pro His His Ile Thr Glu Ala Glu Tyr Lys Ala Val Ala Arg Ala  
                   170                  175                  180

ctg cgc ggt gcc gta gag atg gat cct cgt caa aca gga atc cca tcc 691  
 Leu Arg Gly Ala Val Glu Met Asp Pro Arg Gln Thr Gly Ile Pro Ser  
                   185                  190                  195

act aag gga gcg ctc tagacatgaa ctcttctccc atc 729  
 Thr Lys Gly Ala Leu  
                   200

<210> 394

<211> 202

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 394

Met Thr Val Ala Pro Arg Ile Gly Thr Ala Thr Arg Thr Thr Ser Glu  
   1                  5                  10                  15

Ser Asp Ile Thr Val Glu Ile Asn Leu Asp Gly Thr Gly Lys Val Asp  
                   20                  25                  30

Ile Asp Thr Gly Leu Pro Phe Phe Asp His Met Leu Thr Ala Phe Gly  
                   35                  40                  45

Val His Gly Ser Phe Asp Leu Lys Val His Ala Lys Gly Asp Ile Glu  
   50                  55                  60

Ile Asp Ala His His Thr Val Glu Asp Thr Ala Ile Val Leu Gly Gln  
   65                  70                  75                  80

Ala Leu Leu Asp Ala Ile Gly Asp Lys Lys Gly Ile Arg Arg Phe Ala  
                   85                  90                  95

Ser Cys Gln Leu Pro Met Asp Glu Ala Leu Val Glu Ser Val Val Asp  
                   100                  105                  110

Ile Ser Gly Arg Pro Tyr Phe Val Ile Ser Gly Glu Pro Asp His Met  
                   115                  120                  125

Ile Thr Ser Val Ile Gly Gly His Tyr Ala Thr Val Ile Asn Glu His  
                   130                  135                  140

Phe Phe Glu Thr Leu Ala Leu Asn Ser Arg Ile Thr Leu His Val Ile  
   145                  150                  155                  160

Cys His Tyr Gly Arg Asp Pro His His Ile Thr Glu Ala Glu Tyr Lys  
                   165                  170                  175

Ala Val Ala Arg Ala Leu Arg Gly Ala Val Glu Met Asp Pro Arg Gln  
                   180                  185                  190

Thr Gly Ile Pro Ser Thr Lys Gly Ala Leu  
                   195                  200

<210> 395



Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala Ala Gln Ala  
 185 190 195

gca gcg ctt gcg agt ttg aat tct gcc gat gag ttg atg gaa cgg gtg 739  
 Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met Glu Arg Val  
 200 205 210

gag gaa acc gtc gaa aag cgt gat gct gtg gtg tca gcg ctt ggt gct 787  
 Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala Leu Gly Ala  
 215 220 225

gcg ccg acg cag gcc aat ttc gtc tgg ctg ccg ggc gag ggc gcc gct 835  
 Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu Gly Ala Ala  
 230 235 240 245

gag ttg gcg gct aaa ttg gcc gag cac ggc atc gtg att cgc gcg ttc 883  
 Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile Arg Ala Phe  
 250 255 260

ccc gag ggt gcg cgc att tcg gtg acc aac gcc gag gaa act gac aag 931  
 Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu Thr Asp Lys  
 265 270 275

ctg ctg cgc gcg tgg gag gcc atc aat gct ggg tagtctttgg cgttttgcgg 984  
 Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly  
 280 285

tgc 987

&lt;210&gt; 396

&lt;211&gt; 288

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 396

Met Gly Ala Val Glu Leu Arg Glu Ala Leu Ala Glu His Leu Glu Val  
 1 5 10 15

Glu Phe Asp Gln Val Thr Val Gly Cys Gly Ser Ser Ala Leu Cys Gln  
 20 25 30

Gln Leu Val Gln Ala Thr Cys Ala Gln Gly Asp Glu Val Ile Phe Pro  
 35 40 45

Trp Arg Ser Phe Glu Ala Tyr Pro Ile Phe Ala Gln Val Ala Gly Ala  
 50 55 60

Thr Pro Val Ala Ile Pro Leu Thr Ala Asp Gln Asn His Asp Leu Asp  
 65 70 75 80

Ala Met Ala Ala Ala Ile Thr Asp Lys Thr Arg Leu Ile Phe Ile Cys  
 85 90 95

Asn Pro Asn Asn Pro Ser Gly Thr Thr Ile Thr Gln Ala Gln Phe Asp  
 100 105 110

Asn Phe Met Glu Lys Val Pro Asn Asp Val Val Val Gly Leu Asp Glu  
 115 120 125

Ala Tyr Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu

130	135	140
Glu Ile His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys 145 150 155 160		
Ala Tyr Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala 165 170 175		
Glu Ile Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn 180 185 190		
Ser Ala Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu 195 200 205		
Leu Met Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val 210 215 220		
Ser Ala Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro 225 230 235 240		
Gly Glu Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile 245 250 255		
Val Ile Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala 260 265 270		
Glu Glu Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly 275 280 285		

&lt;210&gt; 397

&lt;211&gt; 545

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(522)

&lt;223&gt; FRXA00446

&lt;400&gt; 397

atg gaa aag gtt cca aac gat gtc gtt gtt ggg ctg gat gag gct tat Met Glu Lys Val Pro Asn Asp Val Val Val Gly Leu Asp Glu Ala Tyr 1 5 10 15 48
ttt gag ttc aac cgc gcg gac gac acc cca gtt gcc act gag gaa atc Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu Glu Ile 20 25 30 96
cac cgc cac gac aac gtg att ggt ttg cgc acg ttc tcc aag gcg tat His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys Ala Tyr 35 40 45 144
ggc ctg gcg ggc ttg cgt gtt ggt tac gcc ttc gga aac gca gag atc Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala Glu Ile 50 55 60 192
atc gca gcg atg aat aag gtg gct att cct ttc gcg gtg aat tca gca 240

Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala  
 65 70 75 80  
 gct cag gcg gca gcg ctt gcg agt ttg aat tct gcc gat gag ttg atg 288  
 Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met  
 85 90 95  
 gaa cgg gtg gag gaa acc gtc gaa aag cgt gat gct gtg gtg tca gcg 336  
 Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala  
 100 105 110  
 ctt ggt gct gcg ccg acg cag gcc aat ttc gtc tgg ctg ccg ggc gag 384  
 Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu  
 115 120 125  
 ggc gcc gct gag ttg gcg gct aaa ttg gcc gag cac ggc atc gtg att 432  
 Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile  
 130 135 140  
 cgc gcg ttc ccc gag ggt gcg cgc att tcg gtg acc aac gcc gag gaa 480  
 Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu  
 145 150 155 160  
 act gac aag ctg ctg cgc gcg tgg gag gcc atc aat gct ggg 522  
 Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly  
 165 170  
 tagtcttttg cgtttttgccg tgc 545

&lt;210&gt; 398

&lt;211&gt; 174

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 398

Met Glu Lys Val Pro Asn Asp Val Val Val Gly Leu Asp Glu Ala Tyr  
 1 5 10 15  
 Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu Glu Ile  
 20 25 30  
 His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys Ala Tyr  
 35 40 45  
 Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala Glu Ile  
 50 55 60  
 Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala  
 65 70 75 80  
 Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met  
 85 90 95  
 Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala  
 100 105 110  
 Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu  
 115 120 125  
 Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile

130	135	140	
Arg Ala Phe Pro Glu Gly	Ala Arg Ile Ser Val Thr Asn Ala Glu Glu		
145	150	155	160
Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly			
	165	170	
<210> 399			
<211> 1221			
<212> DNA			
<213> Corynebacterium glutamicum			
<220>			
<221> CDS			
<222> (101)..(1198)			
<223> RXA01105			
<400> 399			
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gctttgaaaa cctccccacc accgacgagg cctaagaaaa atg acc aaa att act 115			
Met Thr Lys Ile Thr 5			
1			
ttg agc gat ttg cca ttg cgt gaa gaa ctg cgc ggt gag cac gct tac 163			
Leu Ser Asp Leu Pro Leu Arg Glu Glu Leu Arg Gly Glu His Ala Tyr 20			
10 15			
ggc gca ccc cag ctc aac gtt gat att cgc ctc aac acc aac gaa aac 211			
Gly Ala Pro Gln Leu Asn Val Asp Ile Arg Leu Asn Thr Asn Glu Asn 35			
25 30			
cct tac cca ccg tca gag gca ttg gtc gct gac ttg gtt gcc acc gtg 259			
Pro Tyr Pro Pro Ser Glu Ala Leu Val Ala Asp Leu Val Ala Thr Val 50			
40 45			
gat aag atc gcc acc gag ctg aac cgc tac cca gag cgc gat gct gtg 307			
Asp Lys Ile Ala Thr Glu Leu Asn Arg Tyr Pro Glu Arg Asp Ala Val 65			
55 60			
gaa ctg cgt gat gag ttg gct gcg tac atc acc aag caa acc ggc gtg 355			
Glu Leu Arg Asp Glu Leu Ala Ala Tyr Ile Thr Lys Gln Thr Gly Val 85			
70 75 80			
gct gtc acc agg gat aac ctg tgg gct gcc aat ggt tcc aat gaa att 403			
Ala Val Thr Arg Asp Asn Leu Trp Ala Ala Asn Gly Ser Asn Glu Ile 100			
90 95			
ctg cag cag ctg ctg cag gct ttt ggt gga cct gga cgc acc gcg ttg 451			
Leu Gln Gln Leu Leu Gln Ala Phe Gly Gly Pro Gly Arg Thr Ala Leu 115			
105 110			
gga ttc caa ccc agc tat tcc atg cac cca att ttg gct aaa ggc acc 499			
Gly Phe Gln Pro Ser Tyr Ser Met His Pro Ile Leu Ala Lys Gly Thr 130			
120 125			
cac act gaa ttc att gcg gtg tcc cga ggt gct gat ttc cgc atc gat 547			
His Thr Glu Phe Ile Ala Val Ser Arg Gly Ala Asp Phe Arg Ile Asp 145			
135 140			

atg gat gtg gcg ctg gaa gaa att cgt gca aag cag cct gac att gtt	595
Met Asp Val Ala Leu Glu Glu Ile Arg Ala Lys Gln Pro Asp Ile Val	
150 155 160 165	
ttt gtc acc acc ccg aac aac ccg acc ggt gat gtg acc tcg ctg gac	643
Phe Val Thr Thr Pro Asn Asn Pro Thr Gly Asp Val Thr Ser Leu Asp	
170 175 180	
gat gtt gag cgc atc atc aac gtt gcc cca ggc atc gtg atc gtg gat	691
Asp Val Glu Arg Ile Ile Asn Val Ala Pro Gly Ile Val Ile Val Asp	
185 190 195	
gaa gct tat gcg gaa ttc tcc cca tca cct tca gca acc act ctt ctg	739
Glu Ala Tyr Ala Glu Phe Ser Pro Ser Pro Ser Ala Thr Thr Leu Leu	
200 205 210	
gag aag tac cca acc aag ctg gtg gtg tcc cgc acc atg agt aag gct	787
Glu Lys Tyr Pro Thr Lys Leu Val Val Ser Arg Thr Met Ser Lys Ala	
215 220 225	
ttt gat ttc gca ggt gga cgc ctc ggc tac ttc gtg gcc aac cca gcg	835
Phe Asp Phe Ala Gly Gly Arg Leu Gly Tyr Phe Val Ala Asn Pro Ala	
230 235 240 245	
ttt atc gac gcc gtg atg cta gtc cgc ctt ccg tat cat ctt tca gcg	883
Phe Ile Asp Ala Val Met Leu Val Arg Leu Pro Tyr His Leu Ser Ala	
250 255 260	
ctg agc caa gca gcc gca atc gta gcg ctg cgt cac tcc gct gac acg	931
Leu Ser Gln Ala Ala Ala Ile Val Ala Leu Arg His Ser Ala Asp Thr	
265 270 275	
ctg gga acc gtc gaa aag ctc tct gta gag cgt gtt cgc gtg gca gca	979
Leu Gly Thr Val Glu Lys Leu Ser Val Glu Arg Val Arg Val Ala Ala	
280 285 290	
cgc ttg gag gaa ctg ggc tac gct gtg gtt cca agt gag tcc aac ttt	
1027 Arg Leu Glu Glu Leu Gly Tyr Ala Val Val Pro Ser Glu Ser Asn Phe	
295 300 305	
gtg ttc ttt gga gat ttc tcc gat cag cac gcg gca tgg cag gca ttt	
1075 Val Phe Phe Gly Asp Phe Ser Asp Gln His Ala Ala Trp Gln Ala Phe	
310 315 320 325	
ttg gat agg gga gtg ctc atc cgc gat gtg gga atc gct ggg cac ttg	
1123 Leu Asp Arg Gly Val Leu Ile Arg Asp Val Gly Ile Ala Gly His Leu	
330 335 340	
cgc act acc att ggt gtg cct gag gaa aat gat gcg ttt ttg gac gca	
1171 Arg Thr Thr Ile Gly Val Pro Glu Glu Asn Asp Ala Phe Leu Asp Ala	
345 350 355	
gct gca gag atc atc aag ctg aac ctg taagagagaa gaatttttca	
1218 Ala Ala Glu Ile Ile Lys Leu Asn Leu	
360 365	

Tyr His Leu Ser Ala Leu Ser Gln Ala Ala Ala Ile Val Ala Leu Arg  
260 265 270



<400> 401																	
ggtaa	acatg	cgggc	cttaag	aactt	gtgtt	gaggc	cgctt	ggatt	cgggc	accgag	ctcg					60	
aagaatt	ttcg	attca	acctt	ttaag	ggaga	actttt	tcgcc	atg	ttg	aat	gtc	act				115	
								Met	Leu	Asn	Val	Thr				5	
								1									
gac	ctg	cga	ggt	caa	aca	cca	tcc	aag	agc	gac	atc	cga	cgt	gct	ttg	163	
Asp	Leu	Arg	Gly	Gln	Thr	Pro	Ser	Lys	Ser	Asp	Ile	Arg	Arg	Ala	Leu		
				10					15					20			
cca	cgt	ggt	ggc	act	gac	gtg	tgg	tct	gtg	ctt	ccc	ata	gtg	cag	cct	211	
Pro	Arg	Gly	Gly	Thr	Asp	Val	Trp	Ser	Val	Leu	Pro	Ile	Val	Gln	Pro		
				25					30					35			
gtt	gta	gaa	gat	gtc	caa	aac	cgc	ggc	gct	gaa	gct	gct	ttg	gat	tac	259	
Val	Val	Glu	Asp	Val	Gln	Asn	Arg	Gly	Ala	Glu	Ala	Ala	Leu	Asp	Tyr		
		40					45					50					
ggc	gag	aag	ttc	gac	cat	att	cgc	ccc	gcc	tcg	gtg	cgg	gtg	cca	gct	307	
Gly	Glu	Lys	Phe	Asp	His	Ile	Arg	Pro	Ala	Ser	Val	Arg	Val	Pro	Ala		
		55					60					65					
gag	gtt	att	gct	gca	gca	gaa	aac	acc	tta	gat	ccg	ttg	gtg	cgt	gaa	355	
Glu	Val	Ile	Ala	Ala	Ala	Glu	Asn	Thr	Leu	Asp	Pro	Leu	Val	Arg	Glu		
70							75					80			85		
tcg	att	gaa	gag	tcg	att	cgt	cgc	gtc	cgc	aag	gtt	cac	gct	gag	caa	403	
Ser	Ile	Glu	Glu	Ser	Ile	Arg	Arg	Val	Arg	Lys	Val	His	Ala	Glu	Gln		
				90							95			100			

aag cca tcc gag cac acc act gaa ctt tca cca ggt ggc acc gtc act	451
Lys Pro Ser Glu His Thr Thr Glu Leu Ser Pro Gly Gly Thr Val Thr	
105 110 115	
gag cgt ttc atg ccg att gat cgc gtg gga ctg tac gtt cca ggc ggc	499
Glu Arg Phe Met Pro Ile Asp Arg Val Gly Leu Tyr Val Pro Gly Gly	
120 125 130	
aat gcg gtg tac cca tca agc gtg att atg aat act gtc cca gct caa	547
Asn Ala Val Tyr Pro Ser Ser Val Ile Met Asn Thr Val Pro Ala Gln	
135 140 145	
gag gct ggt gtg aac tcc ctt gtg gtt gcg tcg cct cct cag gct gag	595
Glu Ala Gly Val Asn Ser Leu Val Val Ala Ser Pro Pro Gln Ala Glu	
150 155 160 165	
cac ggt ggc tgg cct cac ccc acc att ttg gcg gcg tgt tcc atc ttg	643
His Gly Gly Trp Pro His Pro Thr Ile Leu Ala Ala Cys Ser Ile Leu	
170 175 180	
ggt gtt gat gag gtg tgg gct gtc ggc ggc ggt cag gcc gtg gcg ttg	691
Gly Val Asp Glu Val Trp Ala Val Gly Gly Gly Gln Ala Val Ala Leu	
185 190 195	
ctg gct tat ggt gat gac gct gca ggt ctc gag cct gtg gat atg atc	739
Leu Ala Tyr Gly Asp Asp Ala Ala Gly Leu Glu Pro Val Asp Met Ile	
200 205 210	
act gga cct ggc aat atc ttt gtc acc gct gcg aag cgc ctg gtc agg	787
Thr Gly Pro Gly Asn Ile Phe Val Thr Ala Ala Lys Arg Leu Val Arg	
215 220 225	
gga gtg gta ggt act gat tct gag gct ggc cct aca gaa atc gct gtg	835
Gly Val Val Gly Thr Asp Ser Glu Ala Gly Pro Thr Glu Ile Ala Val	
230 235 240 245	
ctt gct gat gcc tct gcc aac gcc gtc aac gtt gcc tac gat ctg atc	883
Leu Ala Asp Ala Ser Ala Asn Ala Val Asn Val Ala Tyr Asp Leu Ile	
250 255 260	
agc caa gca gaa cac gat gtc atg gct gcg tcc gtg ctc atc act gac	931
Ser Gln Ala Glu His Asp Val Met Ala Ala Ser Val Leu Ile Thr Asp	
265 270 275	
tcc gag cag ctt gcc aag gac gta aac agg gaa atc gag gcg cgt tac	979
Ser Glu Gln Leu Ala Lys Asp Val Asn Arg Glu Ile Glu Ala Arg Tyr	
280 285 290	
tca atc acg cgc aac gcc gag cgc gtc gca gaa gct ttg cgc ggg gcc	
1027 Ser Ile Thr Arg Asn Ala Glu Arg Val Ala Glu Ala Leu Arg Gly Ala	
295 300 305	
cag agt ggc atc gtg ctt gtc gac gac att tcc gtg ggt atc caa gta	
1075 Gln Ser Gly Ile Val Leu Val Asp Asp Ile Ser Val Gly Ile Gln Val	
310 315 320 325	
gcc gat caa tac gca gcg gaa cac ctg gaa atc cac act gag aac gcg	
1123 Ala Asp Gln Tyr Ala Ala Glu His Leu Glu Ile His Thr Glu Asn Ala	

330 335 340  
 cgc gcc gta gca gag cag atc acc aac gcg ggt gcg atc ttc gtg ggc  
 1171  
 Arg Ala Val Ala Glu Gln Ile Thr Asn Ala Gly Ala Ile Phe Val Gly  
 345 350 355  
 gat ttc tca cca gta cca ctg ggt gat tac tcc gca gga tcc aac cac  
 1219  
 Asp Phe Ser Pro Val Pro Leu Gly Asp Tyr Ser Ala Gly Ser Asn His  
 360 365 370  
 gtg ctg cca acc tct gga tcc gct cgt ttc tcc gca ggt cta tcc acg  
 1267  
 Val Leu Pro Thr Ser Gly Ser Ala Arg Phe Ser Ala Gly Leu Ser Thr  
 375 380 385  
 cac acg ttc ctt cgc cca gtc aac ctc att gaa tac gat gag gct gct  
 1315  
 His Thr Phe Leu Arg Pro Val Asn Leu Ile Glu Tyr Asp Glu Ala Ala  
 390 395 400 405  
 ctg aag gac gtc tcg cag gtt gtc atc aac ttt gcc aac gcc gaa gat  
 1363  
 Leu Lys Asp Val Ser Gln Val Val Ile Asn Phe Ala Asn Ala Glu Asp  
 410 415 420  
 ctt cca gcg cac ggc gaa gca atc cgt gca cgc ttt gaa aac ctc ccc  
 1411  
 Leu Pro Ala His Gly Glu Ala Ile Arg Ala Arg Phe Glu Asn Leu Pro  
 425 430 435  
 acc acc gac gag gcc taagaaaaat gaccaaatt act  
 1449  
 Thr Thr Asp Glu Ala  
 440

<210> 402  
 <211> 442  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 402  
 Met Leu Asn Val Thr Asp Leu Arg Gly Gln Thr Pro Ser Lys Ser Asp  
 1 5 10 15  
 Ile Arg Arg Ala Leu Pro Arg Gly Gly Thr Asp Val Trp Ser Val Leu  
 20 25 30  
 Pro Ile Val Gln Pro Val Val Glu Asp Val Gln Asn Arg Gly Ala Glu  
 35 40 45  
 Ala Ala Leu Asp Tyr Gly Glu Lys Phe Asp His Ile Arg Pro Ala Ser  
 50 55 60  
 Val Arg Val Pro Ala Glu Val Ile Ala Ala Ala Glu Asn Thr Leu Asp  
 65 70 75 80  
 Pro Leu Val Arg Glu Ser Ile Glu Glu Ser Ile Arg Arg Val Arg Lys  
 85 90 95

Val	His	Ala	Glu	Gln	Lys	Pro	Ser	Glu	His	Thr	Thr	Glu	Leu	Ser	Pro	100	105	110	
Gly	Gly	Thr	Val	Thr	Glu	Arg	Phe	Met	Pro	Ile	Asp	Arg	Val	Gly	Leu	115	120	125	
Tyr	Val	Pro	Gly	Gly	Asn	Ala	Val	Tyr	Pro	Ser	Ser	Val	Ile	Met	Asn	130	135	140	
Thr	Val	Pro	Ala	Gln	Glu	Ala	Gly	Val	Asn	Ser	Leu	Val	Val	Ala	Ser	145	150	155	160
Pro	Pro	Gln	Ala	Glu	His	Gly	Gly	Trp	Pro	His	Pro	Thr	Ile	Leu	Ala	165	170	175	
Ala	Cys	Ser	Ile	Leu	Gly	Val	Asp	Glu	Val	Trp	Ala	Val	Gly	Gly	Gly	180	185	190	
Gln	Ala	Val	Ala	Leu	Leu	Ala	Tyr	Gly	Asp	Asp	Ala	Ala	Gly	Leu	Glu	195	200	205	
Pro	Val	Asp	Met	Ile	Thr	Gly	Pro	Gly	Asn	Ile	Phe	Val	Thr	Ala	Ala	210	215	220	
Lys	Arg	Leu	Val	Arg	Gly	Val	Val	Gly	Thr	Asp	Ser	Glu	Ala	Gly	Pro	225	230	235	240
Thr	Glu	Ile	Ala	Val	Leu	Ala	Asp	Ala	Ser	Ala	Asn	Ala	Val	Asn	Val	245	250	255	
Ala	Tyr	Asp	Leu	Ile	Ser	Gln	Ala	Glu	His	Asp	Val	Met	Ala	Ala	Ser	260	265	270	
Val	Leu	Ile	Thr	Asp	Ser	Glu	Gln	Leu	Ala	Lys	Asp	Val	Asn	Arg	Glu	275	280	285	
Ile	Glu	Ala	Arg	Tyr	Ser	Ile	Thr	Arg	Asn	Ala	Glu	Arg	Val	Ala	Glu	290	295	300	
Ala	Leu	Arg	Gly	Ala	Gln	Ser	Gly	Ile	Val	Leu	Val	Asp	Asp	Ile	Ser	305	310	315	320
Val	Gly	Ile	Gln	Val	Ala	Asp	Gln	Tyr	Ala	Ala	Glu	His	Leu	Glu	Ile	325	330	335	
His	Thr	Glu	Asn	Ala	Arg	Ala	Val	Ala	Glu	Gln	Ile	Thr	Asn	Ala	Gly	340	345	350	
Ala	Ile	Phe	Val	Gly	Asp	Phe	Ser	Pro	Val	Pro	Leu	Gly	Asp	Tyr	Ser	355	360	365	
Ala	Gly	Ser	Asn	His	Val	Leu	Pro	Thr	Ser	Gly	Ser	Ala	Arg	Phe	Ser	370	375	380	
Ala	Gly	Leu	Ser	Thr	His	Thr	Phe	Leu	Arg	Pro	Val	Asn	Leu	Ile	Glu	385	390	395	400
Tyr	Asp	Glu	Ala	Ala	Leu	Lys	Asp	Val	Ser	Gln	Val	Val	Ile	Asn	Phe	405	410	415	

Ala Asn Ala Glu Asp Leu Pro Ala His Gly Glu Ala Ile Arg Ala Arg  
 420 425 430

Phe Glu Asn Leu Pro Thr Thr Asp Glu Ala  
 435 440

<210> 403  
 <211> 876  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(853)  
 <223> RXC00930

<400> 403  
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ttccggtgga tgatggaagc tagacgacga aagggagcat atg tct ggc cac tca 115  
 Met Ser Gly His Ser  
 1 5

aaa tgg gcg act acc aag cac aag aag gct gct aac gac gcc aag cga 163  
 Lys Trp Ala Thr Thr Lys His Lys Lys Ala Ala Asn Asp Ala Lys Arg  
 10 15 20

ggc aag gaa ttt gcc aag ctg atc aag aac atc gaa gtt gcg gca cgt 211  
 Gly Lys Glu Phe Ala Lys Leu Ile Lys Asn Ile Glu Val Ala Ala Arg  
 25 30 35

aca ggc ggt gga gat ccg tct gcg aac cca acg ctt gat gac atg atc 259  
 Thr Gly Gly Gly Asp Pro Ser Ala Asn Pro Thr Leu Asp Asp Met Ile  
 40 45 50

aag aaa gcc aag aag gct tct gtg ccg aac gat aac atc gaa cgt gca 307  
 Lys Lys Ala Lys Lys Ala Ser Val Pro Asn Asp Asn Ile Glu Arg Ala  
 55 60 65

cgc aag cgt ggc tcc ggc gaa gaa gct ggt ggc gct gac tgg atg aac 355  
 Arg Lys Arg Gly Ser Gly Glu Glu Ala Gly Gly Ala Asp Trp Met Asn  
 70 75 80 85

atc atg tac gag gga tac ggc ccc aac ggc gtt gcc atg ctt atc gag 403  
 Ile Met Tyr Glu Gly Tyr Gly Pro Asn Gly Val Ala Met Leu Ile Glu  
 90 95 100

tgt ctg acc gac aac cgt aac cgc gca gct acc gaa gtt cgc acc gca 451  
 Cys Leu Thr Asp Asn Arg Asn Arg Ala Ala Thr Glu Val Arg Thr Ala  
 105 110 115

atg acc aaa aac ggt ggc aac ttg ggc gag tcc ggt tcc gtg tcc tac 499  
 Met Thr Lys Asn Gly Gly Asn Leu Gly Glu Ser Gly Ser Val Ser Tyr  
 120 125 130

atg ttc acc cgc acc ggt gtc gtc acc gta caa aag ggc gat ctt agt 547  
 Met Phe Thr Arg Thr Gly Val Val Thr Val Gln Lys Gly Asp Leu Ser  
 135 140 145

gaa gat gac gtg ctc atg gct gtt ctt gaa gct ggt gct gaa gaa gtc 595

Glu Asp Asp Val Leu Met Ala Val Leu Glu Ala Gly Ala Glu Glu Val  
 150 155 160 165  
 aac gac aac ggc gat ctg ttc gag gtt acc tgc gca cca act gac att 643  
 Asn Asp Asn Gly Asp Leu Phe Glu Val Thr Cys Ala Pro Thr Asp Ile  
 170 175 180  
 cag gct gtt cgc gac gca ctc gtg gaa gct ggc att gaa gta gaa gat 691  
 Gln Ala Val Arg Asp Ala Leu Val Glu Ala Gly Ile Glu Val Glu Asp  
 185 190 195  
 tct gaa tca gac ttc cgg gca tct gtt cag gtc ccc ctg gac gct gac 739  
 Ser Glu Ser Asp Phe Arg Ala Ser Val Gln Val Pro Leu Asp Ala Asp  
 200 205 210  
 ggt gca cgc aag atc ttc aag ctt gtg gac gcg ttg gaa gat tcc gac 787  
 Gly Ala Arg Lys Ile Phe Lys Leu Val Asp Ala Leu Glu Asp Ser Asp  
 215 220 225  
 gat gtg caa aac gtc tac acc aac atc gac ttg agc gat gag gtt ttg 835  
 Asp Val Gln Asn Val Tyr Thr Asn Ile Asp Leu Ser Asp Glu Val Leu  
 230 235 240 245  
 aca gag ctg gaa aac gac tagttcgtat tttccgcact ccg 876  
 Thr Glu Leu Glu Asn Asp  
 250

&lt;210&gt; 404

&lt;211&gt; 251

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 404

Met Ser Gly His Ser Lys Trp Ala Thr Thr Lys His Lys Lys Ala Ala  
 1 5 10 15  
 Asn Asp Ala Lys Arg Gly Lys Glu Phe Ala Lys Leu Ile Lys Asn Ile  
 20 25 30  
 Glu Val Ala Ala Arg Thr Gly Gly Gly Asp Pro Ser Ala Asn Pro Thr  
 35 40 45  
 Leu Asp Asp Met Ile Lys Lys Ala Lys Lys Ala Ser Val Pro Asn Asp  
 50 55 60  
 Asn Ile Glu Arg Ala Arg Lys Arg Gly Ser Gly Glu Glu Ala Gly Gly  
 65 70 75 80  
 Ala Asp Trp Met Asn Ile Met Tyr Glu Gly Tyr Gly Pro Asn Gly Val  
 85 90 95  
 Ala Met Leu Ile Glu Cys Leu Thr Asp Asn Arg Asn Arg Ala Ala Thr  
 100 105 110  
 Glu Val Arg Thr Ala Met Thr Lys Asn Gly Gly Asn Leu Gly Glu Ser  
 115 120 125  
 Gly Ser Val Ser Tyr Met Phe Thr Arg Thr Gly Val Val Thr Val Gln  
 130 135 140

Lys Gly Asp Leu Ser Glu Asp Asp Val Leu Met Ala Val Leu Glu Ala  
 145 150 155 160  
 Gly Ala Glu Glu Val Asn Asp Asn Gly Asp Leu Phe Glu Val Thr Cys  
 165 170 175  
 Ala Pro Thr Asp Ile Gln Ala Val Arg Asp Ala Leu Val Glu Ala Gly  
 180 185 190  
 Ile Glu Val Glu Asp Ser Glu Ser Asp Phe Arg Ala Ser Val Gln Val  
 195 200 205  
 Pro Leu Asp Ala Asp Gly Ala Arg Lys Ile Phe Lys Leu Val Asp Ala  
 210 215 220  
 Leu Glu Asp Ser Asp Asp Val Gln Asn Val Tyr Thr Asn Ile Asp Leu  
 225 230 235 240  
 Ser Asp Glu Val Leu Thr Glu Leu Glu Asn Asp  
 245 250

<210> 405  
 <211> 547  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(547)  
 <223> RXC01096

<400> 405  
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 gttttgctgt aaaagcaaca acgattaagg aagaaatctt atg aag cca cgc gtg 115  
 Met Lys Pro Arg Val  
 1 5  
 ctg tca gca tta ggc att gga gct ggc gcc ctg gtt gtc tgg atc agc 163  
 Leu Ser Ala Leu Gly Ile Gly Ala Gly Ala Leu Val Val Trp Ile Ser  
 10 15 20  
 tca cgc atg aac tgg gta acc atc gag gct ttc gac gat aaa tca ggt 211  
 Ser Arg Met Asn Trp Val Thr Ile Glu Ala Phe Asp Asp Lys Ser Gly  
 25 30 35  
 agt gtc acc caa tct att gtg ggt gca acc tgg tct aca gaa atc atg 259  
 Ser Val Thr Gln Ser Ile Val Gly Ala Thr Trp Ser Thr Glu Ile Met  
 40 45 50  
 gcg ctt gca ctt gct ttg ctc gct gcc ttc gcc gcc gcg ttg gtg ctc 307  
 Ala Leu Ala Leu Ala Leu Leu Ala Ala Phe Ala Ala Ala Leu Val Leu  
 55 60 65  
 aag cgc atg ggt cgg cgc atc att ggt ggt att tcg gcg ctg atc gcg 355  
 Lys Arg Met Gly Arg Arg Ile Ile Gly Gly Ile Ser Ala Leu Ile Ala  
 70 75 80 85  
 gtg ggt gcc agc ctg tct cca ctc gcg ctt ctc acc caa gac cca gac 403  
 Val Gly Ala Ser Leu Ser Pro Leu Ala Leu Leu Thr Gln Asp Pro Asp

	90	95	100	
gca gaa cgg gcc cga acc ctg ctg acc tcc ggt gtg gcc tca cag aag				451
Ala Glu Arg Ala Arg Thr Leu Leu Thr Ser Gly Val Ala Ser Gln Lys				
	105	110	115	
gct aat tcc gga acc ctg ctg tct gat tgg gcg gag atc atc aat acc				499
Ala Asn Ser Gly Thr Leu Leu Ser Asp Trp Ala Glu Ile Ile Asn Thr				
	120	125	130	
acc acc cat cca ctg gcg gca gtg gta gcc atg att ggc tgc gcg cta				547
Thr Thr His Pro Leu Ala Ala Val Val Ala Met Ile Gly Cys Ala Leu				
	135	140	145	

&lt;210&gt; 406

&lt;211&gt; 149

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 406

Met Lys Pro Arg Val Leu Ser Ala Leu Gly Ile Gly Ala Gly Ala Leu
1 5 10 15

Val Val Trp Ile Ser Ser Arg Met Asn Trp Val Thr Ile Glu Ala Phe
20 25 30

Asp Asp Lys Ser Gly Ser Val Thr Gln Ser Ile Val Gly Ala Thr Trp
35 40 45

Ser Thr Glu Ile Met Ala Leu Ala Leu Ala Leu Ala Ala Phe Ala
50 55 60

Ala Ala Leu Val Leu Lys Arg Met Gly Arg Arg Ile Ile Gly Gly Ile
65 70 75 80

Ser Ala Leu Ile Ala Val Gly Ala Ser Leu Ser Pro Leu Ala Leu Leu
85 90 95

Thr Gln Asp Pro Asp Ala Glu Arg Ala Arg Thr Leu Leu Thr Ser Gly
100 105 110

Val Ala Ser Gln Lys Ala Asn Ser Gly Thr Leu Leu Ser Asp Trp Ala
115 120 125

Glu Ile Ile Asn Thr Thr Thr His Pro Leu Ala Ala Val Val Ala Met
130 135 140

Ile Gly Cys Ala Leu
145

&lt;210&gt; 407

&lt;211&gt; 1020

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(997)

&lt;223&gt; RXC01656



&lt;400&gt; 407

tcggcaagca tggcttcacg gtcctcaaaa aagtgggtcta atgcaagtga ctgaaagtgg 60

atctaccgct agtccacttt gtggcggttg atcatctgtc atg acc gaa act caa 115  
 Met Thr Glu Thr Gln  
 1 5

gaa act tac caa gca acc act cgt gtg aag cgc ggc ctt gcc gac atg 163  
 Glu Thr Tyr Gln Ala Thr Thr Arg Val Lys Arg Gly Leu Ala Asp Met  
 10 15 20

ctc aag ggt ggt gtg atc atg gat gtg gtc acc cct gaa caa gcg cgc 211  
 Leu Lys Gly Gly Val Ile Met Asp Val Val Thr Pro Glu Gln Ala Arg  
 25 30 35

atc gcc gaa gat gca ggt gcc agc gca gtt atg gca ctc gag cgc gtt 259  
 Ile Ala Glu Asp Ala Gly Ala Ser Ala Val Met Ala Leu Glu Arg Val  
 40 45 50

ccc gcc gat atc cgt tct cag ggc ggc gtt gct cgc atg agt gat cct 307  
 Pro Ala Asp Ile Arg Ser Gln Gly Gly Val Ala Arg Met Ser Asp Pro  
 55 60 65

gac ctg atc gaa gga atc gtc aat gcg gtc tcc atc ccg gtc atg gcg 355  
 Asp Leu Ile Glu Gly Ile Val Asn Ala Val Ser Ile Pro Val Met Ala  
 70 75 80 85

aaa gct cgc atc ggt cac ttc gtg gaa gct cag gtt ctg gaa gct ctc 403  
 Lys Ala Arg Ile Gly His Phe Val Glu Ala Gln Val Leu Glu Ala Leu  
 90 95 100

ggt gtt gat ttc atc gac gag tcc gaa gtt ctc agc cct gcc gac tac 451  
 Gly Val Asp Phe Ile Asp Glu Ser Glu Val Leu Ser Pro Ala Asp Tyr  
 105 110 115

acg cac cac atc aac aag tgg aag ttc gac gtt cct ttc gtc tgt ggc 499  
 Thr His His Ile Asn Lys Trp Lys Phe Asp Val Pro Phe Val Cys Gly  
 120 125 130

gcg acc aac ctc ggc gaa gct ttg cga cgc atc acc gaa ggc gct gca 547  
 Ala Thr Asn Leu Gly Glu Ala Leu Arg Arg Ile Thr Glu Gly Ala Ala  
 135 140 145

atg atc cgt tcc aag ggc gaa gcc ggc acc ggc gat gtc tct gaa gct 595  
 Met Ile Arg Ser Lys Gly Glu Ala Gly Thr Gly Asp Val Ser Glu Ala  
 150 155 160 165

gtc cgt cac ctg cgc acc atc cgc ggc gac atc aat cgc ctg cgc tcc 643  
 Val Arg His Leu Arg Thr Ile Arg Gly Asp Ile Asn Arg Leu Arg Ser  
 170 175 180

ctg gat gag gat gaa ctc ttc gtc gcc gcc aag gaa ttc cag gca cca 691  
 Leu Asp Glu Asp Glu Leu Phe Val Ala Ala Lys Glu Phe Gln Ala Pro  
 185 190 195

tac gac ctg gtc cgc gaa gtc gcc tcc acc ggc aag ctc cct gtg gtc 739  
 Tyr Asp Leu Val Arg Glu Val Ala Ser Thr Gly Lys Leu Pro Val Val  
 200 205 210

acc ttc gtt gca ggt ggc gtc gca acc cca gcc gac gct gca ctc gtg 787

Thr Phe Val Ala Gly Gly Val Ala Thr Pro Ala Asp Ala Ala Leu Val  
 215 220 225  
 cgc caa atg ggc gcc gaa ggc gtc ttt gtc ggc tcc ggc atc ttc aaa 835  
 Arg Gln Met Gly Ala Glu Gly Val Phe Val Gly Ser Gly Ile Phe Lys  
 230 235 240 245  
 tcc ggc aat cca gcc gcc cgc gcc gca gcg atc gtc aag gct gca acg 883  
 Ser Gly Asn Pro Ala Ala Arg Ala Ala Ile Val Lys Ala Ala Thr  
 250 255 260  
 ctt ttc gac gac ccc tcc gtc att gcc gac gta tcc cgc ggc ctg ggt 931  
 Leu Phe Asp Asp Pro Ser Val Ile Ala Asp Val Ser Arg Gly Leu Gly  
 265 270 275  
 gaa gcc atg gtg ggc atc aac gta tcc gac gtt cca gca cca cac cga 979  
 Glu Ala Met Val Gly Ile Asn Val Ser Asp Val Pro Ala Pro His Arg  
 280 285 290  
 ctc gcc gag cgc ggc tgg tgatcggtgg agtttttagct ctc  
 1020  
 Leu Ala Glu Arg Gly Trp  
 295

&lt;210&gt; 408

&lt;211&gt; 299

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 408

Met Thr Glu Thr Gln Glu Thr Tyr Gln Ala Thr Thr Arg Val Lys Arg  
 1 5 10 15  
 Gly Leu Ala Asp Met Leu Lys Gly Gly Val Ile Met Asp Val Val Thr  
 20 25 30  
 Pro Glu Gln Ala Arg Ile Ala Glu Asp Ala Gly Ala Ser Ala Val Met  
 35 40 45  
 Ala Leu Glu Arg Val Pro Ala Asp Ile Arg Ser Gln Gly Gly Val Ala  
 50 55 60  
 Arg Met Ser Asp Pro Asp Leu Ile Glu Gly Ile Val Asn Ala Val Ser  
 65 70 75 80  
 Ile Pro Val Met Ala Lys Ala Arg Ile Gly His Phe Val Glu Ala Gln  
 85 90 95  
 Val Leu Glu Ala Leu Gly Val Asp Phe Ile Asp Glu Ser Glu Val Leu  
 100 105 110  
 Ser Pro Ala Asp Tyr Thr His His Ile Asn Lys Trp Lys Phe Asp Val  
 115 120 125  
 Pro Phe Val Cys Gly Ala Thr Asn Leu Gly Glu Ala Leu Arg Arg Ile  
 130 135 140  
 Thr Glu Gly Ala Ala Met Ile Arg Ser Lys Gly Glu Ala Gly Thr Gly  
 145 150 155 160

Asp Val Ser Glu Ala Val Arg His Leu Arg Thr Ile Arg Gly Asp Ile  
 165 170 175  
 Asn Arg Leu Arg Ser Leu Asp Glu Asp Glu Leu Phe Val Ala Ala Lys  
 180 185 190  
 Glu Phe Gln Ala Pro Tyr Asp Leu Val Arg Glu Val Ala Ser Thr Gly  
 195 200 205  
 Lys Leu Pro Val Val Thr Phe Val Ala Gly Gly Val Ala Thr Pro Ala  
 210 215 220  
 Asp Ala Ala Leu Val Arg Gln Met Gly Ala Glu Gly Val Phe Val Gly  
 225 230 235 240  
 Ser Gly Ile Phe Lys Ser Gly Asn Pro Ala Ala Arg Ala Ala Ala Ile  
 245 250 255  
 Val Lys Ala Ala Thr Leu Phe Asp Asp Pro Ser Val Ile Ala Asp Val  
 260 265 270  
 Ser Arg Gly Leu Gly Glu Ala Met Val Gly Ile Asn Val Ser Asp Val  
 275 280 285  
 Pro Ala Pro His Arg Leu Ala Glu Arg Gly Trp  
 290 295

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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1042)  
 <223> RXC01158

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 Met Ser Ile Val Glu  
 1 5  
 cac atc aaa gag ttt cga cgc cga ctt ctt atc gct ctg gcg ggc atc 163  
 His Ile Lys Glu Phe Arg Arg Arg Leu Leu Ile Ala Leu Ala Gly Ile  
 10 15 20  
 ctc gtg ggc acc att atc ggc ttt att tgg tac gat ttc tca ttt tgg 211  
 Leu Val Gly Thr Ile Ile Gly Phe Ile Trp Tyr Asp Phe Ser Phe Trp  
 25 30 35  
 cag atc ccc act ttg ggc gag ctg ctg agg gat ccg tac tgt tct ctg 259  
 Gln Ile Pro Thr Leu Gly Glu Leu Leu Arg Asp Pro Tyr Cys Ser Leu  
 40 45 50  
 cct gct gaa tcc cgc tgg gcc atg agc gac tca gag gaa tgt cga ctg 307  
 Pro Ala Glu Ser Arg Trp Ala Met Ser Asp Ser Glu Glu Cys Arg Leu  
 55 60 65

ctc gca acc ggc ccg ttt gat cca ttc atg ctt cgc ctt aaa gta gcg	355
Leu Ala Thr Gly Pro Phe Asp Pro Phe Met Leu Arg Leu Lys Val Ala	
70 75 80 85	
gcg ttg gtg ggt atg gtt ctt ggc tca ccc gtg tgg ctg agc cag ctg	403
Ala Leu Val Gly Met Val Leu Gly Ser Pro Val Trp Leu Ser Gln Leu	
90 95 100	
tgg ggc ttt atc acc cca ggt ttg atg aag aat gag cgc cgt tac acc	451
Trp Gly Phe Ile Thr Pro Gly Leu Met Lys Asn Glu Arg Arg Tyr Thr	
105 110 115	
gca atc ttc gtc acg att gct gtt gtg ctg ttt gtc ggc ggt gct gtt	499
Ala Ile Phe Val Thr Ile Ala Val Val Leu Phe Val Gly Gly Ala Val	
120 125 130	
ctt gcg tac ttc gtc gtt gca tat ggt ttg gag ttc ctc ctt acc att	547
Leu Ala Tyr Phe Val Val Ala Tyr Gly Leu Glu Phe Leu Leu Thr Ile	
135 140 145	
ggt gga gac acc cag gca gcg gcc ctg act ggt gat aag tac ttc gga	595
Gly Gly Asp Thr Gln Ala Ala Leu Thr Gly Asp Lys Tyr Phe Gly	
150 155 160 165	
ttc ttg ctc gcg ttg ttg gcg att ttc ggc gtg agc ttc gaa gtt cca	643
Phe Leu Leu Ala Leu Leu Ala Ile Phe Gly Val Ser Phe Glu Val Pro	
170 175 180	
ctg gtg atc ggc atg ctc aac att gtg ggt atc ttg cct tac gat gcc	691
Leu Val Ile Gly Met Leu Asn Ile Val Gly Ile Leu Pro Tyr Asp Ala	
185 190 195	
att aaa gat aag cga cgc atg atc atc atg att ttg ttc gtg ttc gct	739
Ile Lys Asp Lys Arg Arg Met Ile Ile Met Ile Leu Phe Val Phe Ala	
200 205 210	
gct ttc atg aca ccc ggc cag gat cct ttc acc atg ttg gtg ttg gcg	787
Ala Phe Met Thr Pro Gly Gln Asp Pro Phe Thr Met Leu Val Leu Ala	
215 220 225	
ctt tca ctc acc gtt ctg gta gag ctt gcc ctg cag ttc tgt cgc ttc	835
Leu Ser Leu Thr Val Leu Val Glu Leu Ala Leu Gln Phe Cys Arg Phe	
230 235 240 245	
aac gac aaa cgc cgg gac aag aag cgc cca gaa tgg ctt gat ggc gat	883
Asn Asp Lys Arg Arg Asp Lys Lys Arg Pro Glu Trp Leu Asp Gly Asp	
250 255 260	
gac ctc tct gca tca cca ctg gat act tct gct ggt gga gaa gat gct	931
Asp Leu Ser Ala Ser Pro Leu Asp Thr Ser Ala Gly Gly Glu Asp Ala	
265 270 275	
cca agc cca gtc gaa acc cca gag gcg gtg gag cct tcg cgg atg ctg	979
Pro Ser Pro Val Glu Thr Pro Glu Ala Val Glu Pro Ser Arg Met Leu	
280 285 290	
aac cca agt ggg gag gcg tcg ata agc tat aaa ccc ggg cgc gcc gac	1027
Asn Pro Ser Gly Glu Ala Ser Ile Ser Tyr Lys Pro Gly Arg Ala Asp	
295 300 305	

ttc ggt gac gtg ctc tagggcctag ccaggtaccc tta  
 1065  
 Phe Gly Asp Val Leu  
 310

<210> 410  
 <211> 314  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 410  
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 Ala Leu Ala Gly Ile Leu Val Gly Thr Ile Ile Gly Phe Ile Trp Tyr  
                   20                  25                  30  
 Asp Phe Ser Phe Trp Gln Ile Pro Thr Leu Gly Glu Leu Leu Arg Asp  
           35                  40                  45  
 Pro Tyr Cys Ser Leu Pro Ala Glu Ser Arg Trp Ala Met Ser Asp Ser  
           50                  55                  60  
 Glu Glu Cys Arg Leu Leu Ala Thr Gly Pro Phe Asp Pro Phe Met Leu  
   65                  70                  75                  80  
 Arg Leu Lys Val Ala Ala Leu Val Gly Met Val Leu Gly Ser Pro Val  
                   85                  90                  95  
 Trp Leu Ser Gln Leu Trp Gly Phe Ile Thr Pro Gly Leu Met Lys Asn  
                   100                  105                  110  
 Glu Arg Arg Tyr Thr Ala Ile Phe Val Thr Ile Ala Val Val Leu Phe  
           115                  120                  125  
 Val Gly Gly Ala Val Leu Ala Tyr Phe Val Val Ala Tyr Gly Leu Glu  
   130                  135                  140  
 Phe Leu Leu Thr Ile Gly Gly Asp Thr Gln Ala Ala Ala Leu Thr Gly  
   145                  150                  155                  160  
 Asp Lys Tyr Phe Gly Phe Leu Leu Ala Leu Leu Ala Ile Phe Gly Val  
                   165                  170                  175  
 Ser Phe Glu Val Pro Leu Val Ile Gly Met Leu Asn Ile Val Gly Ile  
                   180                  185                  190  
 Leu Pro Tyr Asp Ala Ile Lys Asp Lys Arg Arg Met Ile Ile Met Ile  
           195                  200                  205  
 Leu Phe Val Phe Ala Ala Phe Met Thr Pro Gly Gln Asp Pro Phe Thr  
   210                  215                  220  
 Met Leu Val Leu Ala Leu Ser Leu Thr Val Leu Val Glu Leu Ala Leu  
   225                  230                  235                  240  
 Gln Phe Cys Arg Phe Asn Asp Lys Arg Arg Asp Lys Lys Arg Pro Glu  
                   245                  250                  255  
 Trp Leu Asp Gly Asp Asp Leu Ser Ala Ser Pro Leu Asp Thr Ser Ala

	260		265		270
Gly Gly Glu Asp Ala Pro Ser Pro Val Glu Thr Pro Glu Ala Val Glu					
275		280		285	
Pro Ser Arg Met Leu Asn Pro Ser Gly Glu Ala Ser Ile Ser Tyr Lys					
290		295		300	
Pro Gly Arg Ala Asp Phe Gly Asp Val Leu					
305		310			

<210> 411  
 <211> 1413  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1390)  
 <223> RXA02458

<400> 411  
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 ggtggtgaac aaaacaaatc ttccacacat aacatctatt atg gtc ttt gtg tct 115  
 Met Val Phe Val Ser 5  
 gat tcg tct atc tct ttg ccc att tgg gat gct ccg cgc gct cgc ggc 163  
 Asp Ser Ser Ile Ser Leu Pro Ile Trp Asp Ala Pro Arg Ala Arg Gly 20  
 ccc ata gtc tcg gac ctg gct atc cct ggt tcc aag tcg atc acc aac 211  
 Pro Ile Val Ser Asp Leu Ala Ile Pro Gly Ser Lys Ser Ile Thr Asn 35  
 cgc gcc ctc atc ttg gct gcg ctc gca tca act cca tcc acc atc att 259  
 Arg Ala Leu Ile Leu Ala Ala Leu Ala Ser Thr Pro Ser Thr Ile Ile 50  
 gat gtc ctt cgt agt cgt gat acc gat ctc atg act gat ggt cta cgc 307  
 Asp Val Leu Arg Ser Arg Asp Thr Asp Leu Met Thr Asp Gly Leu Arg 65  
 agc ctc gga atc acc att act gaa gag gca gtc gat cgc tac cgc gtt 355  
 Ser Leu Gly Ile Thr Ile Thr Glu Glu Ala Val Asp Arg Tyr Arg Val 85  
 gag ccc gga cag ttg tct gct ggc tcc gtt gag tgt ggt ctt gct ggt 403  
 Glu Pro Gly Gln Leu Ser Ala Gly Ser Val Glu Cys Gly Leu Ala Gly 100  
 acg gtc atg cgc ttt ttg cct cct gtt gct gct ttc gct gat ggt cct 451  
 Thr Val Met Arg Phe Leu Pro Pro Val Ala Ala Phe Ala Asp Gly Pro 115  
 gtt cat ttt gat ggc gat cct caa gct cgt gtt cgt ccg atg acc agc 499  
 Val His Phe Asp Gly Asp Pro Gln Ala Arg Val Arg Pro Met Thr Ser 120 125 130

att ttg gat gcg ctg cgt tcg ctt ggt gtg gag gta gac aac aac aat	547
Ile Leu Asp Ala Leu Arg Ser Leu Gly Val Glu Val Asp Asn Asn Asn	
135 140 145	
ctg cct ttc act gtt aat gct ggt gag gtc cct gag ggt ggc gtg gtt	595
Leu Pro Phe Thr Val Asn Ala Gly Glu Val Pro Glu Gly Gly Val Val	
150 155 160 165	
gag att gat gct tcc ggc tca tct cag ttt gtt tct ggt ctt ttg ctt	643
Glu Ile Asp Ala Ser Gly Ser Ser Gln Phe Val Ser Gly Leu Leu Leu	
170 175 180	
tca gcg cct cgt ttt aaa aat ggc gtc acc gtt aag cac gtc ggt ggt	691
Ser Ala Pro Arg Phe Lys Asn Gly Val Thr Val Lys His Val Gly Gly	
185 190 195	
cgt ctg ccg agc atg ccg cat att gag atg acc gtc gat atg ctt cgt	739
Arg Leu Pro Ser Met Pro His Ile Glu Met Thr Val Asp Met Leu Arg	
200 205 210	
tcc gca ggc att gag atc gaa gag tca gaa aat cag tgg gtt gtt cat	787
Ser Ala Gly Ile Glu Ile Glu Glu Ser Glu Asn Gln Trp Val Val His	
215 220 225	
cct ggt gag atc ttg ggt ccg acc tgg cgc att gag ccg gat ctt tct	835
Pro Gly Glu Ile Leu Gly Arg Thr Trp Arg Ile Glu Pro Asp Leu Ser	
230 235 240 245	
aat gcg act ccg ttc cta gct gcc gct gcg gtc act ggt gga acc atc	883
Asn Ala Thr Pro Phe Leu Ala Ala Ala Val Thr Gly Gly Thr Ile	
250 255 260	
aag att aac cac tgg cca atc aaa act act cag cct ggc gat gct att	931
Lys Ile Asn His Trp Pro Ile Lys Thr Thr Gln Pro Gly Asp Ala Ile	
265 270 275	
cgt tcg att ctt gag cgc atg ggc tgc gaa gtt gag ctg gtt gct cag	979
Arg Ser Ile Leu Glu Arg Met Gly Cys Glu Val Glu Leu Val Ala Gln	
280 285 290	
ggt gaa ggt tac gat ctg tcg gtg act ggt ccg gtt gct ctc aag ggc	
1027	
Gly Glu Gly Tyr Asp Leu Ser Val Thr Gly Pro Val Ala Leu Lys Gly	
295 300 305	
att gag atc gat atg tcc gat atc ggt gag ttg acc cct acc gtg gcg	
1075	
Ile Glu Ile Asp Met Ser Asp Ile Gly Glu Leu Thr Pro Thr Val Ala	
310 315 320 325	
gcg ttg gct gcg ttg gcg tcg aca gag tct cgt ttg acc ggt att gct	
1123	
Ala Leu Ala Ala Leu Ala Ser Thr Glu Ser Arg Leu Thr Gly Ile Ala	
330 335 340	
cat ctt cgt ggc cat gag acg gat cgt ttg gct gcg ttg act gcg gag	
1171	
His Leu Arg Gly His Glu Thr Asp Arg Leu Ala Ala Leu Thr Ala Glu	
345 350 355	

atc aac aaa ctt ggt gga aag tgc act gag ctt aag gat ggt ctg ttg

1219

Ile Asn Lys Leu Gly Gly Lys Cys Thr Glu Leu Lys Asp Gly Leu Leu  
360 365 370

att gag cct gcg tcg ctg cac ggt ggt gtg tgg cat tca tat gct gat

1267

Ile Glu Pro Ala Ser Leu His Gly Gly Val Trp His Ser Tyr Ala Asp  
375 380 385

cac cgt atg gct act gct ggt gcg atc att ggc ctc gcg gtt gat ggc

1315

His Arg Met Ala Thr Ala Gly Ala Ile Ile Gly Leu Ala Val Asp Gly  
390 395 400 405

gtt cag gtt gaa gac att aag acc act tcc aaa act ttc cct ggt ttt

1363

Val Gln Val Glu Asp Ile Lys Thr Thr Ser Lys Thr Phe Pro Gly Phe  
410 415 420

gaa aat gtt tgg gag gag atg gtt ggc tagacgcagc tatgacgaat

1410

Glu Asn Val Trp Glu Glu Met Val Gly  
425 430

ccg

1413

<210> 412

<211> 430

<212> PRT

<213> Corynebacterium glutamicum

<400> 412

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Pro Arg Ala Arg Gly Pro Ile Val Ser Asp Leu Ala Ile Pro Gly Ser  
20 25 30

Lys Ser Ile Thr Asn Arg Ala Leu Ile Leu Ala Ala Leu Ala Ser Thr  
35 40 45

Pro Ser Thr Ile Ile Asp Val Leu Arg Ser Arg Asp Thr Asp Leu Met  
50 55 60

Thr Asp Gly Leu Arg Ser Leu Gly Ile Thr Ile Thr Glu Glu Ala Val  
65 70 75 80

Asp Arg Tyr Arg Val Glu Pro Gly Gln Leu Ser Ala Gly Ser Val Glu  
85 90 95

Cys Gly Leu Ala Gly Thr Val Met Arg Phe Leu Pro Pro Val Ala Ala  
100 105 110

Phe Ala Asp Gly Pro Val His Phe Asp Gly Asp Pro Gln Ala Arg Val  
115 120 125

Arg Pro Met Thr Ser Ile Leu Asp Ala Leu Arg Ser Leu Gly Val Glu  
130 135 140



Val	Asp	Asn	Asn	Asn	Leu	Pro	Phe	Thr	Val	Asn	Ala	Gly	Glu	Val	Pro	145	150	155	160
Glu	Gly	Gly	Val	Val	Glu	Ile	Asp	Ala	Ser	Gly	Ser	Ser	Gln	Phe	Val	165	170		175
Ser	Gly	Leu	Leu	Leu	Ser	Ala	Pro	Arg	Phe	Lys	Asn	Gly	Val	Thr	Val	180	185		190
Lys	His	Val	Gly	Gly	Arg	Leu	Pro	Ser	Met	Pro	His	Ile	Glu	Met	Thr	195	200		205
Val	Asp	Met	Leu	Arg	Ser	Ala	Gly	Ile	Glu	Ile	Glu	Glu	Ser	Glu	Asn	210	215		220
Gln	Trp	Val	Val	His	Pro	Gly	Glu	Ile	Leu	Gly	Arg	Thr	Trp	Arg	Ile	225	230		235
Glu	Pro	Asp	Leu	Ser	Asn	Ala	Thr	Pro	Phe	Leu	Ala	Ala	Ala	Ala	Val	245	250		255
Thr	Gly	Gly	Thr	Ile	Lys	Ile	Asn	His	Trp	Pro	Ile	Lys	Thr	Thr	Gln	260	265		270
Pro	Gly	Asp	Ala	Ile	Arg	Ser	Ile	Leu	Glu	Arg	Met	Gly	Cys	Glu	Val	275	280		285
Glu	Leu	Val	Ala	Gln	Gly	Glu	Gly	Tyr	Asp	Leu	Ser	Val	Thr	Gly	Pro	290	295		300
Val	Ala	Leu	Lys	Gly	Ile	Glu	Ile	Asp	Met	Ser	Asp	Ile	Gly	Glu	Leu	305	310		315
Thr	Pro	Thr	Val	Ala	Ala	Leu	Ala	Ala	Leu	Ala	Ser	Thr	Glu	Ser	Arg	325	330		335
Leu	Thr	Gly	Ile	Ala	His	Leu	Arg	Gly	His	Glu	Thr	Asp	Arg	Leu	Ala	340	345		350
Ala	Leu	Thr	Ala	Glu	Ile	Asn	Lys	Leu	Gly	Gly	Lys	Cys	Thr	Glu	Leu	355	360		365
Lys	Asp	Gly	Leu	Leu	Ile	Glu	Pro	Ala	Ser	Leu	His	Gly	Gly	Val	Trp	370	375		380
His	Ser	Tyr	Ala	Asp	His	Arg	Met	Ala	Thr	Ala	Gly	Ala	Ile	Ile	Gly	385	390		395
Leu	Ala	Val	Asp	Gly	Val	Gln	Val	Glu	Asp	Ile	Lys	Thr	Thr	Ser	Lys	405	410		415
Thr	Phe	Pro	Gly	Phe	Glu	Asn	Val	Trp	Glu	Glu	Met	Val	Gly			420	425		430

&lt;210&gt; 413

&lt;211&gt; 1266

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

<220>  
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 <222> (101)..(1243)  
 <223> RXA02790

<400> 413

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agggaaattt cccaggatga accaaatccg aaaccgccgg atg gag ccc gtc tac 115
              Met Glu Pro Val Tyr
              1                    5

gta aag cgc cgc caa cgg ttt att gcc gtg acg atc gct tca ctc atc 163
Val Lys Arg Arg Gln Arg Phe Ile Ala Val Thr Ile Ala Ser Leu Ile
              10                    15                    20

ctc att atc ggt gcc atc atc tat atc ggt gta gcc acc tca aac cgg 211
Leu Ile Ile Gly Ala Ile Ile Tyr Ile Gly Val Ala Thr Ser Asn Arg
              25                    30                    35

acg cca cat gac tat gaa ggc tcc gga aac ggt gtg gtt cag ctg gtc 259
Thr Pro His Asp Tyr Glu Gly Ser Gly Asn Gly Val Val Gln Leu Val
              40                    45                    50

gaa atc cct gaa ggt tcc tcc ata tca gag ctc ggc cca gag ttg gaa 307
Glu Ile Pro Glu Gly Ser Ser Ile Ser Glu Leu Gly Pro Glu Leu Glu
              55                    60                    65

gaa cga gat atc gtg gcc acc aac tca gcg ttc caa aca gcg gcc agc 355
Glu Arg Asp Ile Val Ala Thr Asn Ser Ala Phe Gln Thr Ala Ala Ser
              70                    75                    80                    85

aac aac ccc aac gcg ggt agt gta cag cca ggt ttc tac cgt ctg cag 403
Asn Asn Pro Asn Ala Gly Ser Val Gln Pro Gly Phe Tyr Arg Leu Gln
              90                    95                    100

gaa caa atg aac gca gca gct gca gtg tcg gct ctg ctt gat cca gac 451
Glu Gln Met Asn Ala Ala Ala Ala Val Ser Ala Leu Leu Asp Pro Asp
              105                    110                    115

aac cag gtt gat ctc ctc gac att cac ggc ggc gcc acc ttg atg gac 499
Asn Gln Val Asp Leu Leu Asp Ile His Gly Gly Ala Thr Leu Met Asp
              120                    125                    130

gtc act gtt gtc ggc gga aac acc cgc gcg gga atc tac tcc cag atc 547
Val Thr Val Val Gly Gly Asn Thr Arg Ala Gly Ile Tyr Ser Gln Ile
              135                    140                    145

gca gcc gtg acc tgc acc gaa ggc tcc gcc aac tgc atc acc gct gag 595
Ala Ala Val Thr Cys Thr Glu Gly Ser Ala Asn Cys Ile Thr Ala Glu
              150                    155                    160                    165

gat ttg cag cag gtt gcc tcc acc gtg tcg cct gca gaa ttg ggt gtc 643
Asp Leu Gln Gln Val Ala Ser Thr Val Ser Pro Ala Glu Leu Gly Val
              170                    175                    180

cca gat tgg gca atc gct gct gtg gaa gct cgc gga act gat cca aag 691
Pro Asp Trp Ala Ile Ala Ala Val Glu Ala Arg Gly Thr Asp Pro Lys
              185                    190                    195

cgc ctc gaa ggc ctg atc atg cct ggc caa tac gtg gtg gat cca tcc 739

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Arg	Leu	Glu	Gly	Leu	Ile	Met	Pro	Gly	Gln	Tyr	Val	Val	Asp	Pro	Ser		
		200					205					210					
aac	gac	gcc	cag	gga	atc	ctc	acc	gat	ctg	atc	acg	cga	tca	gca	aac	787	
Asn	Asp	Ala	Gln	Gly	Ile	Leu	Thr	Asp	Leu	Ile	Thr	Arg	Ser	Ala	Asn		
	215					220					225						
cat	ttc	caa	gaa	acc	gac	atc	acg	ggc	cgt	gca	gat	gcc	atc	gga	ctt	835	
His	Phe	Gln	Glu	Thr	Asp	Ile	Thr	Gly	Arg	Ala	Asp	Ala	Ile	Gly	Leu		
	230				235					240					245		
act	cca	tat	gag	ctg	gtc	acc	gca	gca	tct	tta	atc	gag	cgc	gaa	gca	883	
Thr	Pro	Tyr	Glu	Leu	Val	Thr	Ala	Ala	Ser	Leu	Ile	Glu	Arg	Glu	Ala		
				250					255					260			
cca	gca	gga	gat	ttt	gat	aag	gtc	gcc	cgc	gtc	atc	ttg	aac	cgt	ctc	931	
Pro	Ala	Gly	Asp	Phe	Asp	Lys	Val	Ala	Arg	Val	Ile	Leu	Asn	Arg	Leu		
			265					270					275				
gcc	gag	cca	atg	cag	ctg	caa	ttc	gac	tcc	acc	gtc	aac	tac	ggt	ctg	979	
Ala	Glu	Pro	Met	Gln	Leu	Gln	Phe	Asp	Ser	Thr	Val	Asn	Tyr	Gly	Leu		
		280					285					290					
tct	gaa	caa	gaa	gta	gca	acc	acc	gac	gaa	gac	cgt	cag	acc	gtc	acc		
1027																	
Ser	Glu	Gln	Glu	Val	Ala	Thr	Thr	Asp	Glu	Asp	Arg	Gln	Thr	Val	Thr		
	295					300					305						
cca	tgg	aac	act	tac	gcc	atg	gac	ggc	ctg	cca	caa	acc	ccc	atc	gcc		
1075																	
Pro	Trp	Asn	Thr	Tyr	Ala	Met	Asp	Gly	Leu	Pro	Gln	Thr	Pro	Ile	Ala		
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gca	gta	tcc	acc	gaa	gca	ctc	caa	gcc	atg	gaa	aac	cct	gca	gaa	gga		
1123																	
Ala	Val	Ser	Thr	Glu	Ala	Leu	Gln	Ala	Met	Glu	Asn	Pro	Ala	Glu	Gly		
				330				335						340			
aac	tgg	ctg	tac	ttt	gtc	acc	atc	gac	acc	gat	gga	acc	acc	gtg	ttc		
1171																	
Asn	Trp	Leu	Tyr	Phe	Val	Thr	Ile	Asp	Thr	Asp	Gly	Thr	Thr	Val	Phe		
			345					350					355				
aac	gac	acc	ttc	gaa	gag	cac	gaa	gcc	gac	att	gag	caa	gct	ttg	aac		
1219																	
Asn	Asp	Thr	Phe	Glu	Glu	His	Glu	Ala	Asp	Ile	Glu	Gln	Ala	Leu	Asn		
		360					365					370					
agt	ggc	gtt	cta	gac	agc	aac	cga	taaggatcag	cgaataaaaat	tgg							
1266																	
Ser	Gly	Val	Leu	Asp	Ser	Asn	Arg										
	375					380											

&lt;210&gt; 414

&lt;211&gt; 381

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 414

Met Glu Pro Val Tyr Val Lys Arg Arg Gln Arg Phe Ile Ala Val Thr

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Ile Ala Ser Leu	Ile Leu Ile Ile	Gly Ala Ile Ile	Tyr Ile Gly Val
20		25	30
Ala Thr Ser Asn	Arg Thr Pro His	Asp Tyr Glu Gly	Ser Gly Asn Gly
35	40	45	
Val Val Gln Leu	Val Glu Ile Pro	Glu Gly Ser Ser	Ile Ser Glu Leu
50	55	60	
Gly Pro Glu Leu	Glu Glu Arg Asp	Ile Val Ala Thr	Asn Ser Ala Phe
65	70	75	80
Gln Thr Ala Ala	Ser Asn Asn Pro	Asn Ala Gly Ser	Val Gln Pro Gly
	85	90	95
Phe Tyr Arg Leu	Gln Glu Gln Met	Asn Ala Ala Ala	Val Ser Ala
100		105	110
Leu Leu Asp Pro	Asp Asn Gln Val	Asp Leu Leu Asp	Ile His Gly Gly
115	120	125	
Ala Thr Leu Met	Asp Val Thr Val	Val Gly Gly Asn	Thr Arg Ala Gly
130	135	140	
Ile Tyr Ser Gln	Ile Ala Ala Val	Thr Cys Thr Glu	Gly Ser Ala Asn
145	150	155	160
Cys Ile Thr Ala	Glu Asp Leu Gln	Gln Val Ala Ser	Thr Val Ser Pro
	165	170	175
Ala Glu Leu Gly	Val Pro Asp Trp	Ala Ile Ala Ala	Val Glu Ala Arg
180		185	190
Gly Thr Asp Pro	Lys Arg Leu Glu	Gly Leu Ile Met	Pro Gly Gln Tyr
195	200	205	
Val Val Asp Pro	Ser Asn Asp Ala	Gln Gly Ile Leu	Thr Asp Leu Ile
210	215	220	
Thr Arg Ser Ala	Asn His Phe Gln	Glu Thr Asp Ile	Thr Gly Arg Ala
225	230	235	240
Asp Ala Ile Gly	Leu Thr Pro Tyr	Glu Leu Val Thr	Ala Ala Ser Leu
	245	250	255
Ile Glu Arg Glu	Ala Pro Ala Gly	Asp Phe Asp Lys	Val Ala Arg Val
260		265	270
Ile Leu Asn Arg	Leu Ala Glu Pro	Met Gln Leu Gln	Phe Asp Ser Thr
275	280	285	
Val Asn Tyr Gly	Leu Ser Glu Gln	Glu Val Ala Thr	Thr Asp Glu Asp
290	295	300	
Arg Gln Thr Val	Thr Pro Trp Asn	Thr Tyr Ala Met	Asp Gly Leu Pro
305	310	315	320
Gln Thr Pro Ile	Ala Ala Val Ser	Thr Glu Ala Leu	Gln Ala Met Glu
	325	330	335

Asn Pro Ala Glu Gly Asn Trp Leu Tyr Phe Val Thr Ile Asp Thr Asp  
340 345 350

Gly Thr Thr Val Phe Asn Asp Thr Phe Glu Glu His Glu Ala Asp Ile  
355 360 365

Glu Gln Ala Leu Asn Ser Gly Val Leu Asp Ser Asn Arg  
370 375 380

<210> 415

<211> 644

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(621)

<223> RXN00954

<400> 415

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1 5 10 15

gcg tac aac cct gcg att gcg cat gtg cag ccg gtt cgc cag gcg ctg 96  
Ala Tyr Asn Pro Ala Ile Ala His Val Gln Pro Val Arg Gln Ala Leu  
20 25 30

aaa ttc ccc acc atc ttc aac acg ctt gga cca ttg ctg tcc ccg gcg 144  
Lys Phe Pro Thr Ile Phe Asn Thr Leu Gly Pro Leu Leu Ser Pro Ala  
35 40 45

cgc ccg gag cgt cag atc atg ggc gtg gcc aat gcc aat cat gga cag 192  
Arg Pro Glu Arg Gln Ile Met Gly Val Ala Asn Ala Asn His Gly Gln  
50 55 60

ctc atc gcc gag gtc ttc cgc gag ttg ggc cgt aca cgc gcg ctt gtt 240  
Leu Ile Ala Glu Val Phe Arg Glu Leu Gly Arg Thr Arg Ala Leu Val  
65 70 75 80

gtg cat ggc gca ggc acc gat gag atc gca gtc cac ggc acc acc ttg 288  
Val His Gly Ala Gly Thr Asp Glu Ile Ala Val His Gly Thr Thr Leu  
85 90 95

gtg tgg gag ctt aaa gaa gac ggc acc atc gag cat tac acc atc gag 336  
Val Trp Glu Leu Lys Glu Asp Gly Thr Ile Glu His Tyr Thr Ile Glu  
100 105 110

cct gag gac ctt ggc ctt ggc cgc tac acc ctt gag gat ctc gta ggt 384  
Pro Glu Asp Leu Gly Leu Gly Arg Tyr Thr Leu Glu Asp Leu Val Gly  
115 120 125

ggc ctc ggc act gag aac gcc gaa gct atg cgc gct act ttc gcg ggc 432  
Gly Leu Gly Thr Glu Asn Ala Glu Ala Met Arg Ala Thr Phe Ala Gly  
130 135 140

acc ggc cct gat gca cac cgt gat gcg ttg gct gcg tcc gca ggt gcg 480  
Thr Gly Pro Asp Ala His Arg Asp Ala Leu Ala Ala Ser Ala Gly Ala  
145 150 155 160

atg ttc tac ctc aac ggc gat gtc gac tcc ttg aaa gat ggt gca caa 528  
 Met Phe Tyr Leu Asn Gly Asp Val Asp Ser Leu Lys Asp Gly Ala Gln  
                   165                                  170                                  175

aag gcg ctt tcc ttg ctt gcc gac ggc acc acc cag gca tgg ttg gcc 576  
 Lys Ala Leu Ser Leu Leu Ala Asp Gly Thr Thr Gln Ala Trp Leu Ala  
                   180                                  185                                  190

aag cac gaa gag atc gat tac tca gaa aag gag tct tcc aat gac 621  
 Lys His Glu Glu Ile Asp Tyr Ser Glu Lys Glu Ser Ser Asn Asp  
                   195                                  200                                  205

tagtaataat ctgcccacag tgt 644

<210> 416

<211> 207

<212> PRT

<213> Corynebacterium glutamicum

<400> 416

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Ala Tyr Asn Pro Ala Ile Ala His Val Gln Pro Val Arg Gln Ala Leu  
                   20                                  25                                  30

Lys Phe Pro Thr Ile Phe Asn Thr Leu Gly Pro Leu Leu Ser Pro Ala  
                   35                                  40                                  45

Arg Pro Glu Arg Gln Ile Met Gly Val Ala Asn Ala Asn His Gly Gln  
                   50                                  55                                  60

Leu Ile Ala Glu Val Phe Arg Glu Leu Gly Arg Thr Arg Ala Leu Val  
   65                                  70                                  75                                  80

Val His Gly Ala Gly Thr Asp Glu Ile Ala Val His Gly Thr Thr Leu  
                   85                                  90                                  95

Val Trp Glu Leu Lys Glu Asp Gly Thr Ile Glu His Tyr Thr Ile Glu  
                   100                                  105                                  110

Pro Glu Asp Leu Gly Leu Gly Arg Tyr Thr Leu Glu Asp Leu Val Gly  
                   115                                  120                                  125

Gly Leu Gly Thr Glu Asn Ala Glu Ala Met Arg Ala Thr Phe Ala Gly  
   130                                  135                                  140

Thr Gly Pro Asp Ala His Arg Asp Ala Leu Ala Ala Ser Ala Gly Ala  
   145                                  150                                  155                                  160

Met Phe Tyr Leu Asn Gly Asp Val Asp Ser Leu Lys Asp Gly Ala Gln  
                   165                                  170                                  175

Lys Ala Leu Ser Leu Leu Ala Asp Gly Thr Thr Gln Ala Trp Leu Ala  
                   180                                  185                                  190

Lys His Glu Glu Ile Asp Tyr Ser Glu Lys Glu Ser Ser Asn Asp  
                   195                                  200                                  205

<210> 417  
 <211> 611  
 <212> DNA  
 <213> Corynebacterium glutamicum

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 <223> FRXA00954

<400> 417  
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 gtt cgc cag gcg ctg aaa ttc ccc acc atc ttc aac acg ctt gga cca 96  
 Val Arg Gln Ala Leu Lys Phe Pro Thr Ile Phe Asn Thr Leu Gly Pro  
 20 25 30  
 ttg ctg tcc ccg gcg cgc ccg gag cgt cag atc atg ggc gtg gcc aat 144  
 Leu Leu Ser Pro Ala Arg Pro Glu Arg Gln Ile Met Gly Val Ala Asn  
 35 40 45  
 gcc aat cat gga cag ctc atc gcc gag gtc ttc cgc gag ttg ggc cgt 192  
 Ala Asn His Gly Gln Leu Ile Ala Glu Val Phe Arg Glu Leu Gly Arg  
 50 55 60  
 aca cgc gcg ctt gtt gtg cat ggc gca ggc acc gat gag atc gca gtc 240  
 Thr Arg Ala Leu Val Val His Gly Ala Gly Thr Asp Glu Ile Ala Val  
 65 70 75 80  
 cac ggc acc acc ttg gtg tgg gag ctt aaa gaa gac ggc acc atc gag 288  
 His Gly Thr Thr Leu Val Trp Glu Leu Lys Glu Asp Gly Thr Ile Glu  
 85 90 95  
 cat tac acc atc gag cct gag gac ctt ggc ctt ggc cgc tac acc ctt 336  
 His Tyr Thr Ile Glu Pro Glu Asp Leu Gly Leu Gly Arg Tyr Thr Leu  
 100 105 110  
 gag gat ctc gta ggt ggc ctc ggc act gag aac gcc gaa gct atg cgc 384  
 Glu Asp Leu Val Gly Gly Leu Gly Thr Glu Asn Ala Glu Ala Met Arg  
 115 120 125  
 gct act ttc gcg ggc acc ggc cct gat gca cac cgt gat gcg ttg gct 432  
 Ala Thr Phe Ala Gly Thr Gly Pro Asp Ala His Arg Asp Ala Leu Ala  
 130 135 140  
 gcg tcc gca ggt gcg atg ttc tac ctc aac ggc gat gtc gac tcc ttg 480  
 Ala Ser Ala Gly Ala Met Phe Tyr Leu Asn Gly Asp Val Asp Ser Leu  
 145 150 155 160  
 aaa gat ggt gca caa aag gcg ctt tcc ttg ctt gcc gac ggc acc acc 528  
 Lys Asp Gly Ala Gln Lys Ala Leu Ser Leu Leu Ala Asp Gly Thr Thr  
 165 170 175  
 cag gca tgg ttg gcc aag cac gaa gag atc gat tac tca gaa aag gag 576  
 Gln Ala Trp Leu Ala Lys His Glu Glu Ile Asp Tyr Ser Glu Lys Glu  
 180 185 190  
 tct tcc aat gac tagtaataat ctgcccacag tgt 611

Ser Ser Asn Asp  
195

<210> 418  
<211> 196  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 418  
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Val Arg Gln Ala Leu Lys Phe Pro Thr Ile Phe Asn Thr Leu Gly Pro  
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Leu Leu Ser Pro Ala Arg Pro Glu Arg Gln Ile Met Gly Val Ala Asn  
35 40 45  
Ala Asn His Gly Gln Leu Ile Ala Glu Val Phe Arg Glu Leu Gly Arg  
50 55 60  
Thr Arg Ala Leu Val Val His Gly Ala Gly Thr Asp Glu Ile Ala Val  
65 70 75 80  
His Gly Thr Thr Leu Val Trp Glu Leu Lys Glu Asp Gly Thr Ile Glu  
85 90 95  
His Tyr Thr Ile Glu Pro Glu Asp Leu Gly Leu Gly Arg Tyr Thr Leu  
100 105 110  
Glu Asp Leu Val Gly Gly Leu Gly Thr Glu Asn Ala Glu Ala Met Arg  
115 120 125  
Ala Thr Phe Ala Gly Thr Gly Pro Asp Ala His Arg Asp Ala Leu Ala  
130 135 140  
Ala Ser Ala Gly Ala Met Phe Tyr Leu Asn Gly Asp Val Asp Ser Leu  
145 150 155 160  
Lys Asp Gly Ala Gln Lys Ala Leu Ser Leu Leu Ala Asp Gly Thr Thr  
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Gln Ala Trp Leu Ala Lys His Glu Glu Ile Asp Tyr Ser Glu Lys Glu  
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Ser Ser Asn Asp  
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<210> 419  
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<212> DNA  
<213> Corynebacterium glutamicum

<220>  
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<222> (101) .. (1654)  
<223> RXN00957

<400> 419



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Met Ser Thr Asn Pro  
1 5  
cat gtt ttc tcc cta gat gtc cgc tat cac gag gat gct tct gca ttg 163  
His Val Phe Ser Leu Asp Val Arg Tyr His Glu Asp Ala Ser Ala Leu  
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ttt gcc cac ttg ggt ggc aca acc gca gat gat gca gcc ctg ttg gaa 211  
Phe Ala His Leu Gly Gly Thr Thr Ala Asp Asp Ala Ala Leu Leu Glu  
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Ser Ala Asp Ile Thr Thr Lys Asn Gly Ile Ser Ser Leu Ala Val Leu  
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Lys Ser Ser Val Arg Ile Thr Cys Thr Gly Asn Thr Val Val Thr Gln  
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Pro Leu Thr Asp Ser Gly Arg Ala Val Val Ala Arg Leu Thr Gln Gln  
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Leu Gly Gln Tyr Asn Thr Ala Glu Asn Thr Phe Ser Phe Pro Ala Ser  
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Asp Ala Val Asp Glu Arg Glu Arg Leu Thr Ala Pro Ser Thr Ile Glu  
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Val Leu Arg Lys Leu Gln Phe Glu Ser Gly Tyr Ser Asp Ala Ser Leu  
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cca ctg ctc atg ggc ggt ttc gcg ttt gat ttc tta gaa acc ttt gaa 547  
Pro Leu Leu Met Gly Gly Phe Ala Phe Asp Phe Leu Glu Thr Phe Glu  
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Thr Leu Pro Ala Val Glu Glu Ser Val Asn Thr Tyr Pro Asp Tyr Gln  
150 155 160 165  
ttc gtc ctc gcg gaa atc gtc ctg gac atc aat cac cag gac cag acc 643  
Phe Val Leu Ala Glu Ile Val Leu Asp Ile Asn His Gln Asp Gln Thr  
170 175 180  
gcc aaa ctc gcc ggc gtc tcc aac gcc cca ggc gag ctc gag gcc gag 691  
Ala Lys Leu Ala Gly Val Ser Asn Ala Pro Gly Glu Leu Glu Ala Glu  
185 190 195  
ctc aac aag ctt tca ttg ctt atc gac gcc gcc ctc ccc gca acc gaa 739  
Leu Asn Lys Leu Ser Leu Leu Ile Asp Ala Ala Leu Pro Ala Thr Glu  
200 205 210  
cac gcc tac caa acc acc cct cac gac ggc gac act ctt cgc gtt gtg 787  
His Ala Tyr Gln Thr Thr Pro His Asp Gly Asp Thr Leu Arg Val Val  
215 220 225

gct gat att ccc gat gct cag ttc cgc acc cag atc aat gag ctg aaa	835
Ala Asp Ile Pro Asp Ala Gln Phe Arg Thr Gln Ile Asn Glu Leu Lys	
230 235 240 245	
gaa aac att tac aac ggt gac atc tac caa gtt gtc ccg gcg cgc act	883
Glu Asn Ile Tyr Asn Gly Asp Ile Tyr Gln Val Val Pro Ala Arg Thr	
250 255 260	
ttc acc gca cca tgt cct gat gca ttc gct gct tat ctg cag ctg cgt	931
Phe Thr Ala Pro Cys Pro Asp Ala Phe Ala Ala Tyr Leu Gln Leu Arg	
265 270 275	
gcc acc aac ccg tcg ccg tac atg ttc tat atc cgt ggc ctc aac gaa	979
Ala Thr Asn Pro Ser Pro Tyr Met Phe Tyr Ile Arg Gly Leu Asn Glu	
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1123 Arg Pro Arg Gly Leu Asn Pro Asp Gly Ser Ile Asn Asp Glu Leu Asp	
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atc cgc aat gag ttg gat atg cgc act gat gcc aaa gag atc gcg gag	
1171 Ile Arg Asn Glu Leu Asp Met Arg Thr Asp Ala Lys Glu Ile Ala Glu	
345 350 355	
cac acc atg ctt gtc gat ctc gcc cgc aac gac ctg gcc cgc gtc tcg	
1219 His Thr Met Leu Val Asp Leu Ala Arg Asn Asp Leu Ala Arg Val Ser	
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gtc cca gcg tcg cgc cgg gtt gcg gat ctt ttg cag gtg gat cgc tat	
1267 Val Pro Ala Ser Arg Arg Val Ala Asp Leu Leu Gln Val Asp Arg Tyr	
375 380 385	
tcc cgc gtg atg cac ttg gtg tcc cgt gtg acg gcg acg ttg gac cca	
1315 Ser Arg Val Met His Leu Val Ser Arg Val Thr Ala Thr Leu Asp Pro	
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410 415 420	
ttg acc ggc gct ccg aag ttg cgc gct atg gag ctg ttg cgc ggc gtc	
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425 430 435	

gaa aag cgc agg cgt ggt tct tat ggt ggg gca gtg ggg tac ctg cgc  
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 Glu Lys Arg Arg Arg Gly Ser Tyr Gly Gly Ala Val Gly Tyr Leu Arg  
           440                                  445                                  450

ggc aat ggc gat atg gat aat tgc att gtt att cgt tcg gcg ttt gtc  
 1507  
 Gly Asn Gly Asp Met Asp Asn Cys Ile Val Ile Arg Ser Ala Phe Val  
           455                                  460                                  465

cag gat ggt gtg gct gct gtg cag gct ggt gct ggt gtg gtc cgc gat  
 1555  
 Gln Asp Gly Val Ala Ala Val Gln Ala Gly Ala Gly Val Val Arg Asp  
 470                                  475                                  480                                  485

tct aat cct caa tct gaa gcc gat gag acg ttg cac aag gcg tat gcc  
 1603  
 Ser Asn Pro Gln Ser Glu Ala Asp Glu Thr Leu His Lys Ala Tyr Ala  
                                   490                                  495                                  500

gtg ttg aat gcc att gcg ctt gct gct ggt tcc act ttg gag gtc atc  
 1651  
 Val Leu Asn Ala Ile Ala Leu Ala Ala Gly Ser Thr Leu Glu Val Ile  
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 1677  
 Arg

<210> 420  
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 <212> PRT  
 <213> Corynebacterium glutamicum

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 Ala Ala Leu Leu Glu Ser Ala Asp Ile Thr Thr Lys Asn Gly Ile Ser  
                                   35                                  40                                  45  
 Ser Leu Ala Val Leu Lys Ser Ser Val Arg Ile Thr Cys Thr Gly Asn  
                                   50                                  55                                  60  
 Thr Val Val Thr Gln Pro Leu Thr Asp Ser Gly Arg Ala Val Val Ala  
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 Arg Leu Thr Gln Gln Leu Gly Gln Tyr Asn Thr Ala Glu Asn Thr Phe  
                                   85                                  90                                  95  
 Ser Phe Pro Ala Ser Asp Ala Val Asp Glu Arg Glu Arg Leu Thr Ala  
                                   100                                  105                                  110  
 Pro Ser Thr Ile Glu Val Leu Arg Lys Leu Gln Phe Glu Ser Gly Tyr  
                                   115                                  120                                  125

Ser	Asp	Ala	Ser	Leu	Pro	Leu	Leu	Met	Gly	Gly	Phe	Ala	Phe	Asp	Phe
130						135					140				
Leu	Glu	Thr	Phe	Glu	Thr	Leu	Pro	Ala	Val	Glu	Glu	Ser	Val	Asn	Thr
145					150					155					160
Tyr	Pro	Asp	Tyr	Gln	Phe	Val	Leu	Ala	Glu	Ile	Val	Leu	Asp	Ile	Asn
				165					170					175	
His	Gln	Asp	Gln	Thr	Ala	Lys	Leu	Ala	Gly	Val	Ser	Asn	Ala	Pro	Gly
			180					185					190		
Glu	Leu	Glu	Ala	Glu	Leu	Asn	Lys	Leu	Ser	Leu	Leu	Ile	Asp	Ala	Ala
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Leu	Pro	Ala	Thr	Glu	His	Ala	Tyr	Gln	Thr	Thr	Pro	His	Asp	Gly	Asp
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Thr	Leu	Arg	Val	Val	Ala	Asp	Ile	Pro	Asp	Ala	Gln	Phe	Arg	Thr	Gln
225					230					235					240
Ile	Asn	Glu	Leu	Lys	Glu	Asn	Ile	Tyr	Asn	Gly	Asp	Ile	Tyr	Gln	Val
				245					250					255	
Val	Pro	Ala	Arg	Thr	Phe	Thr	Ala	Pro	Cys	Pro	Asp	Ala	Phe	Ala	Ala
			260					265					270		
Tyr	Leu	Gln	Leu	Arg	Ala	Thr	Asn	Pro	Ser	Pro	Tyr	Met	Phe	Tyr	Ile
		275					280					285			
Arg	Gly	Leu	Asn	Glu	Gly	Arg	Ser	Tyr	Glu	Leu	Phe	Gly	Ala	Ser	Pro
	290					295					300				
Glu	Ser	Asn	Leu	Lys	Phe	Thr	Ala	Ala	Asn	Arg	Glu	Leu	Gln	Leu	Tyr
305					310					315					320
Pro	Ile	Ala	Gly	Thr	Arg	Pro	Arg	Gly	Leu	Asn	Pro	Asp	Gly	Ser	Ile
				325					330					335	
Asn	Asp	Glu	Leu	Asp	Ile	Arg	Asn	Glu	Leu	Asp	Met	Arg	Thr	Asp	Ala
			340					345					350		
Lys	Glu	Ile	Ala	Glu	His	Thr	Met	Leu	Val	Asp	Leu	Ala	Arg	Asn	Asp
		355					360					365			
Leu	Ala	Arg	Val	Ser	Val	Pro	Ala	Ser	Arg	Arg	Val	Ala	Asp	Leu	Leu
	370					375					380				
Gln	Val	Asp	Arg	Tyr	Ser	Arg	Val	Met	His	Leu	Val	Ser	Arg	Val	Thr
385					390					395					400
Ala	Thr	Leu	Asp	Pro	Glu	Leu	Asp	Ala	Leu	Asp	Ala	Tyr	Arg	Ala	Cys
				405					410					415	
Met	Asn	Met	Gly	Thr	Leu	Thr	Gly	Ala	Pro	Lys	Leu	Arg	Ala	Met	Glu
			420					425					430		
Leu	Leu	Arg	Gly	Val	Glu	Lys	Arg	Arg	Arg	Gly	Ser	Tyr	Gly	Gly	Ala
		435					440					445			

Val Gly Tyr Leu Arg Gly Asn Gly Asp Met Asp Asn Cys Ile Val Ile  
 450 455 460

Arg Ser Ala Phe Val Gln Asp Gly Val Ala Ala Val Gln Ala Gly Ala  
 465 470 475 480

Gly Val Val Arg Asp Ser Asn Pro Gln Ser Glu Ala Asp Glu Thr Leu  
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<210> 421  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(1128)  
 <223> FRXA00957

<400> 421

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aac act tac ccc gat tac cag ttc gtc ctc gcg gaa atc gtc ctg gac	96
Asn Thr Tyr Pro Asp Tyr Gln Phe Val Leu Ala Glu Ile Val Leu Asp	
20 25 30	
atc aat cac cag gac cag acc gcc aaa ctc gcc ggc gtc tcc aac gcc	144
Ile Asn His Gln Asp Gln Thr Ala Lys Leu Ala Gly Val Ser Asn Ala	
35 40 45	
cca ggc gag ctc gag gcc gag ctc aac aag ctt tca ttg ctt atc gac	192
Pro Gly Glu Leu Glu Ala Glu Leu Asn Lys Leu Ser Leu Leu Ile Asp	
50 55 60	
gcc gcc ctc ccc gca acc gaa cac gcc tac caa acc acc cct cac gac	240
Ala Ala Leu Pro Ala Thr Glu His Ala Tyr Gln Thr Thr Pro His Asp	
65 70 75 80	
ggc gac act ctt cgc gtt gtg gct gat att ccc gat gct cag ttc cgc	288
Gly Asp Thr Leu Arg Val Val Ala Asp Ile Pro Asp Ala Gln Phe Arg	
85 90 95	
acc cag atc aat gag ctg aaa gaa aac att tac aac ggt gac atc tac	336
Thr Gln Ile Asn Glu Leu Lys Glu Asn Ile Tyr Asn Gly Asp Ile Tyr	
100 105 110	
caa gtt gtc ccg gcg cgc act ttc acc gca cca tgt cct gat gca ttc	384
Gln Val Val Pro Ala Arg Thr Phe Thr Ala Pro Cys Pro Asp Ala Phe	
115 120 125	
gct gct tat ctg cag ctg cgt gcc acc aac ccg tcg ccg tac atg ttc	432
Ala Ala Tyr Leu Gln Leu Arg Ala Thr Asn Pro Ser Pro Tyr Met Phe	

130	135	140	
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tcc cct gag tcc aac ctc aag ttc acc gct gct aac cgt gag ctg cag Ser Pro Glu Ser Asn Leu Lys Phe Thr Ala Ala Asn Arg Glu Leu Gln 165 170 175			528
ctg tac cca atc gca ggt acc cgc ccc cgt gga ctc aac cca gat ggc Leu Tyr Pro Ile Ala Gly Thr Arg Pro Arg Gly Leu Asn Pro Asp Gly 180 185 190			576
tcc atc aac gat gag cta gat atc cgc aat gag ttg gat atg cgc act Ser Ile Asn Asp Glu Leu Asp Ile Arg Asn Glu Leu Asp Met Arg Thr 195 200 205			624
gat gcc aaa gag atc gcg gag cac acc atg ctt gtc gat ctc gcc cgc Asp Ala Lys Glu Ile Ala Glu His Thr Met Leu Val Asp Leu Ala Arg 210 215 220			672
aac gac ctg gcc cgc gtc tcg gtc cca gcg tcg cgc cgg gtt gcg gat Asn Asp Leu Ala Arg Val Ser Val Pro Ala Ser Arg Arg Val Ala Asp 225 230 235 240			720
ctt ttg cag gtg gat cgc tat tcc cgc gtg atg cac ttg gtg tcc cgt Leu Leu Gln Val Asp Arg Tyr Ser Arg Val Met His Leu Val Ser Arg 245 250 255			768
gtg acg gcg acg ttg gac cca gag ctt gat gct ttg gac gcc tat cgg Val Thr Ala Thr Leu Asp Pro Glu Leu Asp Ala Leu Asp Ala Tyr Arg 260 265 270			816
gcg tgc atg aat atg ggc acg ttg acc ggc gct ccg aag ttg cgc gct Ala Cys Met Asn Met Gly Thr Leu Thr Gly Ala Pro Lys Leu Arg Ala 275 280 285			864
atg gag ctg ttg cgc ggc gtc gaa aag cgc agg cgt ggt tct tat ggt Met Glu Leu Leu Arg Gly Val Glu Lys Arg Arg Arg Gly Ser Tyr Gly 290 295 300			912
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gtt att cgt tcg gcg ttt gtc cag gat ggt gtg gct gct gtg cag gct 1008 Val Ile Arg Ser Ala Phe Val Gln Asp Gly Val Ala Ala Val Gln Ala 325 330 335			
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acg ttg cac aag gcg tat gcc gtg ttg aat gcc att gcg ctt gct gct 1104 Thr Leu His Lys Ala Tyr Ala Val Leu Asn Ala Ile Ala Leu Ala Ala 355 360 365			

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 Ile Asn His Gln Asp Gln Thr Ala Lys Leu Ala Gly Val Ser Asn Ala  
                       35                      40                      45  
 Pro Gly Glu Leu Glu Ala Glu Leu Asn Lys Leu Ser Leu Leu Ile Asp  
           50                      55                      60  
 Ala Ala Leu Pro Ala Thr Glu His Ala Tyr Gln Thr Thr Pro His Asp  
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 Gly Asp Thr Leu Arg Val Val Ala Asp Ile Pro Asp Ala Gln Phe Arg  
                       85                      90                      95  
 Thr Gln Ile Asn Glu Leu Lys Glu Asn Ile Tyr Asn Gly Asp Ile Tyr  
                       100                      105                      110  
 Gln Val Val Pro Ala Arg Thr Phe Thr Ala Pro Cys Pro Asp Ala Phe  
                       115                      120                      125  
 Ala Ala Tyr Leu Gln Leu Arg Ala Thr Asn Pro Ser Pro Tyr Met Phe  
   130                      135                      140  
 Tyr Ile Arg Gly Leu Asn Glu Gly Arg Ser Tyr Glu Leu Phe Gly Ala  
 145                      150                      155                      160  
 Ser Pro Glu Ser Asn Leu Lys Phe Thr Ala Ala Asn Arg Glu Leu Gln  
                       165                      170                      175  
 Leu Tyr Pro Ile Ala Gly Thr Arg Pro Arg Gly Leu Asn Pro Asp Gly  
                       180                      185                      190  
 Ser Ile Asn Asp Glu Leu Asp Ile Arg Asn Glu Leu Asp Met Arg Thr  
                       195                      200                      205  
 Asp Ala Lys Glu Ile Ala Glu His Thr Met Leu Val Asp Leu Ala Arg  
   210                      215                      220  
 Asn Asp Leu Ala Arg Val Ser Val Pro Ala Ser Arg Arg Val Ala Asp  
 225                      230                      235                      240  
 Leu Leu Gln Val Asp Arg Tyr Ser Arg Val Met His Leu Val Ser Arg  
                       245                      250                      255  
 Val Thr Ala Thr Leu Asp Pro Glu Leu Asp Ala Leu Asp Ala Tyr Arg

260					265					270						
Ala	Cys	Met	Asn	Met	Gly	Thr	Leu	Thr	Gly	Ala	Pro	Lys	Leu	Arg	Ala	
275					280					285						
Met	Glu	Leu	Leu	Arg	Gly	Val	Glu	Lys	Arg	Arg	Arg	Gly	Ser	Tyr	Gly	
290					295					300						
Gly	Ala	Val	Gly	Tyr	Leu	Arg	Gly	Asn	Gly	Asp	Met	Asp	Asn	Cys	Ile	
305					310					315					320	
Val	Ile	Arg	Ser	Ala	Phe	Val	Gln	Asp	Gly	Val	Ala	Ala	Val	Gln	Ala	
325					330					335						
Gly	Ala	Gly	Val	Val	Arg	Asp	Ser	Asn	Pro	Gln	Ser	Glu	Ala	Asp	Glu	
340					345					350						
Thr	Leu	His	Lys	Ala	Tyr	Ala	Val	Leu	Asn	Ala	Ile	Ala	Leu	Ala	Ala	
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1045)  
 <223> RXA02687

<400> 423  
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 Met Ser Asp Ala Pro 5  
 act gtt gtg gcc tat ttg ggg cct gcc gga acc ttc acc gaa gaa gcc 163  
 Thr Val Val Ala Tyr Leu Gly Pro Ala Gly Thr Phe Thr Glu Glu Ala 20  
 ctc tac aaa ttt gcc gac gcc ggc gta ttc ggc gac ggt gag atc gag 211  
 Leu Tyr Lys Phe Ala Asp Ala Gly Val Phe Gly Asp Gly Glu Ile Glu 35  
 cag cta cca gcc aaa tcg cca caa gaa gct gtc gac gcc gtc cgc cac 259  
 Gln Leu Pro Ala Lys Ser Pro Gln Glu Ala Val Asp Ala Val Arg His 50  
 ggc acc gcc cag ttc gcg gtg gtc gcc atc gaa aac ttc gtc gac ggc 307  
 Gly Thr Ala Gln Phe Ala Val Val Ala Ile Glu Asn Phe Val Asp Gly 65  
 ccc gtc acc ccc acc ttc gac gcc ctt gac cag ggc tcc aac gtg caa 355  
 Pro Val Thr Pro Thr Phe Asp Ala Leu Asp Gln Gly Ser Asn Val Gln 85  
 70 75 80



atc atc gcc gaa gaa gaa ctc gac atc gcc ttt tcc atc atg gtc cgg	403
Ile Ile Ala Glu Glu Glu Leu Asp Ile Ala Phe Ser Ile Met Val Arg	
90 95 100	
cca ggg act tcg ctt gcc gac gtc aaa acc ctc gcc acc cac ccg gtt	451
Pro Gly Thr Ser Leu Ala Asp Val Lys Thr Leu Ala Thr His Pro Val	
105 110 115	
ggg tac caa caa gtg aaa aac tgg atg gca acc acc att ccg gac gcc	499
Gly Tyr Gln Gln Val Lys Asn Trp Met Ala Thr Thr Ile Pro Asp Ala	
120 125 130	
atg tat ctt tca gca agc tcc aac ggc gcc ggc gca caa atg gtt gcc	547
Met Tyr Leu Ser Ala Ser Ser Asn Gly Ala Gly Ala Gln Met Val Ala	
135 140 145	
gaa gga acc gcc gac gca gcc gca gcg ccc tcc cgc gca gcc gaa ctc	595
Glu Gly Thr Ala Asp Ala Ala Ala Pro Ser Arg Ala Ala Glu Leu	
150 155 160 165	
ttc gga ctg gaa cgc ctt gtt gat gat gtc gcc gac gtc cgt ggc gcc	643
Phe Gly Leu Glu Arg Leu Val Asp Asp Val Ala Asp Val Arg Gly Ala	
170 175 180	
cgc acc cgc ttc gtt gct gtc caa gcc caa gca gcc gtt tcc gaa ccg	691
Arg Thr Arg Phe Val Ala Val Gln Ala Gln Ala Ala Val Ser Glu Pro	
185 190 195	
acc ggc cac gac cgc acc tcc gtc att ttc tcc cta ccg aat gtg cca	739
Thr Gly His Asp Arg Thr Ser Val Ile Phe Ser Leu Pro Asn Val Pro	
200 205 210	
ggc agc ctc gtg cgc gcc ctc aac gaa ttc gcc atc cgc ggc gtt gac	787
Gly Ser Leu Val Arg Ala Leu Asn Glu Phe Ala Ile Arg Gly Val Asp	
215 220 225	
ctc acc cgc atc gaa tcc cgc ccc acc cgc aaa gtc ttc gga acc tac	835
Leu Thr Arg Ile Glu Ser Arg Pro Thr Arg Lys Val Phe Gly Thr Tyr	
230 235 240 245	
cgc ttc cac ctg gac ata tcc gga cat atc cgc gat atc ccc gtc gcc	883
Arg Phe His Leu Asp Ile Ser Gly His Ile Arg Asp Ile Pro Val Ala	
250 255 260	
gaa gcc ctc cgc gca ctc cac ctc caa gcc gaa gaa ctc gtc ttc gtc	931
Glu Ala Leu Arg Ala Leu His Leu Gln Ala Glu Glu Leu Val Phe Val	
265 270 275	
ggc tcc tgg ccc tcc aac cgt gcg gaa gac agc acg ccc caa acc gac	979
Gly Ser Trp Pro Ser Asn Arg Ala Glu Asp Ser Thr Pro Gln Thr Asp	
280 285 290	
caa cta gct aag cta cac aag gcg gac gaa tgg gtt cgc gca gca agc	
1027	
Gln Leu Ala Lys Leu His Lys Ala Asp Glu Trp Val Arg Ala Ala Ser	
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gaa gga agg aaa ctt aac tagccatggc cggccggatt att	
1068	
Glu Gly Arg Lys Leu Asn	
310 315	

&lt;210&gt; 424

&lt;211&gt; 315

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 424

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		20						25					30		
Asp	Gly	Glu	Ile	Glu	Gln	Leu	Pro	Ala	Lys	Ser	Pro	Gln	Glu	Ala	Val
		35					40					45			
Asp	Ala	Val	Arg	His	Gly	Thr	Ala	Gln	Phe	Ala	Val	Val	Ala	Ile	Glu
	50					55					60				
Asn	Phe	Val	Asp	Gly	Pro	Val	Thr	Pro	Thr	Phe	Asp	Ala	Leu	Asp	Gln
65					70					75					80
Gly	Ser	Asn	Val	Gln	Ile	Ile	Ala	Glu	Glu	Glu	Leu	Asp	Ile	Ala	Phe
				85					90					95	
Ser	Ile	Met	Val	Arg	Pro	Gly	Thr	Ser	Leu	Ala	Asp	Val	Lys	Thr	Leu
			100					105					110		
Ala	Thr	His	Pro	Val	Gly	Tyr	Gln	Gln	Val	Lys	Asn	Trp	Met	Ala	Thr
		115					120					125			
Thr	Ile	Pro	Asp	Ala	Met	Tyr	Leu	Ser	Ala	Ser	Ser	Asn	Gly	Ala	Gly
	130					135						140			
Ala	Gln	Met	Val	Ala	Glu	Gly	Thr	Ala	Asp	Ala	Ala	Ala	Ala	Pro	Ser
145					150				155					160	
Arg	Ala	Ala	Glu	Leu	Phe	Gly	Leu	Glu	Arg	Leu	Val	Asp	Asp	Val	Ala
			165						170					175	
Asp	Val	Arg	Gly	Ala	Arg	Thr	Arg	Phe	Val	Ala	Val	Gln	Ala	Gln	Ala
			180					185					190		
Ala	Val	Ser	Glu	Pro	Thr	Gly	His	Asp	Arg	Thr	Ser	Val	Ile	Phe	Ser
		195					200					205			
Leu	Pro	Asn	Val	Pro	Gly	Ser	Leu	Val	Arg	Ala	Leu	Asn	Glu	Phe	Ala
	210					215					220				
Ile	Arg	Gly	Val	Asp	Leu	Thr	Arg	Ile	Glu	Ser	Arg	Pro	Thr	Arg	Lys
225					230					235					240
Val	Phe	Gly	Thr	Tyr	Arg	Phe	His	Leu	Asp	Ile	Ser	Gly	His	Ile	Arg
			245						250					255	
Asp	Ile	Pro	Val	Ala	Glu	Ala	Leu	Arg	Ala	Leu	His	Leu	Gln	Ala	Glu
			260					265					270		
Glu	Leu	Val	Phe	Val	Gly	Ser	Trp	Pro	Ser	Asn	Arg	Ala	Glu	Asp	Ser
		275					280					285			

Thr Pro Gln Thr Asp Gln Leu Ala Lys Leu His Lys Ala Asp Glu Trp  
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Val Arg Ala Ala Ser Glu Gly Arg Lys Leu Asn  
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<210> 425

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<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1330)

<223> RXN01698

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 Met Leu Gly Met Leu  
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cga tgg act aca gca ggt gaa tcc cac ggc cag gcg ctt atc gcc acg 163  
 Arg Trp Thr Thr Ala Gly Glu Ser His Gly Gln Ala Leu Ile Ala Thr  
 10 15 20

gtt gaa cac atg cca gca ggc gtg ccc gtg act aaa gat gag gtc tcg 211  
 Val Glu His Met Pro Ala Gly Val Pro Val Thr Lys Asp Glu Val Ser  
 25 30 35

tat caa ttg gcg cgc cga cgc ctt gga tat ggt cgc ggc gct cgc atg 259  
 Tyr Gln Leu Ala Arg Arg Arg Leu Gly Tyr Gly Arg Gly Ala Arg Met  
 40 45 50

aag ttt gag caa gac gcg ttg acc ttc ctc acc ggc atc cgc cac ggc 307  
 Lys Phe Glu Gln Asp Ala Leu Thr Phe Leu Thr Gly Ile Arg His Gly  
 55 60 65

ctc act ttg ggt agc ccc atc tca atc atg atc ggc aac act gag tgg 355  
 Leu Thr Leu Gly Ser Pro Ile Ser Ile Met Ile Gly Asn Thr Glu Trp  
 70 75 80 85

gat aag tgg acc acc atc atg tcc tct gac gct ttg gac atg gaa gac 403  
 Asp Lys Trp Thr Thr Ile Met Ser Ser Asp Ala Leu Asp Met Glu Asp  
 90 95 100

cca gat aac gtt gcg gcg atg tct tcg ggt cgg ggc gca aaa ctg act 451  
 Pro Asp Asn Val Ala Ala Met Ser Ser Gly Arg Gly Ala Lys Leu Thr  
 105 110 115

cgt ccg cgt cca ggc cac gct gat tac gca ggc atg ctc aag tac gga 499  
 Arg Pro Arg Pro Gly His Ala Asp Tyr Ala Gly Met Leu Lys Tyr Gly  
 120 125 130

ttc gat gat gcc cgc aac gtg ctg gag cgt tct tca gcc cgt gag acg 547  
 Phe Asp Asp Ala Arg Asn Val Leu Glu Arg Ser Ser Ala Arg Glu Thr  
 135 140 145

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Ala Ala Arg Val Ala Ala Ala Thr Val Ala Arg Ser Phe Leu Arg Glu	
150 155 160 165	
acc ttg ggc gtg gaa gtg ctt tcc cac gta att tcc att ggt gcg tcc	643
Thr Leu Gly Val Glu Val Leu Ser His Val Ile Ser Ile Gly Ala Ser	
170 175 180	
gag cct tac act ggc gcg gag cca acc ttt gca gat att caa gca atc	691
Glu Pro Tyr Thr Gly Ala Glu Pro Thr Phe Ala Asp Ile Gln Ala Ile	
185 190 195	
gat gat tcc cca gtt cgt gca ttc ggt aaa gac gct gaa gaa tcc atg	739
Asp Asp Ser Pro Val Arg Ala Phe Gly Lys Asp Ala Glu Glu Ser Met	
200 205 210	
atc gcg gaa atc gag gcc gca aag aaa gcc ggc gat acc ctc ggt ggc	787
Ile Ala Glu Ile Glu Ala Ala Lys Lys Ala Gly Asp Thr Leu Gly Gly	
215 220 225	
atc gtg gaa gtg att gtt gaa ggc ctg ccc atc ggt ttg ggc tca cac	835
Ile Val Glu Val Ile Val Glu Gly Leu Pro Ile Gly Leu Gly Ser His	
230 235 240 245	
att tct ggc gaa gat cgc ctc gat gcg cag atc gca gct gca ctc atg	883
Ile Ser Gly Glu Asp Arg Leu Asp Ala Gln Ile Ala Ala Ala Leu Met	
250 255 260	
ggc att cag gcc atc aag ggc gtg gaa atc ggt gac ggt ttc gaa gaa	931
Gly Ile Gln Ala Ile Lys Gly Val Glu Ile Gly Asp Gly Phe Glu Glu	
265 270 275	
gct cgt cga cgt ggc tcc gaa gcc cac gat gaa gtg ttc ctg gat gac	979
Ala Arg Arg Arg Gly Ser Glu Ala His Asp Glu Val Phe Leu Asp Asp	
280 285 290	
aac ggc gta tac cgc aac acc aac cgt gca ggt ggc ctc gaa ggc ggc	
1027	
Asn Gly Val Tyr Arg Asn Thr Asn Arg Ala Gly Gly Leu Glu Gly Gly	
295 300 305	
atg acc aac ggt gaa acc ctg cgc gtt cgt gct ggc atg aag cca att	
1075	
Met Thr Asn Gly Glu Thr Leu Arg Val Arg Ala Gly Met Lys Pro Ile	
310 315 320 325	
tct act gtg cct cgc gcc ctg aaa acc att gat atg gaa aac ggc aag	
1123	
Ser Thr Val Pro Arg Ala Leu Lys Thr Ile Asp Met Glu Asn Gly Lys	
330 335 340	
gca gca acc gga atc cac cag cgt tcc gac gtg tgc gct gtt cca gcc	
1171	
Ala Ala Thr Gly Ile His Gln Arg Ser Asp Val Cys Ala Val Pro Ala	
345 350 355	
gcc ggt gtc gtt gca gaa gca atg gtc acc ctg gtt ctc gcc cgc gca	
1219	
Ala Gly Val Val Ala Glu Ala Met Val Thr Leu Val Leu Ala Arg Ala	
360 365 370	

gtc ctg cag aaa ttc ggc ggt gac tcc ctg agc gaa acc aag agc aac  
 1267  
 Val Leu Gln Lys Phe Gly Gly Asp Ser Leu Ser Glu Thr Lys Ser Asn  
 375 380 385

att gac acc tac ctc aaa aac att gag gaa cga atg aaa ttc gaa ggt  
 1315  
 Ile Asp Thr Tyr Leu Lys Asn Ile Glu Glu Arg Met Lys Phe Glu Gly  
 390 395 400 405

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 Leu Glu Asp Gly Ala  
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<210> 426  
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 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 426  
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 Ala Leu Ile Ala Thr Val Glu His Met Pro Ala Gly Val Pro Val Thr  
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 Lys Asp Glu Val Ser Tyr Gln Leu Ala Arg Arg Arg Leu Gly Tyr Gly  
 35 40 45  
 Arg Gly Ala Arg Met Lys Phe Glu Gln Asp Ala Leu Thr Phe Leu Thr  
 50 55 60  
 Gly Ile Arg His Gly Leu Thr Leu Gly Ser Pro Ile Ser Ile Met Ile  
 65 70 75 80  
 Gly Asn Thr Glu Trp Asp Lys Trp Thr Thr Ile Met Ser Ser Asp Ala  
 85 90 95  
 Leu Asp Met Glu Asp Pro Asp Asn Val Ala Ala Met Ser Ser Gly Arg  
 100 105 110  
 Gly Ala Lys Leu Thr Arg Pro Arg Pro Gly His Ala Asp Tyr Ala Gly  
 115 120 125  
 Met Leu Lys Tyr Gly Phe Asp Asp Ala Arg Asn Val Leu Glu Arg Ser  
 130 135 140  
 Ser Ala Arg Glu Thr Ala Ala Arg Val Ala Ala Ala Thr Val Ala Arg  
 145 150 155 160  
 Ser Phe Leu Arg Glu Thr Leu Gly Val Glu Val Leu Ser His Val Ile  
 165 170 175  
 Ser Ile Gly Ala Ser Glu Pro Tyr Thr Gly Ala Glu Pro Thr Phe Ala  
 180 185 190  
 Asp Ile Gln Ala Ile Asp Asp Ser Pro Val Arg Ala Phe Gly Lys Asp  
 195 200 205

Ala Glu Glu Ser Met Ile Ala Glu Ile Glu Ala Ala Lys Lys Ala Gly  
 210 215 220

Asp Thr Leu Gly Gly Ile Val Glu Val Ile Val Glu Gly Leu Pro Ile  
 225 230 235 240

Gly Leu Gly Ser His Ile Ser Gly Glu Asp Arg Leu Asp Ala Gln Ile  
 245 250 255

Ala Ala Ala Leu Met Gly Ile Gln Ala Ile Lys Gly Val Glu Ile Gly  
 260 265 270

Asp Gly Phe Glu Glu Ala Arg Arg Arg Gly Ser Glu Ala His Asp Glu  
 275 280 285

Val Phe Leu Asp Asp Asn Gly Val Tyr Arg Asn Thr Asn Arg Ala Gly  
 290 295 300

Gly Leu Glu Gly Gly Met Thr Asn Gly Glu Thr Leu Arg Val Arg Ala  
 305 310 315 320

Gly Met Lys Pro Ile Ser Thr Val Pro Arg Ala Leu Lys Thr Ile Asp  
 325 330 335

Met Glu Asn Gly Lys Ala Ala Thr Gly Ile His Gln Arg Ser Asp Val  
 340 345 350

Cys Ala Val Pro Ala Ala Gly Val Val Ala Glu Ala Met Val Thr Leu  
 355 360 365

Val Leu Ala Arg Ala Val Leu Gln Lys Phe Gly Gly Asp Ser Leu Ser  
 370 375 380

Glu Thr Lys Ser Asn Ile Asp Thr Tyr Leu Lys Asn Ile Glu Glu Arg  
 385 390 395 400

Met Lys Phe Glu Gly Leu Glu Asp Gly Ala  
 405 410

<210> 427  
 <211> 1013  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(990)  
 <223> FRXA01698

<400> 427

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ttg gac atg gaa gac cca gat aac gtt gcg gcg atg tct tcg ggt cgg	96
Leu Asp Met Glu Asp Pro Asp Asn Val Ala Ala Met Ser Ser Gly Arg	
20 25 30	
ggc gca aaa ctg act cgt ccg cgt cca ggc cac gct gat tac gca ggc	144
Gly Ala Lys Leu Thr Arg Pro Arg Pro Gly His Ala Asp Tyr Ala Gly	

35					40					45						
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Met	Leu	Lys	Tyr	Gly	Phe	Asp	Asp	Ala	Arg	Asn	Val	Leu	Glu	Arg	Ser	
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tca	gcc	cgt	gag	acg	gca	gca	cgc	gtg	gca	gca	gca	acc	gtt	gcg	cgt	240
Ser	Ala	Arg	Glu	Thr	Ala	Ala	Arg	Val	Ala	Ala	Ala	Thr	Val	Ala	Arg	
	65				70					75					80	
tcc	ttc	ctg	cgt	gaa	acc	ttg	ggc	gtg	gaa	gtg	ctt	tcc	cac	gta	att	288
Ser	Phe	Leu	Arg	Glu	Thr	Leu	Gly	Val	Glu	Val	Leu	Ser	His	Val	Ile	
				85					90					95		
tcc	att	ggc	gcg	tcc	gag	cct	tac	act	ggc	gcg	gag	cca	acc	ttt	gca	336
Ser	Ile	Gly	Ala	Ser	Glu	Pro	Tyr	Thr	Gly	Ala	Glu	Pro	Thr	Phe	Ala	
			100					105					110			
gat	att	caa	gca	atc	gat	gat	tcc	cca	gtt	cgt	gca	ttc	ggc	aaa	gac	384
Asp	Ile	Gln	Ala	Ile	Asp	Asp	Ser	Pro	Val	Arg	Ala	Phe	Gly	Lys	Asp	
		115					120					125				
gct	gaa	gaa	tcc	atg	atc	gcg	gaa	atc	gag	gcc	gca	aag	aaa	gcc	ggc	432
Ala	Glu	Glu	Ser	Met	Ile	Ala	Glu	Ile	Glu	Ala	Ala	Lys	Lys	Ala	Gly	
	130					135					140					
gat	acc	ctc	ggc	ggc	atc	gtg	gaa	gtg	att	gtt	gaa	ggc	ctg	ccc	atc	480
Asp	Thr	Leu	Gly	Gly	Ile	Val	Glu	Val	Ile	Val	Glu	Gly	Leu	Pro	Ile	
	145				150					155					160	
ggc	ttg	ggc	tca	cac	att	tct	ggc	gaa	gat	cgc	ctc	gat	gcg	cag	atc	528
Gly	Leu	Gly	Ser	His	Ile	Ser	Gly	Glu	Asp	Arg	Leu	Asp	Ala	Gln	Ile	
				165					170					175		
gca	gct	gca	ctc	atg	ggc	att	cag	gcc	atc	aag	ggc	gtg	gaa	atc	ggc	576
Ala	Ala	Ala	Leu	Met	Gly	Ile	Gln	Ala	Ile	Lys	Gly	Val	Glu	Ile	Gly	
			180				185						190			
gac	ggc	ttc	gaa	gaa	gct	cgt	cga	cgt	ggc	tcc	gaa	gcc	cac	gat	gaa	624
Asp	Gly	Phe	Glu	Glu	Ala	Arg	Arg	Arg	Gly	Ser	Glu	Ala	His	Asp	Glu	
		195					200					205				
gtg	ttc	ctg	gat	gac	aac	ggc	gta	tac	cgc	aac	acc	aac	cgt	gca	ggc	672
Val	Phe	Leu	Asp	Asp	Asn	Gly	Val	Tyr	Arg	Asn	Thr	Asn	Arg	Ala	Gly	
	210					215					220					
ggc	ctc	gaa	ggc	ggc	atg	acc	aac	ggc	gaa	acc	ctg	cgc	gtt	cgt	gct	720
Gly	Leu	Glu	Gly	Gly	Met	Thr	Asn	Gly	Glu	Thr	Leu	Arg	Val	Arg	Ala	
	225				230					235					240	
ggc	atg	aag	cca	att	tct	act	gtg	cct	cgc	gcc	ctg	aaa	acc	att	gat	768
Gly	Met	Lys	Pro	Ile	Ser	Thr	Val	Pro	Arg	Ala	Leu	Lys	Thr	Ile	Asp	
				245					250					255		
atg	gaa	aac	ggc	aag	gca	gca	acc	gga	atc	cac	cag	cgt	tcc	gac	gtg	816
Met	Glu	Asn	Gly	Lys	Ala	Ala	Thr	Gly	Ile	His	Gln	Arg	Ser	Asp	Val	
			260					265					270			
tgc	gct	gtt	cca	gcc	gcc	ggc	gtc	gtt	gca	gaa	gca	atg	gtc	acc	ctg	864
Cys	Ala	Val	Pro	Ala	Ala	Gly	Val	Val	Ala	Glu	Ala	Met	Val	Thr	Leu	
		275					280					285				

gtt ctc gcc cgc gca gtc ctg cag aaa ttc ggc ggt gac tcc ctg agc 912  
 Val Leu Ala Arg Ala Val Leu Gln Lys Phe Gly Gly Asp Ser Leu Ser  
 290 295 300

gaa acc aag agc aac att gac acc tac ctc aaa aac att gag gaa cga 960  
 Glu Thr Lys Ser Asn Ile Asp Thr Tyr Leu Lys Asn Ile Glu Glu Arg  
 305 310 315 320

atg aaa ttc gaa ggt tta gag gat gga gcg taatgaagtg aatgatcaaa  
 1010  
 Met Lys Phe Glu Gly Leu Glu Asp Gly Ala  
 325 330

ttc  
 1013

<210> 428  
 <211> 330  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 428  
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Gly Ala Lys Leu Thr Arg Pro Arg Pro Gly His Ala Asp Tyr Ala Gly  
 35 40 45

Met Leu Lys Tyr Gly Phe Asp Asp Ala Arg Asn Val Leu Glu Arg Ser  
 50 55 60

Ser Ala Arg Glu Thr Ala Ala Arg Val Ala Ala Ala Thr Val Ala Arg  
 65 70 75 80

Ser Phe Leu Arg Glu Thr Leu Gly Val Glu Val Leu Ser His Val Ile  
 85 90 95

Ser Ile Gly Ala Ser Glu Pro Tyr Thr Gly Ala Glu Pro Thr Phe Ala  
 100 105 110

Asp Ile Gln Ala Ile Asp Asp Ser Pro Val Arg Ala Phe Gly Lys Asp  
 115 120 125

Ala Glu Glu Ser Met Ile Ala Glu Ile Glu Ala Ala Lys Lys Ala Gly  
 130 135 140

Asp Thr Leu Gly Gly Ile Val Glu Val Ile Val Glu Gly Leu Pro Ile  
 145 150 155 160

Gly Leu Gly Ser His Ile Ser Gly Glu Asp Arg Leu Asp Ala Gln Ile  
 165 170 175

Ala Ala Ala Leu Met Gly Ile Gln Ala Ile Lys Gly Val Glu Ile Gly  
 180 185 190

Asp Gly Phe Glu Glu Ala Arg Arg Arg Gly Ser Glu Ala His Asp Glu



195	200	205
Val Phe Leu Asp Asp Asn Gly Val Tyr Arg Asn Thr Asn Arg Ala Gly 210 215 220		
Gly Leu Glu Gly Gly Met Thr Asn Gly Glu Thr Leu Arg Val Arg Ala 225 230 240		
Gly Met Lys Pro Ile Ser Thr Val Pro Arg Ala Leu Lys Thr Ile Asp 245 250 255		
Met Glu Asn Gly Lys Ala Ala Thr Gly Ile His Gln Arg Ser Asp Val 260 265 270		
Cys Ala Val Pro Ala Ala Gly Val Val Ala Glu Ala Met Val Thr Leu 275 280 285		
Val Leu Ala Arg Ala Val Leu Gln Lys Phe Gly Gly Asp Ser Leu Ser 290 295 300		
Glu Thr Lys Ser Asn Ile Asp Thr Tyr Leu Lys Asn Ile Glu Glu Arg 305 310 315 320		
Met Lys Phe Glu Gly Leu Glu Asp Gly Ala 325 330		

&lt;210&gt; 429

&lt;211&gt; 906

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(883)

&lt;223&gt; RXA01095

&lt;400&gt; 429

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ataaccttaa acacagcatt ggttggaagg aggttggggc atg gtt gca aca gag 115  
Met Val Ala Thr Glu  
1 5

aac cgc atg ttg atg gaa atc gct gcg gaa ata tcg gct cgg gaa gca 163  
Asn Arg Met Leu Met Glu Ile Ala Ala Glu Ile Ser Ala Arg Glu Ala  
10 15 20

acg ctt ggt ttt caa gaa gtc aaa act aaa tct cga tca gca ggt ctc 211  
Thr Leu Gly Phe Gln Glu Val Lys Thr Lys Ser Arg Ser Ala Gly Leu  
25 30 35

acg gcg gct ttc gat att gct tca gtc ttt ttt tcg tct gga tgt aat 259  
Thr Ala Ala Phe Asp Ile Ala Ser Val Phe Phe Ser Ser Gly Cys Asn  
40 45 50

gtc gta gtc gcc ttt gat cgt ttt gca tcc aat tgg tct gat cat tcg 307  
Val Val Val Ala Phe Asp Arg Phe Ala Ser Asn Trp Ser Asp His Ser  
55 60 65

gat cat gtg gac tac gct gca cag gtt gcg ggt ttt ggc gca tca atg 355

Asp	His	Val	Asp	Tyr	Ala	Ala	Gln	Val	Ala	Gly	Phe	Gly	Ala	Ser	Met	
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ctt	gca	tat	acg	gtg	cgc	agg	gga	cag	ttt	gat	acc	gca	gta	cgc	gat	403
Leu	Ala	Tyr	Thr	Val	Arg	Arg	Gly	Gln	Phe	Asp	Thr	Ala	Val	Arg	Asp	
				90					95					100		
atc	agg	gac	atc	aaa	tct	gaa	gta	gac	att	ccc	att	ctg	ctt	cat	gat	451
Ile	Arg	Asp	Ile	Lys	Ser	Glu	Val	Asp	Ile	Pro	Ile	Leu	Leu	His	Asp	
			105					110					115			
ccc	atc	atc	gat	ccg	tat	caa	atc	cac	gaa	gcc	cgc	gtc	atg	ggc	atc	499
Pro	Ile	Ile	Asp	Pro	Tyr	Gln	Ile	His	Glu	Ala	Arg	Val	Met	Gly	Ile	
		120					125					130				
gac	gct	ctt	caa	ttc	ccc	gta	tgg	gcg	atg	gaa	caa	gct	cga	ctg	gaa	547
Asp	Ala	Leu	Gln	Phe	Pro	Val	Trp	Ala	Met	Glu	Gln	Ala	Arg	Leu	Glu	
	135					140					145					
tct	ttg	gtg	gac	cgc	acc	gaa	tca	ttg	ggc	atg	aca	gcc	atc	gtg	tct	595
Ser	Leu	Val	Asp	Arg	Thr	Glu	Ser	Leu	Gly	Met	Thr	Ala	Ile	Val	Ser	
150				155					160					165		
gtg	cga	aac	cac	gaa	gaa	gcg	cat	cgt	gca	gtg	gac	gca	gga	gcg	aca	643
Val	Arg	Asn	His	Glu	Glu	Ala	His	Arg	Ala	Val	Asp	Ala	Gly	Ala	Thr	
			170					175					180			
gtg	gta	gca	att	gat	att	act	ggc	tat	acc	ggc	tca	ctc	act	ttg	cct	691
Val	Val	Ala	Ile	Asp	Ile	Thr	Gly	Tyr	Thr	Gly	Ser	Leu	Thr	Leu	Pro	
			185				190						195			
gaa	gcg	ttt	tcg	ggc	atc	acc	caa	ttc	atg	ccc	aaa	gag	gta	gcc	cgc	739
Glu	Ala	Phe	Ser	Gly	Ile	Thr	Gln	Phe	Met	Pro	Lys	Glu	Val	Ala	Arg	
	200						205					210				
att	gtg	ctc	gga	ggc	tgc	agc	agc	cct	aaa	gaa	ctc	atg	cgg	ttt	gca	787
Ile	Val	Leu	Gly	Gly	Cys	Ser	Ser	Pro	Lys	Glu	Leu	Met	Arg	Phe	Ala	
	215					220				225						
cga	cat	tct	gca	gac	gcc	atc	ttt	ggt	cca	cat	gca	gac	ctc	gcc	acc	835
Arg	His	Ser	Ala	Asp	Ala	Ile	Phe	Val	Pro	His	Ala	Asp	Leu	Ala	Thr	
230				235					240					245		
aca	aaa	tct	ctt	gtg	aca	gca	ggc	atg	cat	cca	gcg	tgc	cca	tcg	cgt	883
Thr	Lys	Ser	Leu	Val	Thr	Ala	Gly	Met	His	Pro	Ala	Cys	Pro	Ser	Arg	
			250				255						260			
tgaagaggtg	ctctgtggtc	agc														906

&lt;210&gt; 430

&lt;211&gt; 261

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 430

Met	Val	Ala	Thr	Glu	Asn	Arg	Met	Leu	Met	Glu	Ile	Ala	Ala	Glu	Ile
1				5				10						15	

Ser	Ala	Arg	Glu	Ala	Thr	Leu	Gly	Phe	Gln	Glu	Val	Lys	Thr	Lys	Ser
			20				25						30		

Arg Ser Ala Gly Leu Thr Ala Ala Phe Asp Ile Ala Ser Val Phe Phe  
                   35                                  40                                  45  
 Ser Ser Gly Cys Asn Val Val Val Ala Phe Asp Arg Phe Ala Ser Asn  
           50  55                                  60  
 Trp Ser Asp His Ser Asp His Val Asp Tyr Ala Ala Gln Val Ala Gly  
   65  70                                  75                                  80  
 Phe Gly Ala Ser Met Leu Ala Tyr Thr Val Arg Arg Gly Gln Phe Asp  
                                   85                                  90                                  95  
 Thr Ala Val Arg Asp Ile Arg Asp Ile Lys Ser Glu Val Asp Ile Pro  
                   100                                  105                                  110  
 Ile Leu Leu His Asp Pro Ile Ile Asp Pro Tyr Gln Ile His Glu Ala  
           115                                  120                                  125  
 Arg Val Met Gly Ile Asp Ala Leu Gln Phe Pro Val Trp Ala Met Glu  
           130                                  135                                  140  
 Gln Ala Arg Leu Glu Ser Leu Val Asp Arg Thr Glu Ser Leu Gly Met  
   145                                  150                                  155                                  160  
 Thr Ala Ile Val Ser Val Arg Asn His Glu Glu Ala His Arg Ala Val  
                   165                                  170                                  175  
 Asp Ala Gly Ala Thr Val Val Ala Ile Asp Ile Thr Gly Tyr Thr Gly  
                   180                                  185                                  190  
 Ser Leu Thr Leu Pro Glu Ala Phe Ser Gly Ile Thr Gln Phe Met Pro  
           195                                  200                                  205  
 Lys Glu Val Ala Arg Ile Val Leu Gly Gly Cys Ser Ser Pro Lys Glu  
           210                                  215                                  220  
 Leu Met Arg Phe Ala Arg His Ser Ala Asp Ala Ile Phe Val Pro His  
   225                                  230                                  235                                  240  
 Ala Asp Leu Ala Thr Thr Lys Ser Leu Val Thr Ala Gly Met His Pro  
                   245                                  250                                  255  
 Ala Cys Pro Ser Arg  
                   260

&lt;210&gt; 431

&lt;211&gt; 1545

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1522)

&lt;223&gt; RXA00955

&lt;400&gt; 431

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aagcacgaag agatcgatta ctcagaaaag gagtcttcca atg act agt aat aat 115

																Met 1	Thr	Ser	Asn	Asn 5	
ctg	ccc	aca	gtg	ttg	gaa	agc	atc	gtc	gag	ggg	cgt	cgc	gga	cac	ctg	163					
Leu	Pro	Thr	Val	Leu	Glu	Ser	Ile	Val	Glu	Gly	Arg	Arg	Gly	His	Leu						
				10					15					20							
gag	gaa	att	cgc	gct	cgc	atc	gct	cac	gtg	gat	gtg	gat	gcg	ctt	cca	211					
Glu	Glu	Ile	Arg	Ala	Arg	Ile	Ala	His	Val	Asp	Val	Asp	Ala	Leu	Pro						
				25					30					35							
aaa	tcc	acc	cgt	tct	ctg	ttt	gat	tcc	ctc	aac	cag	ggg	agg	gga	ggg	259					
Lys	Ser	Thr	Arg	Ser	Leu	Phe	Asp	Ser	Leu	Asn	Gln	Gly	Arg	Gly	Gly						
				40					45					50							
gcg	cgt	ttc	atc	atg	gag	tgc	aag	tcc	gca	tcg	cct	tct	ttg	gga	atg	307					
Ala	Arg	Phe	Ile	Met	Glu	Cys	Lys	Ser	Ala	Ser	Pro	Ser	Leu	Gly	Met						
				55					60					65							
att	cgt	gag	cac	tac	cag	ccg	ggg	gaa	atc	gct	cgc	gtg	tac	tct	cgc	355					
Ile	Arg	Glu	His	Tyr	Gln	Pro	Gly	Glu	Ile	Ala	Arg	Val	Tyr	Ser	Arg						
				70					75					80							
tac	gcc	agc	ggc	att	tcc	gtg	ctg	tgc	gag	ccg	gat	cgt	ttt	ggg	ggc	403					
Tyr	Ala	Ser	Gly	Ile	Ser	Val	Leu	Cys	Glu	Pro	Asp	Arg	Phe	Gly	Gly						
				90					95					100							
gat	tac	gat	cac	ctc	gct	acc	gtt	gcc	gct	acc	tct	cat	ctt	ccg	gtg	451					
Asp	Tyr	Asp	His	Leu	Ala	Thr	Val	Ala	Ala	Thr	Ser	His	Leu	Pro	Val						
				105					110					115							
ctg	tgc	aaa	gac	ttc	atc	att	gat	cct	gtc	cag	gta	cac	gcg	gcg	cgt	499					
Leu	Cys	Lys	Asp	Phe	Ile	Ile	Asp	Pro	Val	Gln	Val	His	Ala	Ala	Arg						
				120					125					130							
tac	ttt	ggg	gct	gat	gcc	atc	ctg	ctc	atg	ctc	tct	gtg	ctt	gat	gat	547					
Tyr	Phe	Gly	Ala	Asp	Ala	Ile	Leu	Leu	Met	Leu	Ser	Val	Leu	Asp	Asp						
				135					140					145							
gaa	gag	tac	gca	gca	ctc	gct	gcc	gag	gct	gcg	cgt	ttt	gat	ctg	gat	595					
Glu	Glu	Tyr	Ala	Ala	Leu	Ala	Ala	Glu	Ala	Ala	Arg	Phe	Asp	Leu	Asp						
				150					155					160							
atc	ctc	acc	gag	gtt	att	gat	gag	gag	gaa	gtc	gcc	cgc	gcc	atc	aag	643					
Ile	Leu	Thr	Glu	Val	Ile	Asp	Glu	Glu	Glu	Val	Ala	Arg	Ala	Ile	Lys						
				170					175					180							
ctg	ggg	gcg	aag	atc	ttt	ggc	gtc	aac	cac	cgc	aac	ctg	cat	gat	ctg	691					
Leu	Gly	Ala	Lys	Ile	Phe	Gly	Val	Asn	His	Arg	Asn	Leu	His	Asp	Leu						
				185					190					195							
tcc	att	gat	ttg	gat	cgt	tca	cgt	cgc	ctg	tcc	aag	ctc	att	cca	gca	739					
Ser	Ile	Asp	Leu	Asp	Arg	Ser	Arg	Arg	Leu	Ser	Lys	Leu	Ile	Pro	Ala						
				200					205					210							
gat	gcc	gtg	ctc	gtg	tct	gag	tct	ggc	gtg	cgc	gat	acc	gaa	acc	gtc	787					
Asp	Ala	Val	Leu	Val	Ser	Glu	Ser	Gly	Val	Arg	Asp	Thr	Glu	Thr	Val						
				215					220					225							
cgc	cag	cta	ggg	ggg	cac	tcc	aat	gca	ttc	ctc	gtt	ggc	tcc	cag	ctg	835					
Arg	Gln	Leu	Gly	Gly	His	Ser	Asn	Ala	Phe	Leu	Val	Gly	Ser	Gln	Leu						

230	235	240	245	
acc agc cag gaa aac gtc gat ctg gca gcc cgc gaa tta gtc tac ggc	883			
Thr Ser Gln Glu Asn Val Asp Leu Ala Ala Arg Glu Leu Val Tyr Gly				
250 255 260				
ccc aac aaa gtc tgc gga ctc acc tca cca agt gca gca caa acc gct	931			
Pro Asn Lys Val Cys Gly Leu Thr Ser Pro Ser Ala Ala Gln Thr Ala				
265 270 275				
cgc gca gcg ggt gcg gtc tac ggc ggg ctc atc ttc gaa gag gca tcg	979			
Arg Ala Ala Gly Ala Val Tyr Gly Gly Leu Ile Phe Glu Glu Ala Ser				
280 285 290				
cca cgc aat gtt tca cgt gaa aca ttg caa aaa atc atc gcc gca gag				
1027 Pro Arg Asn Val Ser Arg Glu Thr Leu Gln Lys Ile Ile Ala Ala Glu				
295 300 305				
ccc aac ctg cgc tac gtc gcg gtc agc cgt cgc acc tcc ggg tac aag				
1075 Pro Asn Leu Arg Tyr Val Ala Val Ser Arg Arg Thr Ser Gly Tyr Lys				
310 315 320 325				
gat ttg ctt gtc gac ggc atc ttc gcc gta caa atc cac gcc cca ctg				
1123 Asp Leu Leu Val Asp Gly Ile Phe Ala Val Gln Ile His Ala Pro Leu				
330 335 340				
cag gac agc gtc gaa gca gaa aag gca ttg atc gcc gcc gtt cgt gaa				
1171 Gln Asp Ser Val Glu Ala Glu Lys Ala Leu Ile Ala Ala Val Arg Glu				
345 350 355				
gag gtt gga ccg cag gtc cag gtc tgg cgc gcg atc tcg atg tcc agc				
1219 Glu Val Gly Pro Gln Val Gln Val Trp Arg Ala Ile Ser Met Ser Ser				
360 365 370				
ccc ttg ggg gct gaa gtg gca gct gcg gtg gag ggt gac gtc gat aag				
1267 Pro Leu Gly Ala Glu Val Ala Ala Ala Val Glu Gly Asp Val Asp Lys				
375 380 385				
cta att ctt gat gcc cat gaa ggt ggc agc ggg gaa gta ttc gac tgg				
1315 Leu Ile Leu Asp Ala His Glu Gly Gly Ser Gly Glu Val Phe Asp Trp				
390 395 400 405				
gct acg gtg ccg gcc gct gtg aag gca aag tct ttg ctc gcg gga ggc				
1363 Ala Thr Val Pro Ala Ala Val Lys Ala Lys Ser Leu Leu Ala Gly Gly				
410 415 420				
atc tct ccg gac aac gct gcg cag gca ctc gct gtg ggc tgc gca ggt				
1411 Ile Ser Pro Asp Asn Ala Ala Gln Ala Leu Ala Val Gly Cys Ala Gly				
425 430 435				
ttg gac atc aac tct ggc gtg gaa tac ccc gcc ggt gca ggc acg tgg				
1459				

Leu Asp Ile Asn Ser Gly Val Glu Tyr Pro Ala Gly Ala Gly Thr Trp  
 440 445 450

gct ggg gcg aaa gac gcc ggc gcg ctg ctg aaa att tta gcg acc atc  
 1507

Ala Gly Ala Lys Asp Ala Gly Ala Leu Leu Lys Ile Leu Ala Thr Ile  
 455 460 465

tcc aca ttc cat tac taaaggttta aataggatca tga  
 1545  
 Ser Thr Phe His Tyr  
 470

<210> 432

<211> 474

<212> PRT

<213> Corynebacterium glutamicum

<400> 432

Met Thr Ser Asn Asn Leu Pro Thr Val Leu Glu Ser Ile Val Glu Gly  
 1 5 10 15

Arg Arg Gly His Leu Glu Glu Ile Arg Ala Arg Ile Ala His Val Asp  
 20 25 30

Val Asp Ala Leu Pro Lys Ser Thr Arg Ser Leu Phe Asp Ser Leu Asn  
 35 40 45

Gln Gly Arg Gly Gly Ala Arg Phe Ile Met Glu Cys Lys Ser Ala Ser  
 50 55 60

Pro Ser Leu Gly Met Ile Arg Glu His Tyr Gln Pro Gly Glu Ile Ala  
 65 70 75 80

Arg Val Tyr Ser Arg Tyr Ala Ser Gly Ile Ser Val Leu Cys Glu Pro  
 85 90 95

Asp Arg Phe Gly Gly Asp Tyr Asp His Leu Ala Thr Val Ala Ala Thr  
 100 105 110

Ser His Leu Pro Val Leu Cys Lys Asp Phe Ile Ile Asp Pro Val Gln  
 115 120 125

Val His Ala Ala Arg Tyr Phe Gly Ala Asp Ala Ile Leu Leu Met Leu  
 130 135 140

Ser Val Leu Asp Asp Glu Glu Tyr Ala Ala Leu Ala Ala Glu Ala Ala  
 145 150 155 160

Arg Phe Asp Leu Asp Ile Leu Thr Glu Val Ile Asp Glu Glu Glu Val  
 165 170 175

Ala Arg Ala Ile Lys Leu Gly Ala Lys Ile Phe Gly Val Asn His Arg  
 180 185 190

Asn Leu His Asp Leu Ser Ile Asp Leu Asp Arg Ser Arg Arg Leu Ser  
 195 200 205

Lys Leu Ile Pro Ala Asp Ala Val Leu Val Ser Glu Ser Gly Val Arg  
 210 215 220

```

Asp Thr Glu Thr Val Arg Gln Leu Gly Gly His Ser Asn Ala Phe Leu
225                               230                               235                               240

Val Gly Ser Gln Leu Thr Ser Gln Glu Asn Val Asp Leu Ala Ala Arg
                               245                               250                               255

Glu Leu Val Tyr Gly Pro Asn Lys Val Cys Gly Leu Thr Ser Pro Ser
                               260                               265                               270

Ala Ala Gln Thr Ala Arg Ala Ala Gly Ala Val Tyr Gly Gly Leu Ile
                               275                               280                               285

Phe Glu Glu Ala Ser Pro Arg Asn Val Ser Arg Glu Thr Leu Gln Lys
                               290                               295                               300

Ile Ile Ala Ala Glu Pro Asn Leu Arg Tyr Val Ala Val Ser Arg Arg
305                               310                               315                               320

Thr Ser Gly Tyr Lys Asp Leu Leu Val Asp Gly Ile Phe Ala Val Gln
                               325                               330                               335

Ile His Ala Pro Leu Gln Asp Ser Val Glu Ala Glu Lys Ala Leu Ile
                               340                               345                               350

Ala Ala Val Arg Glu Glu Val Gly Pro Gln Val Gln Val Trp Arg Ala
                               355                               360                               365

Ile Ser Met Ser Ser Pro Leu Gly Ala Glu Val Ala Ala Ala Val Glu
                               370                               375                               380

Gly Asp Val Asp Lys Leu Ile Leu Asp Ala His Glu Gly Gly Ser Gly
385                               390                               395                               400

Glu Val Phe Asp Trp Ala Thr Val Pro Ala Ala Val Lys Ala Lys Ser
                               405                               410                               415

Leu Leu Ala Gly Gly Ile Ser Pro Asp Asn Ala Ala Gln Ala Leu Ala
                               420                               425                               430

Val Gly Cys Ala Gly Leu Asp Ile Asn Ser Gly Val Glu Tyr Pro Ala
                               435                               440                               445

Gly Ala Gly Thr Trp Ala Gly Ala Lys Asp Ala Gly Ala Leu Leu Lys
                               450                               455                               460

Ile Leu Ala Thr Ile Ser Thr Phe His Tyr
465                               470

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&lt;210&gt; 433

&lt;211&gt; 494

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(471)

&lt;223&gt; RXA02814

&lt;400&gt; 433

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gcc aaa aac cta gaa gaa cac tcc tac gtg gtc aac cac ctg cgc acc 48
Ala Lys Asn Leu Glu Glu His Ser Tyr Val Val Asn His Leu Arg Thr
  1          5          10          15

atc ctg gaa cca ctg tgc tca caa ttc gac gcc cca aca gtt cct gaa 96
Ile Leu Glu Pro Leu Cys Ser Gln Phe Asp Ala Pro Thr Val Pro Glu
          20          25          30

ctg acc aaa acc aac gaa atg tgg cac ctc gca aca ccc atc gtt ggc 144
Leu Thr Lys Thr Asn Glu Met Trp His Leu Ala Thr Pro Ile Val Gly
          35          40          45

acc ctc aag tac cca cac atc acc gca cta gaa cta gcc ata cga aca 192
Thr Leu Lys Tyr Pro His Ile Thr Ala Leu Glu Leu Ala Ile Arg Thr
          50          55          60

cac ccc acc ccc gcg atc tgt ggc acc ccc acc gac gcc gcc gaa gcc 240
His Pro Thr Pro Ala Ile Cys Gly Thr Pro Thr Asp Ala Ala Glu Ala
  65          70          75          80

ctc atc atc gaa gcg gaa tcc ccc cga aac ttc tac gcc gga gca gcc 288
Leu Ile Ile Glu Ala Glu Ser Pro Arg Asn Phe Tyr Ala Gly Ala Ala
          85          90          95

ggc tgg tgt gac tcc acc gga gac ggc gaa tac atg gta gcc atc cgc 336
Gly Trp Cys Asp Ser Thr Gly Asp Gly Glu Tyr Met Val Ala Ile Arg
          100          105          110

tgc gcc gaa gta tcc gaa gac gga acc tgg gcc aga gca tgg gca ggc 384
Cys Ala Glu Val Ser Glu Asp Gly Thr Trp Ala Arg Ala Trp Ala Gly
          115          120          125

gga ggc atc gtc gcc gaa tca gac gcc caa gaa gag ttt gat gaa acc 432
Gly Gly Ile Val Ala Glu Ser Asp Ala Gln Glu Glu Phe Asp Glu Thr
          130          135          140

acc gcg aag ctc caa acc atc atg cgc tcg ctt ggt ttg tgagatgtgg 481
Thr Ala Lys Leu Gln Thr Ile Met Arg Ser Leu Gly Leu
145          150          155

tcttaaaaca ccg 494

```

&lt;210&gt; 434

&lt;211&gt; 157

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 434

```

Ala Lys Asn Leu Glu Glu His Ser Tyr Val Val Asn His Leu Arg Thr
  1          5          10          15

Ile Leu Glu Pro Leu Cys Ser Gln Phe Asp Ala Pro Thr Val Pro Glu
          20          25          30

Leu Thr Lys Thr Asn Glu Met Trp His Leu Ala Thr Pro Ile Val Gly
          35          40          45

Thr Leu Lys Tyr Pro His Ile Thr Ala Leu Glu Leu Ala Ile Arg Thr
          50          55          60

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His Pro Thr Pro Ala Ile Cys Gly Thr Pro Thr Asp Ala Ala Glu Ala  
 65 70 75 80  
 Leu Ile Ile Glu Ala Glu Ser Pro Arg Asn Phe Tyr Ala Gly Ala Ala  
 85 90 95  
 Gly Trp Cys Asp Ser Thr Gly Asp Gly Glu Tyr Met Val Ala Ile Arg  
 100 105 110  
 Cys Ala Glu Val Ser Glu Asp Gly Thr Trp Ala Arg Ala Trp Ala Gly  
 115 120 125  
 Gly Gly Ile Val Ala Glu Ser Asp Ala Gln Glu Glu Phe Asp Glu Thr  
 130 135 140  
 Thr Ala Lys Leu Gln Thr Ile Met Arg Ser Leu Gly Leu  
 145 150 155

<210> 435  
 <211> 803  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(780)  
 <223> RXA00229

<400> 435  
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 Glu Ala Lys Gly Leu Ala Gln Gly Arg Ala Thr Val Tyr Arg Arg Ile  
 1 5 10 15  
 gac acg ctt ggg tcg cgt gct tcc ggg caa gat tta aat acg ctt ctc 96  
 Asp Thr Leu Gly Ser Arg Ala Ser Gly Gln Asp Leu Asn Thr Leu Leu  
 20 25 30  
 gac gcc gcc ctc tac ctt ggc ttc agc ggc ctg aac atc act cac ccg 144  
 Asp Ala Ala Leu Tyr Leu Gly Phe Ser Gly Leu Asn Ile Thr His Pro  
 35 40 45  
 tac aag caa gca gta tta ccc ctg ctt ggc gaa gtc tcc gaa caa gcc 192  
 Tyr Lys Gln Ala Val Leu Pro Leu Leu Gly Glu Val Ser Glu Gln Ala  
 50 55 60  
 acc caa ctc ggc gca gtg aat act gtc gtt atg gac gcc acc ggc cac 240  
 Thr Gln Leu Gly Ala Val Asn Thr Val Val Met Asp Ala Thr Gly His  
 65 70 75 80  
 acc acc ggc cac aac acc gac gtc tcc gga ttt ggc cgc gga atg gaa 288  
 Thr Thr Gly His Asn Thr Asp Val Ser Gly Phe Gly Arg Gly Met Glu  
 85 90 95  
 gaa ggc ctc ccc aac gcc aag ctc gat tcc gtc gtg cag gtc ggc gcc 336  
 Glu Gly Leu Pro Asn Ala Lys Leu Asp Ser Val Val Gln Val Gly Ala  
 100 105 110  
 ggc ggc gta gaa aac gca gtg gca tac gcc ctg gtc acc cac ggt gtg 384  
 Gly Gly Val Glu Asn Ala Val Ala Tyr Ala Leu Val Thr His Gly Val  
 115 120 125

cag aaa ctt cag gtc gct gac ctc gac act tcc cgc gcg cag gca ctg 432  
 Gln Lys Leu Gln Val Ala Asp Leu Asp Thr Ser Arg Ala Gln Ala Leu  
 130 135 140  
 gca gat gtc atc aac aac gca gtc ggc cgt gaa gcc gtc gtg gga gta 480  
 Ala Asp Val Ile Asn Asn Ala Val Gly Arg Glu Ala Val Val Gly Val  
 145 150 155 160  
 gac gcc cgc ggc atc gaa gac gtc atc gcc gcc gcc gac gga gta gtc 528  
 Asp Ala Arg Gly Ile Glu Asp Val Ile Ala Ala Ala Asp Gly Val Val  
 165 170 175  
 aac gca acc ccc atg gga atg cca gca cac ccc ggc acc gcc ttt gat 576  
 Asn Ala Thr Pro Met Gly Met Pro Ala His Pro Gly Thr Ala Phe Asp  
 180 185 190  
 gtc agc tgc ctc acc aag gat cac tgg gtt ggc gac gtc gtg tac atg 624  
 Val Ser Cys Leu Thr Lys Asp His Trp Val Gly Asp Val Val Tyr Met  
 195 200 205  
 ccc atc gaa act gaa ctt ctc aaa gcc gcc cgt gcc ctc ggc tgc gaa 672  
 Pro Ile Glu Thr Glu Leu Leu Lys Ala Ala Arg Ala Leu Gly Cys Glu  
 210 215 220  
 acc ctc gac gga acc cgc atg gca atc cac caa gcc gtc gat gcc ttc 720  
 Thr Leu Asp Gly Thr Arg Met Ala Ile His Gln Ala Val Asp Ala Phe  
 225 230 235 240  
 cga ctg ttc acc ggc ctc gaa ccc gac gtc tcc cgc atg cgg gaa act 768  
 Arg Leu Phe Thr Gly Leu Glu Pro Asp Val Ser Arg Met Arg Glu Thr  
 245 250 255  
 ttc ctg tcc ctc taaaagagtc agtaaaacct cga 803  
 Phe Leu Ser Leu  
 260

<210> 436  
 <211> 260  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

<400> 436  
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 Asp Thr Leu Gly Ser Arg Ala Ser Gly Gln Asp Leu Asn Thr Leu Leu  
 20 25 30  
 Asp Ala Ala Leu Tyr Leu Gly Phe Ser Gly Leu Asn Ile Thr His Pro  
 35 40 45  
 Tyr Lys Gln Ala Val Leu Pro Leu Leu Gly Glu Val Ser Glu Gln Ala  
 50 55 60  
 Thr Gln Leu Gly Ala Val Asn Thr Val Val Met Asp Ala Thr Gly His  
 65 70 75 80  
 Thr Thr Gly His Asn Thr Asp Val Ser Gly Phe Gly Arg Gly Met Glu  
 85 90 95

Glu Gly Leu Pro Asn Ala Lys Leu Asp Ser Val Val Gln Val Gly Ala  
 100 105 110  
 Gly Gly Val Glu Asn Ala Val Ala Tyr Ala Leu Val Thr His Gly Val  
 115 120 125  
 Gln Lys Leu Gln Val Ala Asp Leu Asp Thr Ser Arg Ala Gln Ala Leu  
 130 135 140  
 Ala Asp Val Ile Asn Asn Ala Val Gly Arg Glu Ala Val Val Gly Val  
 145 150 155 160  
 Asp Ala Arg Gly Ile Glu Asp Val Ile Ala Ala Ala Asp Gly Val Val  
 165 170 175  
 Asn Ala Thr Pro Met Gly Met Pro Ala His Pro Gly Thr Ala Phe Asp  
 180 185 190  
 Val Ser Cys Leu Thr Lys Asp His Trp Val Gly Asp Val Val Tyr Met  
 195 200 205  
 Pro Ile Glu Thr Glu Leu Leu Lys Ala Ala Arg Ala Leu Gly Cys Glu  
 210 215 220  
 Thr Leu Asp Gly Thr Arg Met Ala Ile His Gln Ala Val Asp Ala Phe  
 225 230 235 240  
 Arg Leu Phe Thr Gly Leu Glu Pro Asp Val Ser Arg Met Arg Glu Thr  
 245 250 255  
 Phe Leu Ser Leu  
 260

<210> 437  
 <211> 927  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(904)  
 <223> RXA02093

<400> 437  
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 Met Val Asn Tyr Val  
 1 5  
 gac agg gaa aca acc ctg tgc atc tct ctc gct gct cgt cca tcc aac 163  
 Asp Arg Glu Thr Thr Leu Cys Ile Ser Leu Ala Ala Arg Pro Ser Asn  
 10 15 20  
 cat ggt gtt cgt ttc cac aac tgg ctt tac gct gaa ctt gga ttg aac 211  
 His Gly Val Arg Phe His Asn Trp Leu Tyr Ala Glu Leu Gly Leu Asn  
 25 30 35  
 tac ctg tac aag gct gtt gcc cca gca gat atc acc gct gca gtc gca 259

Tyr	Leu	Tyr	Lys	Ala	Val	Ala	Pro	Ala	Asp	Ile	Thr	Ala	Ala	Val	Ala		
		40					45					50					
ggt	atc	cgt	ggt	ctg	aac	att	cgc	ggc	gca	ggt	gtc	tcc	atg	cca	tac	307	
Gly	Ile	Arg	Gly	Leu	Asn	Ile	Arg	Gly	Ala	Gly	Val	Ser	Met	Pro	Tyr		
	55					60					65						
aag	agc	gat	gtc	atc	cca	ctc	atc	gat	gag	ttg	cat	cct	tcc	gca	gag	355	
Lys	Ser	Asp	Val	Ile	Pro	Leu	Ile	Asp	Glu	Leu	His	Pro	Ser	Ala	Glu		
	70				75					80					85		
cgc	ata	cgt	tct	gtt	aac	acc	atc	gtc	aac	aat	gac	gga	cac	ctt	gtc	403	
Arg	Ile	Arg	Ser	Val	Asn	Thr	Ile	Val	Asn	Asn	Asp	Gly	His	Leu	Val		
				90					95					100			
gga	tac	aac	acc	gac	tac	act	gcg	gtg	tac	cac	ctc	ctt	gaa	gaa	cac	451	
Gly	Tyr	Asn	Thr	Asp	Tyr	Thr	Ala	Val	Tyr	His	Leu	Leu	Glu	Glu	His		
			105					110					115				
cgc	gtg	aac	ccc	aat	gca	cga	gta	gct	atc	aag	gga	tcc	ggc	ggc	atg	499	
Arg	Val	Asn	Pro	Asn	Ala	Arg	Val	Ala	Ile	Lys	Gly	Ser	Gly	Gly	Met		
		120					125					130					
gcc	aat	gct	gtt	gtt	gca	gct	ctt	gct	gag	tat	ggt	ctg	agt	ggc	acc	547	
Ala	Asn	Ala	Val	Val	Ala	Ala	Leu	Ala	Glu	Tyr	Gly	Leu	Ser	Gly	Thr		
	135					140					145						
gtc	gtt	gcc	cgc	aac	cac	acc	acc	ggt	tct	gcg	cta	gct	tcc	cgt	tac	595	
Val	Val	Ala	Arg	Asn	His	Thr	Thr	Gly	Ser	Ala	Leu	Ala	Ser	Arg	Tyr		
	150				155					160					165		
ggt	tgg	gaa	tac	tcc	gca	act	gtt	ccg	gaa	gac	gca	aaa	att	ttg	gtt	643	
Gly	Trp	Glu	Tyr	Ser	Ala	Thr	Val	Pro	Glu	Asp	Ala	Lys	Ile	Leu	Val		
				170				175						180			
aat	gta	acc	cca	atg	gga	atg	aat	gga	cct	gac	caa	gac	gtt	gta	tct	691	
Asn	Val	Thr	Pro	Met	Gly	Met	Asn	Gly	Pro	Asp	Gln	Asp	Val	Val	Ser		
			185					190					195				
ttt	ggt	gag	gat	gaa	gta	gac	cga	gcc	gac	gta	atc	ttt	gac	tgc	gta	739	
Phe	Gly	Glu	Asp	Glu	Val	Asp	Arg	Ala	Asp	Val	Ile	Phe	Asp	Cys	Val		
		200					205					210					
gca	ttc	ccc	gtc	gag	acc	cca	ctg	att	aag	ttg	gcc	aag	gaa	aag	ggt	787	
Ala	Phe	Pro	Val	Glu	Thr	Pro	Leu	Ile	Lys	Leu	Ala	Lys	Glu	Lys	Gly		
	215					220					225						
aag	caa	acc	atc	gac	ggc	gga	gaa	gtt	gcc	gct	ctt	cag	gca	gca	gag	835	
Lys	Gln	Thr	Ile	Asp	Gly	Gly	Glu	Val	Ala	Ala	Leu	Gln	Ala	Ala	Glu		
	230				235				240						245		
cag	ttc	cac	ctc	tac	acc	gga	gtt	ctt	cca	acc	aac	gac	cag	atc	att	883	
Gln	Phe	His	Leu	Tyr	Thr	Gly	Val	Leu	Pro	Thr	Asn	Asp	Gln	Ile	Ile		
				250				255						260			
gct	gcg	gag	gag	ttc	tcc	aag	taaattttctc	tcccctatttt	tta							927	
Ala	Ala	Glu	Glu	Phe	Ser	Lys											
				265													

&lt;210&gt; 438

&lt;211&gt; 268

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 438

Met Val Asn Tyr Val Asp Arg Glu Thr Thr Leu Cys Ile Ser Leu Ala  
 1 5 10 15

Ala Arg Pro Ser Asn His Gly Val Arg Phe His Asn Trp Leu Tyr Ala  
 20 25 30

Glu Leu Gly Leu Asn Tyr Leu Tyr Lys Ala Val Ala Pro Ala Asp Ile  
 35 40 45

Thr Ala Ala Val Ala Gly Ile Arg Gly Leu Asn Ile Arg Gly Ala Gly  
 50 55 60

Val Ser Met Pro Tyr Lys Ser Asp Val Ile Pro Leu Ile Asp Glu Leu  
 65 70 75 80

His Pro Ser Ala Glu Arg Ile Arg Ser Val Asn Thr Ile Val Asn Asn  
 85 90 95

Asp Gly His Leu Val Gly Tyr Asn Thr Asp Tyr Thr Ala Val Tyr His  
 100 105 110

Leu Leu Glu Glu His Arg Val Asn Pro Asn Ala Arg Val Ala Ile Lys  
 115 120 125

Gly Ser Gly Gly Met Ala Asn Ala Val Val Ala Ala Leu Ala Glu Tyr  
 130 135 140

Gly Leu Ser Gly Thr Val Val Ala Arg Asn His Thr Thr Gly Ser Ala  
 145 150 155 160

Leu Ala Ser Arg Tyr Gly Trp Glu Tyr Ser Ala Thr Val Pro Glu Asp  
 165 170 175

Ala Lys Ile Leu Val Asn Val Thr Pro Met Gly Met Asn Gly Pro Asp  
 180 185 190

Gln Asp Val Val Ser Phe Gly Glu Asp Glu Val Asp Arg Ala Asp Val  
 195 200 205

Ile Phe Asp Cys Val Ala Phe Pro Val Glu Thr Pro Leu Ile Lys Leu  
 210 215 220

Ala Lys Glu Lys Gly Lys Gln Thr Ile Asp Gly Gly Glu Val Ala Ala  
 225 230 235 240

Leu Gln Ala Ala Glu Gln Phe His Leu Tyr Thr Gly Val Leu Pro Thr  
 245 250 255

Asn Asp Gln Ile Ile Ala Ala Glu Glu Phe Ser Lys  
 260 265

&lt;210&gt; 439

&lt;211&gt; 951

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101) .. (928)

&lt;223&gt; RXA02791

&lt;400&gt; 439

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accgtgttca acgacacctt cgaagagcac gaagccgaca ttgagcaagc tttgaacagt 60

ggcgttctag acagcaaccg ataaggatca gcgaataaaa ttg ggt tct cac atc 115
                                   Leu Gly Ser His Ile
                                   1                               5

act cac cgg gcg gcc gta ctc ggc tca ccc atc gag cat tcc aaa tcc 163
Thr His Arg Ala Ala Val Leu Gly Ser Pro Ile Glu His Ser Lys Ser
                                   10                               15                               20

cca gtc ctc cac aac acc ggc tat aaa gcc ctc gga ctg gac caa tgg 211
Pro Val Leu His Asn Thr Gly Tyr Lys Ala Leu Gly Leu Asp Gln Trp
                                   25                               30                               35

gaa tac gac cgc ttt gag tgc acc ggc gac atg ctc ccc ggc atc gtc 259
Glu Tyr Asp Arg Phe Glu Cys Thr Gly Asp Met Leu Pro Gly Ile Val
                                   40                               45                               50

tcc ggc gct gat gaa acc tac tgc gga ttc tcc gtc acc atg ccg tct 307
Ser Gly Ala Asp Glu Thr Tyr Cys Gly Phe Ser Val Thr Met Pro Ser
                                   55                               60                               65

aaa ttc gca gct ctt gaa ttc gcc gac gaa gta acc gaa cgc gcc tgc 355
Lys Phe Ala Ala Leu Glu Phe Ala Asp Glu Val Thr Glu Arg Ala Cys
                                   70                               75                               80                               85

gcc atc ggc tcc gca aac acc ttg ctg cgc acg gcc acc gga tgg cgc 403
Ala Ile Gly Ser Ala Asn Thr Leu Leu Arg Thr Ala Thr Gly Trp Arg
                                   90                               95                               100

gcc gac aac acc gac gtc gac ggc atc agg gga gct ctc ggt gaa ctc 451
Ala Asp Asn Thr Asp Val Asp Gly Ile Arg Gly Ala Leu Gly Glu Leu
                                   105                               110                               115

ctc ggc ggc gca tca ctg gcc ggc aaa cac gcc atc gtc atc ggc tcc 499
Leu Gly Gly Ala Ser Leu Ala Gly Lys His Ala Ile Val Ile Gly Ser
                                   120                               125                               130

ggc ggc acc gca cgc ccc gcc atc tgg gca ctc atc gaa gcc ggg gtc 547
Gly Gly Thr Ala Arg Pro Ala Ile Trp Ala Leu Ile Glu Ala Gly Val
                                   135                               140                               145

gcc cgg atc acg gtg ctc aac cgc tcc gat cgc acc gcc gaa ctg caa 595
Ala Arg Ile Thr Val Leu Asn Arg Ser Asp Arg Thr Ala Glu Leu Gln
                                   150                               155                               160                               165

acg ctt ttc gac gaa acc ccc acc acc ttg gcc tac gcc ccg ctc gag 643
Thr Leu Phe Asp Glu Thr Pro Thr Thr Leu Ala Tyr Ala Pro Leu Glu
                                   170                               175                               180

cat ctc cac atc gaa gcc gac gtc gta gtc tct aca gtg ccc tcc gca 691
His Leu His Ile Glu Ala Asp Val Val Val Ser Thr Val Pro Ser Ala
                                   185                               190                               195

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gca atc gca ggc ctc gaa gac acc ctt gcg atc gcc cca gtc ctc gac 739  
 Ala Ile Ala Gly Leu Glu Asp Thr Leu Ala Ile Ala Pro Val Leu Asp  
 200 205 210

gtc atc tac gac ccc tgg cca aca cca ctc gta gaa gtc aca cga gcc 787  
 Val Ile Tyr Asp Pro Trp Pro Thr Pro Leu Val Glu Val Thr Arg Ala  
 215 220 225

aaa ggc ctc aaa gct gtc gga ggc cac gtc atg ctg gca cac cag tcc 835  
 Lys Gly Leu Lys Ala Val Gly Gly His Val Met Leu Ala His Gln Ser  
 230 235 240 245

tac gga cag ttt gaa caa ttc acc gga atg gat gca ccc cgc gat gcc 883  
 Tyr Gly Gln Phe Glu Gln Phe Thr Gly Met Asp Ala Pro Arg Asp Ala  
 250 255 260

atg cgt gag gct ttg gaa gag tct tta ggc atc tca gaa gaa cac 928  
 Met Arg Glu Ala Leu Glu Glu Ser Leu Gly Ile Ser Glu Glu His  
 265 270 275

taagtccccg ccacctcctc aac 951

<210> 440  
 <211> 276  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 440  
 Leu Gly Ser His Ile Thr His Arg Ala Ala Val Leu Gly Ser Pro Ile  
 1 5 10 15  
 Glu His Ser Lys Ser Pro Val Leu His Asn Thr Gly Tyr Lys Ala Leu  
 20 25 30  
 Gly Leu Asp Gln Trp Glu Tyr Asp Arg Phe Glu Cys Thr Gly Asp Met  
 35 40 45  
 Leu Pro Gly Ile Val Ser Gly Ala Asp Glu Thr Tyr Cys Gly Phe Ser  
 50 55 60  
 Val Thr Met Pro Ser Lys Phe Ala Ala Leu Glu Phe Ala Asp Glu Val  
 65 70 75 80  
 Thr Glu Arg Ala Cys Ala Ile Gly Ser Ala Asn Thr Leu Leu Arg Thr  
 85 90 95  
 Ala Thr Gly Trp Arg Ala Asp Asn Thr Asp Val Asp Gly Ile Arg Gly  
 100 105 110  
 Ala Leu Gly Glu Leu Leu Gly Gly Ala Ser Leu Ala Gly Lys His Ala  
 115 120 125  
 Ile Val Ile Gly Ser Gly Gly Thr Ala Arg Pro Ala Ile Trp Ala Leu  
 130 135 140  
 Ile Glu Ala Gly Val Ala Arg Ile Thr Val Leu Asn Arg Ser Asp Arg  
 145 150 155 160  
 Thr Ala Glu Leu Gln Thr Leu Phe Asp Glu Thr Pro Thr Thr Leu Ala  
 165 170 175

Tyr Ala Pro Leu Glu His Leu His Ile Glu Ala Asp Val Val Val Ser  
 180 185 190  
 Thr Val Pro Ser Ala Ala Ile Ala Gly Leu Glu Asp Thr Leu Ala Ile  
 195 200 205  
 Ala Pro Val Leu Asp Val Ile Tyr Asp Pro Trp Pro Thr Pro Leu Val  
 210 215 220  
 Glu Val Thr Arg Ala Lys Gly Leu Lys Ala Val Gly Gly His Val Met  
 225 230 235 240  
 Leu Ala His Gln Ser Tyr Gly Gln Phe Glu Gln Phe Thr Gly Met Asp  
 245 250 255  
 Ala Pro Arg Asp Ala Met Arg Glu Ala Leu Glu Glu Ser Leu Gly Ile  
 260 265 270  
 Ser Glu Glu His  
 275

<210> 441  
 <211> 693  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(670)  
 <223> RXA01699

<400> 441  
 ctgcagaaat tcggcgggtga ctccctgagc gaaaccaaga gcaacattga cacctacctc 60  
 aaaaacattg aggaacgaat gaaattcgaa ggttttagagg atg gag cgt aat gaa 115  
 Met Glu Arg Asn Glu 5  
 1  
 gtg aat gat caa att cac tta gat cat caa tca gat gac acc tct gaa 163  
 Val Asn Asp Gln Ile His Leu Asp His Gln Ser Asp Asp Thr Ser Glu 20  
 10 15  
 tgc tcc tgc ccg atc gtg gtt ctt gtg ggt ttg cca gga gct gga aaa 211  
 Cys Ser Cys Pro Ile Val Val Leu Val Gly Leu Pro Gly Ala Gly Lys 35  
 25 30  
 tcc acc att gga cgt cga tta gcg cgc gcc tta aac act gaa ctc gtc 259  
 Ser Thr Ile Gly Arg Arg Leu Ala Arg Ala Leu Asn Thr Glu Leu Val 50  
 40 45  
 gac tcc gac gaa ctg att gag cgc gcc acc gga aaa gcc tgt ggc gcc 307  
 Asp Ser Asp Glu Leu Ile Glu Arg Ala Thr Gly Lys Ala Cys Gly Ala 65  
 55 60  
 gtg ttc agc gag ctc ggc gag cca gcc ttc cgc gag ctc gag gcc atc 355  
 Val Phe Ser Glu Leu Gly Glu Pro Ala Phe Arg Glu Leu Glu Ala Ile 85  
 70 75 80  
 cac gtg gcc gaa gca ctg aaa tcc tcc gga gtg gtg agc ttg gga ggc 403



His Val Ala Glu Ala Leu Lys Ser Ser Gly Val Val Ser Leu Gly Gly  
                     90                    95                    100  
  
 gga tct gtg ctg aca gaa tcc acc cgt gaa ctg ctc aaa ggc cag gac 451  
 Gly Ser Val Leu Thr Glu Ser Thr Arg Glu Leu Leu Lys Gly Gln Asp  
                     105                    110                    115  
  
 gtg gtc tgg atc gac gtg cca gta gaa gaa ggc atc agg cgc acc gca 499  
 Val Val Trp Ile Asp Val Pro Val Glu Glu Gly Ile Arg Arg Thr Ala  
                     120                    125                    130  
  
 aac gag cgt tcc cgc ccc gtg ctg caa gcc gcc gac ccc gcc gag cac 547  
 Asn Glu Arg Ser Arg Pro Val Leu Gln Ala Ala Asp Pro Ala Glu His  
                     135                    140                    145  
  
 tac cgc aac ctg gtg aaa gtg cgc acc ccg ttg tac gaa gag gtg gca 595  
 Tyr Arg Asn Leu Val Lys Val Arg Thr Pro Leu Tyr Glu Glu Val Ala  
                     150                    155                    160                    165  
  
 acc tac cga ctt cgc acc aac aac cgc agc ccc cag caa gtg gtg gca 643  
 Thr Tyr Arg Leu Arg Thr Asn Asn Arg Ser Pro Gln Gln Val Val Ala  
                     170                    175                    180  
  
 gca gtg ttg cat cat cta gaa atc gat taattaaacc gggcacctga 690  
 Ala Val Leu His His Leu Glu Ile Asp  
                     185                    190  
  
 tta 693

<210> 442  
 <211> 190  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 442  
 Met Glu Arg Asn Glu Val Asn Asp Gln Ile His Leu Asp His Gln Ser  
   1                    5                    10                    15  
  
 Asp Asp Thr Ser Glu Cys Ser Cys Pro Ile Val Val Leu Val Gly Leu  
                     20                    25                    30  
  
 Pro Gly Ala Gly Lys Ser Thr Ile Gly Arg Arg Leu Ala Arg Ala Leu  
                     35                    40                    45  
  
 Asn Thr Glu Leu Val Asp Ser Asp Glu Leu Ile Glu Arg Ala Thr Gly  
                     50                    55                    60  
  
 Lys Ala Cys Gly Ala Val Phe Ser Glu Leu Gly Glu Pro Ala Phe Arg  
   65                    70                    75                    80  
  
 Glu Leu Glu Ala Ile His Val Ala Glu Ala Leu Lys Ser Ser Gly Val  
                     85                    90                    95  
  
 Val Ser Leu Gly Gly Gly Ser Val Leu Thr Glu Ser Thr Arg Glu Leu  
                     100                    105                    110  
  
 Leu Lys Gly Gln Asp Val Val Trp Ile Asp Val Pro Val Glu Glu Gly  
                     115                    120                    125  
  
 Ile Arg Arg Thr Ala Asn Glu Arg Ser Arg Pro Val Leu Gln Ala Ala

130	135	140
Asp Pro Ala Glu His Tyr Arg Asn Leu Val Lys Val Arg Thr Pro Leu		
145	150	155 160
Tyr Glu Glu Val Ala Thr Tyr Arg Leu Arg Thr Asn Asn Arg Ser Pro		
	165	170 175
Gln Gln Val Val Ala Ala Val Leu His His Leu Glu Ile Asp		
	180	185 190

&lt;210&gt; 443

&lt;211&gt; 959

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (97)..(936)

&lt;223&gt; RXA00952

&lt;400&gt; 443

catcctcgtc tccctatccg gccgtggcga caaggacgtt gaccacgtgc gccgcaccct 60

cgaagaaaat ccagaactga tcctgaagga caaccgatg agc cgt tac gac gat	114
Met Ser Arg Tyr Asp Asp	
1 5	

ctt ttt gca cgc ctc gac acg gca ggg gag ggc gcc ttt gtt ccc ttc	162
Leu Phe Ala Arg Leu Asp Thr Ala Gly Glu Gly Ala Phe Val Pro Phe	
10 15 20	

atc atg ctg agc gac cct tca cca gag gag gct ttc cag atc atc tcc	210
Ile Met Leu Ser Asp Pro Ser Pro Glu Glu Ala Phe Gln Ile Ile Ser	
25 30 35	

aca gca atc gaa gct ggc gca gat gca ctg gaa ctt ggc gta cct ttc	258
Thr Ala Ile Glu Ala Gly Ala Asp Ala Leu Glu Leu Gly Val Pro Phe	
40 45 50	

tcc gac cca gtt gcc gat ggc ccc acc gtc gcg gaa tcc cac ctc cgc	306
Ser Asp Pro Val Ala Asp Gly Pro Thr Val Ala Glu Ser His Leu Arg	
55 60 65 70	

gca ctc gac ggc ggc gcc acc gta gac agc gca ctc gag cag atc aag	354
Ala Leu Asp Gly Gly Ala Thr Val Asp Ser Ala Leu Glu Gln Ile Lys	
75 80 85	

cgc gtg cgc gca gcc tac cca gag gtt ccc atc gga atg ctc atc tac	402
Arg Val Arg Ala Ala Tyr Pro Glu Val Pro Ile Gly Met Leu Ile Tyr	
90 95 100	

ggc aac gtt cct ttc acc cgt ggc ttg gat cgc ttc tac caa gag ttc	450
Gly Asn Val Pro Phe Thr Arg Gly Leu Asp Arg Phe Tyr Gln Glu Phe	
105 110 115	

gct gaa gct ggc gca gac tcc atc ctc ctg cca gac gtc cca gtc cga	498
Ala Glu Ala Gly Ala Asp Ser Ile Leu Leu Pro Asp Val Pro Val Arg	
120 125 130	

gaa ggc gca ccg ttt tct gca gca gct gca gca gcc gga att gat ccc 546  
 Glu Gly Ala Pro Phe Ser Ala Ala Ala Ala Ala Gly Ile Asp Pro  
 135 140 145 150  
  
 att tac atc gct ccg gcc aac gcc agc gag aaa acc ctc gag ggt gtc 594  
 Ile Tyr Ile Ala Pro Ala Asn Ala Ser Glu Lys Thr Leu Glu Gly Val  
 155 160 165  
  
 tcc gcc gca tca aag ggc tac atc tac gcc atc tcc cgc gac ggc gtc 642  
 Ser Ala Ala Ser Lys Gly Tyr Ile Tyr Ala Ile Ser Arg Asp Gly Val  
 170 175 180  
  
 acc ggc acc gaa cgt gaa tca tcc acc gac ggc ctg tcc gca gtg gtg 690  
 Thr Gly Thr Glu Arg Glu Ser Ser Thr Asp Gly Leu Ser Ala Val Val  
 185 190 195  
  
 gac aac atc aag aaa ttt gat ggc gca ccc atc ctc ttg ggc ttc ggc 738  
 Asp Asn Ile Lys Lys Phe Asp Gly Ala Pro Ile Leu Leu Gly Phe Gly  
 200 205 210  
  
 atc tca tcc cct cag cac gtg gca gac gcg att gca gcg ggt gct tcc 786  
 Ile Ser Ser Pro Gln His Val Ala Asp Ala Ile Ala Ala Gly Ala Ser  
 215 220 225 230  
  
 ggt gcg atc acg ggt tcc gcg atc acc aag atc att gct tcc cac tgc 834  
 Gly Ala Ile Thr Gly Ser Ala Ile Thr Lys Ile Ile Ala Ser His Cys  
 235 240 245  
  
 gaa ggt gag cac ccg aac ccg tcc acc att cga gat atg gac ggt ttg 882  
 Glu Gly Glu His Pro Asn Pro Ser Thr Ile Arg Asp Met Asp Gly Leu  
 250 255 260  
  
 aag aag gat ctc act gag ttc atc tct gcg atg aag gca gcg acc aag 930  
 Lys Lys Asp Leu Thr Glu Phe Ile Ser Ala Met Lys Ala Ala Thr Lys  
 265 270 275  
  
 aag gtt taggccttta aatgtggcaa tgt 959  
 Lys Val  
 280

&lt;210&gt; 444

&lt;211&gt; 280

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 444

Met Ser Arg Tyr Asp Asp Leu Phe Ala Arg Leu Asp Thr Ala Gly Glu  
 1 5 10 15  
  
 Gly Ala Phe Val Pro Phe Ile Met Leu Ser Asp Pro Ser Pro Glu Glu  
 20 25 30  
  
 Ala Phe Gln Ile Ile Ser Thr Ala Ile Glu Ala Gly Ala Asp Ala Leu  
 35 40 45  
  
 Glu Leu Gly Val Pro Phe Ser Asp Pro Val Ala Asp Gly Pro Thr Val  
 50 55 60  
  
 Ala Glu Ser His Leu Arg Ala Leu Asp Gly Gly Ala Thr Val Asp Ser  
 65 70 75 80

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<210> 445
<211> 1237
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101) .. (1237)
<223> RXN00956
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gccggtgcag gcacgtgggc tggggcgaaa gacgccggcg cgctgctgaa aatttttagcg 60

accatctcca cattccatta ctaaagggtt aaataggatc atg act gaa aaa gaa 115  
Met Thr Glu Lys Glu  
1 5

aac ttg ggc ggc tcc acg ctg ctg cct gca tac ttc ggt gaa ttc ggc 163  
Asn Leu Gly Gly Ser Thr Leu Leu Pro Ala Tyr Phe Gly Glu Phe Gly  
10 15 20

ggc cag ttc gtc gcg gaa tcc ctc ctg cct gct ctc gac cag ctg gag	211
Gly Gln Phe Val Ala Glu Ser Leu Leu Pro Ala Leu Asp Gln Leu Glu	
25 30 35	
aag gcc ttc gtt gac gcg acc aac agc cca gag ttc cgc gaa gaa ctc	259
Lys Ala Phe Val Asp Ala Thr Asn Ser Pro Glu Phe Arg Glu Glu Leu	
40 45 50	
ggc ggc tac ctc cgc gat tac ctc ggc cgc cca acc ccg ctg acc gaa	307
Gly Gly Tyr Leu Arg Asp Tyr Leu Gly Arg Pro Thr Pro Leu Thr Glu	
55 60 65	
tgc tcc aac ctg cca ctc gca ggc gaa ggc aaa ggc ttt gcg cgg atc	355
Cys Ser Asn Leu Pro Leu Ala Gly Glu Gly Lys Gly Phe Ala Arg Ile	
70 75 80 85	
ttc ctc aag cgc gaa gac ctc gtc cac ggc ggt gca cac aaa act aac	403
Phe Leu Lys Arg Glu Asp Leu Val His Gly Gly Ala His Lys Thr Asn	
90 95 100	
cag gtg atc ggc cag gtg ctg ctt gcc aag cgc atg ggc aaa acc cgc	451
Gln Val Ile Gly Gln Val Leu Leu Ala Lys Arg Met Gly Lys Thr Arg	
105 110 115	
atc atc gca gag acc ggc gca ggc cag cac ggc acc gcc acc gct ctc	499
Ile Ile Ala Glu Thr Gly Ala Gly Gln His Gly Thr Ala Thr Ala Leu	
120 125 130	
gca tgt gcg ctc atg ggc ctc gag tgc gtt gtc tac atg ggc gcc aag	547
Ala Cys Ala Leu Met Gly Leu Glu Cys Val Val Tyr Met Gly Ala Lys	
135 140 145	
gac gtt gcc cgc cag cag ccc aac gtc tac cgc atg cag ctg cac ggc	595
Asp Val Ala Arg Gln Gln Pro Asn Val Tyr Arg Met Gln Leu His Gly	
150 155 160 165	
gcg aag gtc atc ccc gtg gaa tct ggt tcc ggc acc ctg aag gac gcc	643
Ala Lys Val Ile Pro Val Glu Ser Gly Ser Gly Thr Leu Lys Asp Ala	
170 175 180	
gtg aat gaa gcg ctg cgc gat tgg acc gca acc ttc cac gag tcc cac	691
Val Asn Glu Ala Leu Arg Asp Trp Thr Ala Thr Phe His Glu Ser His	
185 190 195	
tac ctt ctc ggc acc ccc gcc ggc ccg cac cca ttc cca acc atc gtg	739
Tyr Leu Leu Gly Thr Pro Ala Gly Pro His Pro Phe Pro Thr Ile Val	
200 205 210	
cgt gaa ttc cac aag gtg atc tct gag gaa gcc aag gca cag atg cta	787
Arg Glu Phe His Lys Val Ile Ser Glu Glu Ala Lys Ala Gln Met Leu	
215 220 225	
gag cgc acc ggc aag ctt ccc gac gtt gtg gtc gcc tgt gtc ggt ggt	835
Glu Arg Thr Gly Lys Leu Pro Asp Val Val Val Ala Cys Val Gly Gly	
230 235 240 245	
ggc tcc aac gcc atc ggc atg ttc gca gac ttc att gac gat gaa ggt	883
Gly Ser Asn Ala Ile Gly Met Phe Ala Asp Phe Ile Asp Asp Glu Gly	
250 255 260	

gta gag ctc gtc ggc gct gag cca gcc ggt gaa ggc ctc gac tcc ggc 931  
 Val Glu Leu Val Gly Ala Glu Pro Ala Gly Glu Gly Leu Asp Ser Gly  
                   265                                  270                                  275

aag cac ggc gca acc atc acc aac ggt cag atc ggc atc ctg cac ggc 979  
 Lys His Gly Ala Thr Ile Thr Asn Gly Gln Ile Gly Ile Leu His Gly  
                   280                                  285                                  290

acc cgt tcc tac ctg atg cgc aac tcc gac ggc caa gtg gaa gag tcc  
 1027  
 Thr Arg Ser Tyr Leu Met Arg Asn Ser Asp Gly Gln Val Glu Glu Ser  
                   295                                  300                                  305

tac tcc atc tcc gcc gga ctt gat tac cca ggc gtc ggc cca cag cac  
 1075  
 Tyr Ser Ile Ser Ala Gly Leu Asp Tyr Pro Gly Val Gly Pro Gln His  
 310                                  315                                  320                                  325

gca cac ctg cac gcc acc ggc cgc gcc acc tac gtt ggt atc acc gac  
 1123  
 Ala His Leu His Ala Thr Gly Arg Ala Thr Tyr Val Gly Ile Thr Asp  
                                   330                                  335                                  340

gcc gaa gcc ctc caa gca ttc cag tac ctc gcc cgc tac gaa ggc atc  
 1171  
 Ala Glu Ala Leu Gln Ala Phe Gln Tyr Leu Ala Arg Tyr Glu Gly Ile  
                                   345                                  350                                  355

atc ccc gca ctg gaa tcc tca cac gcg ttc gcc tac gca ctc aag cgc  
 1219  
 Ile Pro Ala Leu Glu Ser Ser His Ala Phe Ala Tyr Ala Leu Lys Arg  
                   360                                  365                                  370

gcc aag acc gcc gaa gta  
 1237  
 Ala Lys Thr Ala Glu Val  
                   375

<210> 446

<211> 379

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 446

Met Thr Glu Lys Glu Asn Leu Gly Gly Ser Thr Leu Leu Pro Ala Tyr  
   1                                  5                                  10                                  15

Phe Gly Glu Phe Gly Gly Gln Phe Val Ala Glu Ser Leu Leu Pro Ala  
                   20                                  25                                  30

Leu Asp Gln Leu Glu Lys Ala Phe Val Asp Ala Thr Asn Ser Pro Glu  
                   35                                  40                                  45

Phe Arg Glu Glu Leu Gly Gly Tyr Leu Arg Asp Tyr Leu Gly Arg Pro  
                   50                                  55                                  60

Thr Pro Leu Thr Glu Cys Ser Asn Leu Pro Leu Ala Gly Glu Gly Lys  
   65                                  70                                  75                                  80

Gly Phe Ala Arg Ile Phe Leu Lys Arg Glu Asp Leu Val His Gly Gly

85								90				95			
Ala	His	Lys	Thr	Asn	Gln	Val	Ile	Gly	Gln	Val	Leu	Leu	Ala	Lys	Arg
			100					105					110		
Met	Gly	Lys	Thr	Arg	Ile	Ile	Ala	Glu	Thr	Gly	Ala	Gly	Gln	His	Gly
		115					120					125			
Thr	Ala	Thr	Ala	Leu	Ala	Cys	Ala	Leu	Met	Gly	Leu	Glu	Cys	Val	Val
	130					135					140				
Tyr	Met	Gly	Ala	Lys	Asp	Val	Ala	Arg	Gln	Gln	Pro	Asn	Val	Tyr	Arg
145					150					155					160
Met	Gln	Leu	His	Gly	Ala	Lys	Val	Ile	Pro	Val	Glu	Ser	Gly	Ser	Gly
				165					170					175	
Thr	Leu	Lys	Asp	Ala	Val	Asn	Glu	Ala	Leu	Arg	Asp	Trp	Thr	Ala	Thr
			180					185						190	
Phe	His	Glu	Ser	His	Tyr	Leu	Leu	Gly	Thr	Pro	Ala	Gly	Pro	His	Pro
		195					200					205			
Phe	Pro	Thr	Ile	Val	Arg	Glu	Phe	His	Lys	Val	Ile	Ser	Glu	Glu	Ala
	210					215					220				
Lys	Ala	Gln	Met	Leu	Glu	Arg	Thr	Gly	Lys	Leu	Pro	Asp	Val	Val	Val
225					230					235					240
Ala	Cys	Val	Gly	Gly	Gly	Ser	Asn	Ala	Ile	Gly	Met	Phe	Ala	Asp	Phe
				245					250					255	
Ile	Asp	Asp	Glu	Gly	Val	Glu	Leu	Val	Gly	Ala	Glu	Pro	Ala	Gly	Glu
			260					265						270	
Gly	Leu	Asp	Ser	Gly	Lys	His	Gly	Ala	Thr	Ile	Thr	Asn	Gly	Gln	Ile
		275					280					285			
Gly	Ile	Leu	His	Gly	Thr	Arg	Ser	Tyr	Leu	Met	Arg	Asn	Ser	Asp	Gly
	290					295					300				
Gln	Val	Glu	Glu	Ser	Tyr	Ser	Ile	Ser	Ala	Gly	Leu	Asp	Tyr	Pro	Gly
305					310					315					320
Val	Gly	Pro	Gln	His	Ala	His	Leu	His	Ala	Thr	Gly	Arg	Ala	Thr	Tyr
				325					330					335	
Val	Gly	Ile	Thr	Asp	Ala	Glu	Ala	Leu	Gln	Ala	Phe	Gln	Tyr	Leu	Ala
			340					345					350		
Arg	Tyr	Glu	Gly	Ile	Ile	Pro	Ala	Leu	Glu	Ser	Ser	His	Ala	Phe	Ala
		355					360					365			
Tyr	Ala	Leu	Lys	Arg	Ala	Lys	Thr	Ala	Glu	Val					
	370					375									

&lt;210&gt; 447

&lt;211&gt; 1231

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1231)

&lt;223&gt; FRXA00956

&lt;400&gt; 447

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 Met Thr Glu Lys Glu  
 1 5

aac ttg ggc ggc tcc acg ctg ctg cct gca tac ttc ggt gaa ttc ggc 163  
 Asn Leu Gly Gly Ser Thr Leu Leu Pro Ala Tyr Phe Gly Glu Phe Gly  
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 Gly Gln Phe Val Ala Glu Ser Leu Leu Pro Ala Leu Asp Gln Leu Glu  
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aag gcc ttc gtt gac gcg acc aac agc cca gag ttc cgc gaa gaa ctc 259  
 Lys Ala Phe Val Asp Ala Thr Asn Ser Pro Glu Phe Arg Glu Glu Leu  
 40 45 50

ggc ggc tac ctc cgc gat tac ctc ggc cgc cca acc ccg ctg acc gaa 307  
 Gly Gly Tyr Leu Arg Asp Tyr Leu Gly Arg Pro Thr Pro Leu Thr Glu  
 55 60 65

tgc tcc aac ctg cca ctc gca ggc gaa ggc aaa ggc ttt gcg cgg atc 355  
 Cys Ser Asn Leu Pro Leu Ala Gly Glu Gly Lys Gly Phe Ala Arg Ile  
 70 75 80 85

ttc ctc aag cgc gaa gac ctc gtc cac ggc ggt gca cac aaa act aac 403  
 Phe Leu Lys Arg Glu Asp Leu Val His Gly Gly Ala His Lys Thr Asn  
 90 95 100

cag gtg atc ggc cag gtg ctg ctt gcc aag cgc atg ggc aaa acc cgc 451  
 Gln Val Ile Gly Gln Val Leu Leu Ala Lys Arg Met Gly Lys Thr Arg  
 105 110 115

atc atc gca gag acc ggc gca ggc cag cac ggc acc gcc acc gct ctc 499  
 Ile Ile Ala Glu Thr Gly Ala Gly Gln His Gly Thr Ala Thr Ala Leu  
 120 125 130

gca tgt gcg ctc atg ggc ctc gag tgc gtt gtc tac atg ggc gcc aag 547  
 Ala Cys Ala Leu Met Gly Leu Glu Cys Val Val Tyr Met Gly Ala Lys  
 135 140 145

gac gtt gcc cgc cag cag ccc aac gtc tac cgc atg cag ctg cac ggc 595  
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 Ala Lys Val Ile Pro Val Glu Ser Gly Ser Gly Thr Leu Lys Asp Ala  
 170 175 180

gtg aat gaa gcg ctg cgc gat tgg acc gca acc ttc cac gag tcc cac 691  
 Val Asn Glu Ala Leu Arg Asp Trp Thr Ala Thr Phe His Glu Ser His  
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Tyr Leu Leu Gly Thr Pro Ala Gly Pro His Pro Phe Pro Thr Ile Val	
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cgt gaa ttc cac aag gtg atc tct gag gaa gcc aag gca cag atg cta	787
Arg Glu Phe His Lys Val Ile Ser Glu Glu Ala Lys Ala Gln Met Leu	
215 220 225	
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Glu Arg Thr Gly Lys Leu Pro Asp Val Val Val Ala Cys Val Gly Gly	
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Gly Ser Asn Ala Ile Gly Met Phe Ala Asp Phe Ile Asp Asp Glu Gly	
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Val Glu Leu Val Gly Ala Glu Pro Ala Gly Glu Gly Leu Asp Ser Gly	
265 270 275	
aag cac ggc gca acc atc acc aac ggt cag atc ggc atc ctg cac ggc	979
Lys His Gly Ala Thr Ile Thr Asn Gly Gln Ile Gly Ile Leu His Gly	
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1219 Ile Pro Ala Leu Glu Ser Ser His Ala Phe Ala Tyr Ala Leu Lys Arg	
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1231 Ala Lys Thr Ala	
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&lt;210&gt; 448

&lt;211&gt; 377

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 448

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Phe	Gly	Glu	Phe	Gly	Gly	Gln	Phe	Val	Ala	Glu	Ser	Leu	Leu	Pro	Ala	20	25	30	
Leu	Asp	Gln	Leu	Glu	Lys	Ala	Phe	Val	Asp	Ala	Thr	Asn	Ser	Pro	Glu	35	40	45	
Phe	Arg	Glu	Glu	Leu	Gly	Gly	Tyr	Leu	Arg	Asp	Tyr	Leu	Gly	Arg	Pro	50	55	60	
Thr	Pro	Leu	Thr	Glu	Cys	Ser	Asn	Leu	Pro	Leu	Ala	Gly	Glu	Gly	Lys	65	70	75	80
Gly	Phe	Ala	Arg	Ile	Phe	Leu	Lys	Arg	Glu	Asp	Leu	Val	His	Gly	Gly	85	90	95	
Ala	His	Lys	Thr	Asn	Gln	Val	Ile	Gly	Gln	Val	Leu	Leu	Ala	Lys	Arg	100	105	110	
Met	Gly	Lys	Thr	Arg	Ile	Ile	Ala	Glu	Thr	Gly	Ala	Gly	Gln	His	Gly	115	120	125	
Thr	Ala	Thr	Ala	Leu	Ala	Cys	Ala	Leu	Met	Gly	Leu	Glu	Cys	Val	Val	130	135	140	
Tyr	Met	Gly	Ala	Lys	Asp	Val	Ala	Arg	Gln	Gln	Pro	Asn	Val	Tyr	Arg	145	150	155	160
Met	Gln	Leu	His	Gly	Ala	Lys	Val	Ile	Pro	Val	Glu	Ser	Gly	Ser	Gly	165	170	175	
Thr	Leu	Lys	Asp	Ala	Val	Asn	Glu	Ala	Leu	Arg	Asp	Trp	Thr	Ala	Thr	180	185	190	
Phe	His	Glu	Ser	His	Tyr	Leu	Leu	Gly	Thr	Pro	Ala	Gly	Pro	His	Pro	195	200	205	
Phe	Pro	Thr	Ile	Val	Arg	Glu	Phe	His	Lys	Val	Ile	Ser	Glu	Glu	Ala	210	215	220	
Lys	Ala	Gln	Met	Leu	Glu	Arg	Thr	Gly	Lys	Leu	Pro	Asp	Val	Val	Val	225	230	235	240
Ala	Cys	Val	Gly	Gly	Gly	Ser	Asn	Ala	Ile	Gly	Met	Phe	Ala	Asp	Phe	245	250	255	
Ile	Asp	Asp	Glu	Gly	Val	Glu	Leu	Val	Gly	Ala	Glu	Pro	Ala	Gly	Glu	260	265	270	
Gly	Leu	Asp	Ser	Gly	Lys	His	Gly	Ala	Thr	Ile	Thr	Asn	Gly	Gln	Ile	275	280	285	
Gly	Ile	Leu	His	Gly	Thr	Arg	Ser	Tyr	Leu	Met	Arg	Asn	Ser	Asp	Gly	290	295	300	
Gln	Val	Glu	Glu	Ser	Tyr	Ser	Ile	Ser	Ala	Gly	Leu	Asp	Tyr	Pro	Gly	305	310	315	320
Val	Gly	Pro	Gln	His	Ala	His	Leu	His	Ala	Thr	Gly	Arg	Ala	Thr	Tyr				

[illegible]

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<212> DNA
<213> Corynebacterium glutamicum
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<223> RXA00064
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Met Ser Ser Val Ser 1 5															
ctg cag gat ttt gat gca gag cga att ggt ttg ttc cac gag gac att 163															
Leu Gln Asp Phe Asp Ala Glu Arg Ile Gly Leu Phe His Glu Asp Ile 10 15 20															
aag cgc aag ttt gat gag ctc aag tca aaa aat ctg aag ctg gat ctt 211															
Lys Arg Lys Phe Asp Glu Leu Lys Ser Lys Asn Leu Lys Leu Asp Leu 25 30 35															
act cgc ggt aag cct tcg tcg gag cag ttg gat ttc gct gat gag ttg 259															
Thr Arg Gly Lys Pro Ser Ser Glu Gln Leu Asp Phe Ala Asp Glu Leu 40 45 50															
ttg gcg ttg cct ggt aag ggt gat ttc aag gct gcg gat ggt act gat 307															
Leu Ala Leu Pro Gly Lys Gly Asp Phe Lys Ala Ala Asp Gly Thr Asp 55 60 65															
gtc cgt aac tat ggc ggg ctg gat ggc atc gtt gat att cgc cag att 355															
Val Arg Asn Tyr Gly Gly Leu Asp Gly Ile Val Asp Ile Arg Gln Ile 70 75 80 85															
tgg gcg gat ttg ctg ggt gtt cct gtg gag cag gtc ttg gcg ggg gat 403															
Trp Ala Asp Leu Leu Gly Val Pro Val Glu Gln Val Leu Ala Gly Asp 90 95 100															
gct tcg agc ttg aac atc atg ttt gat gtg atc agc tgg tcg tac att 451															
Ala Ser Ser Leu Asn Ile Met Phe Asp Val Ile Ser Trp Ser Tyr Ile 105 110 115															
ttc ggt aac aat gat tcg gtt cag cct tgg tcg aag gaa gaa acc gtt 499															
Phe Gly Asn Asn Asp Ser Val Gln Pro Trp Ser Lys Glu Glu Thr Val 120 125 130															

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Lys Trp Ile Cys Pro Val Pro Gly Tyr Asp Arg His Phe Ser Ile Thr	
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Glu Arg Phe Gly Phe Glu Met Ile Ser Val Pro Met Asn Glu Asp Gly	
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Pro Asp Met Asp Ala Val Glu Glu Leu Val Lys Asn Pro Gln Val Lys	
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Gly Met Trp Val Val Pro Val Phe Ser Asn Pro Thr Gly Phe Thr Val	
185 190 195	
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Thr Glu Asp Val Ala Lys Arg Leu Ser Ala Met Glu Thr Ala Ala Pro	
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Asp Phe Arg Val Val Trp Asp Asn Ala Tyr Ala Val His Thr Leu Thr	
215 220 225	
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Asp Glu Phe Pro Glu Val Ile Asp Ile Val Gly Leu Gly Glu Ala Ala	
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Gly Asn Pro Asn Arg Phe Trp Ala Phe Thr Ser Thr Ser Lys Ile Thr	
250 255 260	
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Leu Ala Gly Ala Gly Val Ser Phe Phe Leu Thr Ser Ala Glu Asn Arg	
265 270 275	
aag tgg tac acc ggc cat gcg ggt atc cgt ggc att ggc cct aac aag	979
Lys Trp Tyr Thr Gly His Ala Gly Ile Arg Gly Ile Gly Pro Asn Lys	
280 285 290	
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330 335 340	
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1171 Gln Trp Thr Val Pro Ala Gly Gly Tyr Phe Ile Ser Leu Asp Val Val	
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 Pro Gly Thr Ala Ser Arg Val Ala Glu Leu Ala Lys Glu Ala Gly Ile  
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gcg ttg acg ggt gcg ggt tct tct tac ccg ctg cgt cag gat ccg gag  
 1267  
 Ala Leu Thr Gly Ala Gly Ser Ser Tyr Pro Leu Arg Gln Asp Pro Glu  
           375                                  380                                  385

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 1315  
 Asn Lys Asn Leu Arg Leu Ala Pro Ser Leu Pro Pro Val Glu Glu Leu  
 390                                  395                                  400                                  405

gag gtt gcc atg gat ggc gtg gct acc tgt gtg ctg ttg gca gca gcg  
 1363  
 Glu Val Ala Met Asp Gly Val Ala Thr Cys Val Leu Leu Ala Ala Ala  
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 <213> Corynebacterium glutamicum

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Leu Lys Leu Asp Leu Thr Arg Gly Lys Pro Ser Ser Glu Gln Leu Asp  
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Phe Ala Asp Glu Leu Leu Ala Leu Pro Gly Lys Gly Asp Phe Lys Ala  
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Ala Asp Gly Thr Asp Val Arg Asn Tyr Gly Gly Leu Asp Gly Ile Val  
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Asp Ile Arg Gln Ile Trp Ala Asp Leu Leu Gly Val Pro Val Glu Gln  
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Val Leu Ala Gly Asp Ala Ser Ser Leu Asn Ile Met Phe Asp Val Ile  
                                   100                                  105                                  110

Ser Trp Ser Tyr Ile Phe Gly Asn Asn Asp Ser Val Gln Pro Trp Ser  
                                   115                                  120                                  125

Lys Glu Glu Thr Val Lys Trp Ile Cys Pro Val Pro Gly Tyr Asp Arg  
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His Phe Ser Ile Thr Glu Arg Phe Gly Phe Glu Met Ile Ser Val Pro  
 145                                  150                                  155                                  160

Met	Asn	Glu	Asp	Gly	Pro	Asp	Met	Asp	Ala	Val	Glu	Glu	Leu	Val	Lys	165	170	175	
Asn	Pro	Gln	Val	Lys	Gly	Met	Trp	Val	Val	Pro	Val	Phe	Ser	Asn	Pro	180	185	190	
Thr	Gly	Phe	Thr	Val	Thr	Glu	Asp	Val	Ala	Lys	Arg	Leu	Ser	Ala	Met	195	200	205	
Glu	Thr	Ala	Ala	Pro	Asp	Phe	Arg	Val	Val	Trp	Asp	Asn	Ala	Tyr	Ala	210	215	220	
Val	His	Thr	Leu	Thr	Asp	Glu	Phe	Pro	Glu	Val	Ile	Asp	Ile	Val	Gly	225	230	235	240
Leu	Gly	Glu	Ala	Ala	Gly	Asn	Pro	Asn	Arg	Phe	Trp	Ala	Phe	Thr	Ser	245	250	255	
Thr	Ser	Lys	Ile	Thr	Leu	Ala	Gly	Ala	Gly	Val	Ser	Phe	Phe	Leu	Thr	260	265	270	
Ser	Ala	Glu	Asn	Arg	Lys	Trp	Tyr	Thr	Gly	His	Ala	Gly	Ile	Arg	Gly	275	280	285	
Ile	Gly	Pro	Asn	Lys	Val	Asn	Gln	Leu	Ala	His	Ala	Arg	Tyr	Phe	Gly	290	295	300	
Asp	Ala	Glu	Gly	Val	Arg	Ala	Val	Met	Arg	Lys	His	Ala	Ala	Ser	Leu	305	310	315	320
Ala	Pro	Lys	Phe	Asn	Lys	Val	Leu	Glu	Ile	Leu	Asp	Ser	Arg	Leu	Ala	325	330	335	
Glu	Tyr	Gly	Val	Ala	Gln	Trp	Thr	Val	Pro	Ala	Gly	Gly	Tyr	Phe	Ile	340	345	350	
Ser	Leu	Asp	Val	Val	Pro	Gly	Thr	Ala	Ser	Arg	Val	Ala	Glu	Leu	Ala	355	360	365	
Lys	Glu	Ala	Gly	Ile	Ala	Leu	Thr	Gly	Ala	Gly	Ser	Ser	Tyr	Pro	Leu	370	375	380	
Arg	Gln	Asp	Pro	Glu	Asn	Lys	Asn	Leu	Arg	Leu	Ala	Pro	Ser	Leu	Pro	385	390	395	400
Pro	Val	Glu	Glu	Leu	Glu	Val	Ala	Met	Asp	Gly	Val	Ala	Thr	Cys	Val	405	410	415	
Leu	Leu	Ala	Ala	Ala	Glu	His	Tyr	Ala	Asn							420	425		

&lt;210&gt; 451

&lt;211&gt; 1143

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1120)

&lt;223&gt; RXN00448

&lt;400&gt; 451

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Ile Ser Arg Pro Val Cys Ile Leu Gly Leu Gly Leu Ile Gly Gly Ser
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Leu Leu Arg Asp Leu His Ala Ala Asn His Ser Val Phe Gly Tyr Asn
25 30 35

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Ala Val His Thr His Ala Pro Asn Asn Gly Phe Thr Asp Val Val Ser
90 95 100

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Val Lys Thr Ala Val Tyr Asp Ala Val Lys Ala Arg Asn Met Gln His
105 110 115

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Phe Asp Gln Leu Phe Asp Gly Thr Asp Ile Asn Ser Thr Trp Ile Ser
150 155 160 165

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Ile Trp Lys Asp Val Val Gln Met Ala Leu Ala Val Gly Ala Glu Val
170 175 180

gtc cca tcc cga gtt ggc cca cac gat gca gca gca gca cga gtg tct 691
Val Pro Ser Arg Val Gly Pro His Asp Ala Ala Ala Ala Arg Val Ser
185 190 195

cat tta aca cac atc ctg gct gaa acc ctc gcc atc gtc ggt gac aac 739
His Leu Thr His Ile Leu Ala Glu Thr Leu Ala Ile Val Gly Asp Asn
200 205 210

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 Leu His Glu Ala Arg Glu Gly Leu Thr Ala Glu Gln Pro Asn Ile Glu  
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 Ser Gly Gln Arg Arg Ala Lys Glu Ser Val Ser Pro Thr Ile Thr Ser  
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 65 70 75 80  
 Asp Ser Leu Leu Asp Ala Val His Thr His Ala Pro Asn Asn Gly Phe



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Thr	Asp	Val	Val	Ser	Val	Lys	Thr	Ala	Val	Tyr	Asp	Ala	Val	Lys	Ala		
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Arg	Asn	Met	Gln	His	Arg	Tyr	Val	Gly	Ser	His	Pro	Met	Ala	Gly	Thr		
		115					120					125					
Ala	Asn	Ser	Gly	Trp	Ser	Ala	Ser	Met	Asp	Gly	Leu	Phe	Lys	Arg	Ala		
		130				135					140						
Val	Trp	Val	Val	Thr	Phe	Asp	Gln	Leu	Phe	Asp	Gly	Thr	Asp	Ile	Asn		
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Ser	Thr	Trp	Ile	Ser	Ile	Trp	Lys	Asp	Val	Val	Gln	Met	Ala	Leu	Ala		
				165					170					175			
Val	Gly	Ala	Glu	Val	Val	Pro	Ser	Arg	Val	Gly	Pro	His	Asp	Ala	Ala		
			180					185					190				
Ala	Ala	Arg	Val	Ser	His	Leu	Thr	His	Ile	Leu	Ala	Glu	Thr	Leu	Ala		
		195					200					205					
Ile	Val	Gly	Asp	Asn	Gly	Gly	Ala	Leu	Ser	Leu	Ser	Leu	Ala	Ala	Gly		
		210				215					220						
Ser	Tyr	Arg	Asp	Ser	Thr	Arg	Val	Ala	Gly	Thr	Asp	Pro	Gly	Leu	Val		
					230					235					240		
Arg	Ala	Met	Cys	Glu	Ser	Asn	Ala	Gly	Pro	Leu	Val	Lys	Ala	Leu	Asp		
				245					250					255			
Glu	Ala	Leu	Ala	Ile	Leu	His	Glu	Ala	Arg	Glu	Gly	Leu	Thr	Ala	Glu		
			260					265					270				
Gln	Pro	Asn	Ile	Glu	Gln	Leu	Ala	Asp	Asn	Gly	Tyr	Arg	Ser	Arg	Ile		
		275					280					285					
Arg	Tyr	Glu	Ala	Arg	Ser	Gly	Gln	Arg	Arg	Ala	Lys	Glu	Ser	Val	Ser		
		290				295					300						
Pro	Thr	Ile	Thr	Ser	Ser	Arg	Pro	Val	Leu	Arg	Leu	His	Pro	Gly	Thr		
					310					315					320		
Pro	Asn	Trp	Glu	Lys	Gln	Leu	Ile	His	Ala	Glu	Thr	Leu	Gly	Ala	Arg		
				325					330					335			
Ile	Glu	Val	Phe														
			340														

&lt;210&gt; 453

&lt;211&gt; 689

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(666)

&lt;223&gt; FRXA00448

&lt;400&gt; 453

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Tyr	Val	Gly	Ser	His	Pro	Met	Ala	Gly	Thr	Ala	Asn	Ser	Gly	Trp	Ser	
1				5					10					15		
gca	tcc	atg	gac	gga	ctg	ttc	aaa	cga	gca	gta	tgg	gtg	gtc	acc	ttc	96
Ala	Ser	Met	Asp	Gly	Leu	Phe	Lys	Arg	Ala	Val	Trp	Val	Val	Thr	Phe	
			20				25						30			
gac	cag	ctt	ttc	gac	ggc	acc	gac	atc	aac	tcc	acc	tgg	atc	agc	atc	144
Asp	Gln	Leu	Phe	Asp	Gly	Thr	Asp	Ile	Asn	Ser	Thr	Trp	Ile	Ser	Ile	
		35					40					45				
tgg	aaa	gac	gtc	gtc	caa	atg	gca	ctc	gcc	gtg	ggc	gct	gaa	gtt	gtc	192
Trp	Lys	Asp	Val	Val	Gln	Met	Ala	Leu	Ala	Val	Gly	Ala	Glu	Val	Val	
	50					55					60					
cca	tcc	cga	gtt	ggc	cca	cac	gat	gca	gca	gca	gca	cga	gtg	tct	cat	240
Pro	Ser	Arg	Val	Gly	Pro	His	Asp	Ala	Ala	Ala	Ala	Arg	Val	Ser	His	
65					70					75					80	
tta	aca	cac	atc	ctg	gct	gaa	acc	ctc	gcc	atc	gtc	ggt	gac	aac	ggt	288
Leu	Thr	His	Ile	Leu	Ala	Glu	Thr	Leu	Ala	Ile	Val	Gly	Asp	Asn	Gly	
				85					90					95		
ggc	gca	ctg	tct	ctc	tct	tta	gcc	gct	ggc	agc	tac	cgc	gac	tcc	acc	336
Gly	Ala	Leu	Ser	Leu	Ser	Leu	Ala	Ala	Gly	Ser	Tyr	Arg	Asp	Ser	Thr	
			100					105					110			
cgc	gtt	gca	ggc	acc	gac	cca	gga	ctc	gtc	cgc	gcc	atg	tgt	gaa	agc	384
Arg	Val	Ala	Gly	Thr	Asp	Pro	Gly	Leu	Val	Arg	Ala	Met	Cys	Glu	Ser	
		115					120					125				
aac	gcc	ggc	cca	ctg	gtc	aaa	gcc	ctc	gac	gaa	gca	ctg	gcg	atc	ctc	432
Asn	Ala	Gly	Pro	Leu	Val	Lys	Ala	Leu	Asp	Glu	Ala	Leu	Ala	Ile	Leu	
	130					135					140					
cac	gaa	gcc	cgc	gaa	ggc	ctc	acc	gca	gaa	cag	cca	aac	atc	gag	caa	480
His	Glu	Ala	Arg	Glu	Gly	Leu	Thr	Ala	Glu	Gln	Pro	Asn	Ile	Glu	Gln	
145					150					155					160	
ctt	gcc	gac	aac	ggc	tac	cga	tcc	cgc	atc	cgc	tac	gaa	gcc	cgc	tcc	528
Leu	Ala	Asp	Asn	Gly	Tyr	Arg	Ser	Arg	Ile	Arg	Tyr	Glu	Ala	Arg	Ser	
				165					170					175		
ggc	cag	cga	cgc	gcc	aaa	gaa	tcc	gtt	agc	cct	acc	atc	acc	tca	tcc	576
Gly	Gln	Arg	Arg	Ala	Lys	Glu	Ser	Val	Ser	Pro	Thr	Ile	Thr	Ser	Ser	
			180					185					190			
agg	cca	gtg	ctc	cgt	ctc	cac	ccg	ggc	aca	cca	aac	tgg	gag	aag	cag	624
Arg	Pro	Val	Leu	Arg	Leu	His	Pro	Gly	Thr	Pro	Asn	Trp	Glu	Lys	Gln	
		195					200					205				
ctc	atc	cac	gct	gaa	acc	ctc	ggc	gca	cgg	atc	gaa	gtg	ttc			666
Leu	Ile	His	Ala	Glu	Thr	Leu	Gly	Ala	Arg	Ile	Glu	Val	Phe			
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&lt;210&gt; 454

<211> 222  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 454

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Ala Ser Met Asp Gly Leu Phe Lys Arg Ala Val Trp Val Val Thr Phe
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Asp Gln Leu Phe Asp Gly Thr Asp Ile Asn Ser Thr Trp Ile Ser Ile
          35              40              45

Trp Lys Asp Val Val Gln Met Ala Leu Ala Val Gly Ala Glu Val Val
          50              55              60

Pro Ser Arg Val Gly Pro His Asp Ala Ala Ala Ala Arg Val Ser His
          65              70              75              80

Leu Thr His Ile Leu Ala Glu Thr Leu Ala Ile Val Gly Asp Asn Gly
          85              90              95

Gly Ala Leu Ser Leu Ser Leu Ala Ala Gly Ser Tyr Arg Asp Ser Thr
          100              105              110

Arg Val Ala Gly Thr Asp Pro Gly Leu Val Arg Ala Met Cys Glu Ser
          115              120              125

Asn Ala Gly Pro Leu Val Lys Ala Leu Asp Glu Ala Leu Ala Ile Leu
          130              135              140

His Glu Ala Arg Glu Gly Leu Thr Ala Glu Gln Pro Asn Ile Glu Gln
          145              150              155              160

Leu Ala Asp Asn Gly Tyr Arg Ser Arg Ile Arg Tyr Glu Ala Arg Ser
          165              170              175

Gly Gln Arg Arg Ala Lys Glu Ser Val Ser Pro Thr Ile Thr Ser Ser
          180              185              190

Arg Pro Val Leu Arg Leu His Pro Gly Thr Pro Asn Trp Glu Lys Gln
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Leu Ile His Ala Glu Thr Leu Gly Ala Arg Ile Glu Val Phe
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 <213> Corynebacterium glutamicum

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 <223> FRXA00452

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Val Thr Thr Lys Asp  
1 5

att tcc cgc cca gta tgc atc ctg ggc ctc ggc ctc atc ggc gga tcc 163  
Ile Ser Arg Pro Val Cys Ile Leu Gly Leu Gly Leu Ile Gly Gly Ser  
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ctc ctc cgc gac ctc cat gca gcc aac cac tcc gtc ttc ggc tac aac 211  
Leu Leu Arg Asp Leu His Ala Ala Asn His Ser Val Phe Gly Tyr Asn  
25 30 35

cgc tca cgc tcc ggc gct aaa tca gcc gtc gac gaa ggc ttc gac gtt 259  
Arg Ser Arg Ser Gly Ala Lys Ser Ala Val Asp Glu Gly Phe Asp Val  
40 45 50

tcc gcc gat ctt gaa gca acc ctc cag cgt gca gcc gcc gaa gat gcg 307  
Ser Ala Asp Leu Glu Ala Thr Leu Gln Arg Ala Ala Ala Glu Asp Ala  
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ctc atc gtc ctc gcg gtc ccc atg acc gca atc gat tcg 346  
Leu Ile Val Leu Ala Val Pro Met Thr Ala Ile Asp Ser  
70 75 80

&lt;210&gt; 456

&lt;211&gt; 82

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 456

Val Thr Thr Lys Asp Ile Ser Arg Pro Val Cys Ile Leu Gly Leu Gly  
1 5 10 15

Leu Ile Gly Gly Ser Leu Leu Arg Asp Leu His Ala Ala Asn His Ser  
20 25 30

Val Phe Gly Tyr Asn Arg Ser Arg Ser Gly Ala Lys Ser Ala Val Asp  
35 40 45

Glu Gly Phe Asp Val Ser Ala Asp Leu Glu Ala Thr Leu Gln Arg Ala  
50 55 60

Ala Ala Glu Asp Ala Leu Ile Val Leu Ala Val Pro Met Thr Ala Ile  
65 70 75 80

Asp Ser

&lt;210&gt; 457

&lt;211&gt; 1248

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1225)

&lt;223&gt; RXA00584

&lt;400&gt; 457

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                                         Met His Ser Pro Glu
                                         1                               5
agg caa gaa aaa atg agt tct cca gtc tca ctc gaa aac gcg gcg tca 163
Arg Gln Glu Lys Met Ser Ser Pro Val Ser Leu Glu Asn Ala Ala Ser
                               10                               15                               20
acc agc aac aag cgc gtc gtg gct ttc cac gag ctg cct agc cct aca 211
Thr Ser Asn Lys Arg Val Val Ala Phe His Glu Leu Pro Ser Pro Thr
                               25                               30                               35
gat ctc atc gcc gca aac cca ctg aca cca aag cag gct tcc aag gtg 259
Asp Leu Ile Ala Ala Asn Pro Leu Thr Pro Lys Gln Ala Ser Lys Val
                               40                               45                               50
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Glu Gln Asp Arg Gln Asp Ile Ala Asp Ile Phe Ala Gly Asp Asp Asp
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cgc ctc gtt gtc gtt gtg gga cct tgc tca gtt cac gat cct gaa gca 355
Arg Leu Val Val Val Val Gly Pro Cys Ser Val His Asp Pro Glu Ala
70                               75                               80                               85
gcc atc gat tac gca aac cgc ctg gct ccg ctg gca aag cgc ctt gat 403
Ala Ile Asp Tyr Ala Asn Arg Leu Ala Pro Leu Ala Lys Arg Leu Asp
                               90                               95                               100
cag gac ctc aag att gtc atg cgc gtg tac ttc gag aag cct cgc acc 451
Gln Asp Leu Lys Ile Val Met Arg Val Tyr Phe Glu Lys Pro Arg Thr
                               105                               110                               115
atc gtc gga tgg aag gga ttg atc aat gat cct cac ctc aac gaa acc 499
Ile Val Gly Trp Lys Gly Leu Ile Asn Asp Pro His Leu Asn Glu Thr
                               120                               125                               130
tac gac atc cca gag ggc ttg cgc att gcg cgc aaa gtg ctt atc gac 547
Tyr Asp Ile Pro Glu Gly Leu Arg Ile Ala Arg Lys Val Leu Ile Asp
135                               140                               145
gtt gtg aac ctt gat ctc cca gtc ggc tgc gaa ttc ctc gaa cca aac 595
Val Val Asn Leu Asp Leu Pro Val Gly Cys Glu Phe Leu Glu Pro Asn
150                               155                               160                               165
agc cct cag tac tac gcc gac act gtc gca tgg gga gca atc ggc gct 643
Ser Pro Gln Tyr Tyr Ala Asp Thr Val Ala Trp Gly Ala Ile Gly Ala
                               170                               175                               180
cgt acc acc gaa tct cag gtg cac cgc cag ctg gct tct ggg atg tct 691
Arg Thr Thr Glu Ser Gln Val His Arg Gln Leu Ala Ser Gly Met Ser
                               185                               190                               195
atg cca att ggt ttc aag aac gga act gac gga aac atc cag gtt gca 739
Met Pro Ile Gly Phe Lys Asn Gly Thr Asp Gly Asn Ile Gln Val Ala
200                               205                               210
gtc gac gcg gta cag gct gcc cag aac cca cac ttc ttc ttc gga acc 787
Val Asp Ala Val Gln Ala Ala Gln Asn Pro His Phe Phe Phe Gly Thr
215                               220                               225

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tcc gac gac ggc gcg ctg agc gtc gtg gag acc gca ggc aac agc aac 835  
 Ser Asp Asp Gly Ala Leu Ser Val Val Glu Thr Ala Gly Asn Ser Asn  
 230 235 240 245

tcc cac atc att ttg cgc ggc ggt acc tcc ggc ccg aat cat gat gca 883  
 Ser His Ile Ile Leu Arg Gly Gly Thr Ser Gly Pro Asn His Asp Ala  
 250 255 260

gct tcg gtg gag gcc gtc gtc gag aag ctt ggt gaa aac gct cgt ctc 931  
 Ala Ser Val Glu Ala Val Val Glu Lys Leu Gly Glu Asn Ala Arg Leu  
 265 270 275

atg atc gat gct tcc cat gct aac tcc ggc aag gat cat atc cga cag 979  
 Met Ile Asp Ala Ser His Ala Asn Ser Gly Lys Asp His Ile Arg Gln  
 280 285 290

gtt gag gtt gtt cgt gaa atc gca gag cag att tct ggc ggt tct gaa  
 1027  
 Val Glu Val Val Arg Glu Ile Ala Glu Gln Ile Ser Gly Gly Ser Glu  
 295 300 305

gct gtg gct gga atc atg att gag tcc ttc ctc gtt ggt ggc gca cag  
 1075  
 Ala Val Ala Gly Ile Met Ile Glu Ser Phe Leu Val Gly Gly Ala Gln  
 310 315 320 325

aac ctt gat cct gcg aaa ttg cgc atc aat ggc ggt gaa ggc ctg gtg  
 1123  
 Asn Leu Asp Pro Ala Lys Leu Arg Ile Asn Gly Gly Glu Gly Leu Val  
 330 335 340

tac gga cag tct gtg acc gat aag tgc atc gat att gac acc acc atc  
 1171  
 Tyr Gly Gln Ser Val Thr Asp Lys Cys Ile Asp Ile Asp Thr Thr Ile  
 345 350 355

gat ttg ctc gct gag ctg gcc gca gca gta agg gaa cgc cga gca gca  
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 Ala Lys  
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<210> 458

<211> 375

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 458

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 20 25 30

Leu Pro Ser Pro Thr Asp Leu Ile Ala Ala Asn Pro Leu Thr Pro Lys

35					40					45						
Gln	Ala	Ser	Lys	Val	Glu	Gln	Asp	Arg	Gln	Asp	Ile	Ala	Asp	Ile	Phe	
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Ala	Gly	Asp	Asp	Asp	Arg	Leu	Val	Val	Val	Val	Gly	Pro	Cys	Ser	Val	
65					70					75					80	
His	Asp	Pro	Glu	Ala	Ala	Ile	Asp	Tyr	Ala	Asn	Arg	Leu	Ala	Pro	Leu	
85					90					95						
Ala	Lys	Arg	Leu	Asp	Gln	Asp	Leu	Lys	Ile	Val	Met	Arg	Val	Tyr	Phe	
100					105					110						
Glu	Lys	Pro	Arg	Thr	Ile	Val	Gly	Trp	Lys	Gly	Leu	Ile	Asn	Asp	Pro	
115					120					125						
His	Leu	Asn	Glu	Thr	Tyr	Asp	Ile	Pro	Glu	Gly	Leu	Arg	Ile	Ala	Arg	
130					135					140						
Lys	Val	Leu	Ile	Asp	Val	Val	Asn	Leu	Asp	Leu	Pro	Val	Gly	Cys	Glu	
145					150					155					160	
Phe	Leu	Glu	Pro	Asn	Ser	Pro	Gln	Tyr	Tyr	Ala	Asp	Thr	Val	Ala	Trp	
165					170					175						
Gly	Ala	Ile	Gly	Ala	Arg	Thr	Thr	Glu	Ser	Gln	Val	His	Arg	Gln	Leu	
180					185					190						
Ala	Ser	Gly	Met	Ser	Met	Pro	Ile	Gly	Phe	Lys	Asn	Gly	Thr	Asp	Gly	
195					200					205						
Asn	Ile	Gln	Val	Ala	Val	Asp	Ala	Val	Gln	Ala	Ala	Gln	Asn	Pro	His	
210					215					220						
Phe	Phe	Phe	Gly	Thr	Ser	Asp	Asp	Gly	Ala	Leu	Ser	Val	Val	Glu	Thr	
225					230					235					240	
Ala	Gly	Asn	Ser	Asn	Ser	His	Ile	Ile	Leu	Arg	Gly	Gly	Thr	Ser	Gly	
245					250					255						
Pro	Asn	His	Asp	Ala	Ala	Ser	Val	Glu	Ala	Val	Val	Glu	Lys	Leu	Gly	
260					265					270						
Glu	Asn	Ala	Arg	Leu	Met	Ile	Asp	Ala	Ser	His	Ala	Asn	Ser	Gly	Lys	
275					280					285						
Asp	His	Ile	Arg	Gln	Val	Glu	Val	Val	Arg	Glu	Ile	Ala	Glu	Gln	Ile	
290					295					300						
Ser	Gly	Gly	Ser	Glu	Ala	Val	Ala	Gly	Ile	Met	Ile	Glu	Ser	Phe	Leu	
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325					330					335						
Gly	Glu	Gly	Leu	Val	Tyr	Gly	Gln	Ser	Val	Thr	Asp	Lys	Cys	Ile	Asp	
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Ile	Asp	Thr	Thr	Ile	Asp	Leu	Leu	Ala	Glu	Leu	Ala	Ala	Ala	Val	Arg	
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<210> 459  
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<223> RXA00579

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Met Arg Val Leu Ile  
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Ile Asp Asn Tyr Asp Ser Phe Thr Phe Asn Leu Ala Thr Tyr Val Glu  
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Glu Val Thr Gly Gln Ala Pro Val Val Val Pro Asn Asp Gln Glu Ile  
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Asp Glu Met Leu Phe Asp Ala Val Ile Leu Ser Pro Gly Pro Gly His  
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Ala Gly Val Ala Ala Asp Phe Gly Ile Cys Ala Gly Val Ile Glu Arg  
55 60 65  
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Ala Arg Val Pro Ile Leu Gly Val Cys Leu Gly His Gln Gly Ile Ala  
70 75 80 85  
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Leu Ala Tyr Gly Gly Asp Val Asp Leu Ala Pro Arg Pro Val His Gly  
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Glu Val Ser Gln Ile Thr His Asp Gly Ser Gly Leu Phe Ala Gly Ile  
105 110 115  
cct gaa acg ttt gag gcg gtg cgt tat cac tcg atg gtg gca acc cgc 499  
Pro Glu Thr Phe Glu Ala Val Arg Tyr His Ser Met Val Ala Thr Arg  
120 125 130  
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Leu Pro Glu Ser Leu Lys Ala Thr Ala Thr Ser Asp Asp Gly Leu Ile  
135 140 145  
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Met Ala Leu Ala His Glu Val Leu Pro Gln Trp Gly Val Gln Phe His  
150 155 160 165



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Pro Glu Ser Ile Gly Gly Gln Phe Gly His Gln Ile Ile Lys Asn Phe	
170 175 180	
ctt aat tta gcg cgc aca tat cgc tgg caa ctc acg gag aaa act att	691
Leu Asn Leu Ala Arg Thr Tyr Arg Trp Gln Leu Thr Glu Lys Thr Ile	
185 190 195	
ccg ctc agc gtt gat tca gca gcg gtt ttt gaa aca ttc ttt gcc cat	739
Pro Leu Ser Val Asp Ser Ala Ala Val Phe Glu Thr Phe Phe Ala His	
200 205 210	
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Ser Ser His Ala Phe Trp Leu Asp Asp Ala Gln Gly Thr Ser Tyr Leu	
215 220 225	
ggg gat gcc agc ggt cct ctc gca cgc aca aaa acc cat aat gtc ggc	835
Gly Asp Ala Ser Gly Pro Leu Ala Arg Thr Lys Thr His Asn Val Gly	
230 235 240 245	
gag ggg gat ttc ttc acc tgg cta aag gag gat ctc gcc gcc aac tca	883
Glu Gly Asp Phe Phe Thr Trp Leu Lys Glu Asp Leu Ala Ala Asn Ser	
250 255 260	
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Val Ala Pro Gly Gln Gly Phe Arg Leu Gly Trp Val Gly Tyr Val Gly	
265 270 275	
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Tyr Glu Leu Lys Ala Glu Ala Gly Ala Arg Ala Ala His Thr Ser Ser	
280 285 290	
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Leu Pro Asp Ala His Leu Ile Phe Ala Asp Arg Ala Ile Ala Val Glu	
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tcg gat cag gtt cgg ttg ctg gcg ttg ggg gag cag gac gag tgg ttt	
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Ser Asp Gln Val Arg Leu Leu Ala Leu Gly Glu Gln Asp Glu Trp Phe	
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1123	
Glu Glu Thr Ile Lys Lys Leu His Asn Leu Val Ala Pro Arg Ile Pro	
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Ala Ser Gly His Leu Ala Leu Gln Val Arg Asp Ser Lys Asp Glu Tyr	
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ctc gac aaa att cgc aga gcc cag gag ctg att act cgc ggc gaa tcg	
1219	
Leu Asp Lys Ile Arg Arg Ala Gln Glu Leu Ile Thr Arg Gly Glu Ser	
360 365 370	
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1267	
Tyr Glu Ile Cys Leu Thr Thr Lys Leu Gln Gly Thr Thr Asp Val Ala	

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Gly Ala Tyr Leu Gln Leu Gly Asp Thr Ser Ile Leu Ser Ser Ser Pro 410 415 420		
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Thr Thr Val Lys Thr Ser Lys Leu Phe Asp Val Glu Thr Tyr Ala Thr 490 495 500		
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Val His Gln Leu Val Ser Thr Val Ser Ala Glu Leu Gly Pro Arg Ser 505 510 515		
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Ala Pro Lys Leu Arg Thr Met Glu Ile Ile Asp Glu Leu Glu Ala Ala 535 540 545		
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Pro Arg Gly Ile Tyr Ser Gly Gly Leu Gly Tyr Phe Ser Leu Asp Gly 550 555 560 565		
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Ala Val Asp Leu Ser Met Val Ile Arg Thr Leu Val Ile Gln Asn Asn 570 575 580		

cac gtg gag tac gga gtg ggc ggt gca ctt ctt gct ctg tct gat ccg  
 1891  
 His Val Glu Tyr Gly Val Gly Gly Ala Leu Leu Ala Leu Ser Asp Pro  
                   585                                  590                                  595

gag gct gag tgg gag gaa atc cgc gtt aaa tca cgg cct ctg ctg aat  
 1939  
 Glu Ala Glu Trp Glu Glu Ile Arg Val Lys Ser Arg Pro Leu Leu Asn  
                   600                                  605                                  610

ttg ttt ggg gtt gaa ttc cca tgacgtacct cgtgtgggac ggt  
 1983  
 Leu Phe Gly Val Glu Phe Pro  
           615                                  620

<210> 460  
 <211> 620  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 460  
 Met Arg Val Leu Ile Ile Asp Asn Tyr Asp Ser Phe Thr Phe Asn Leu  
   1                                  5                                  10                                  15

Ala Thr Tyr Val Glu Glu Val Thr Gly Gln Ala Pro Val Val Val Pro  
                   20                                  25                                  30

Asn Asp Gln Glu Ile Asp Glu Met Leu Phe Asp Ala Val Ile Leu Ser  
                   35                                  40                                  45

Pro Gly Pro Gly His Ala Gly Val Ala Ala Asp Phe Gly Ile Cys Ala  
           50                                  55                                  60

Gly Val Ile Glu Arg Ala Arg Val Pro Ile Leu Gly Val Cys Leu Gly  
   65                                  70                                  75                                  80

His Gln Gly Ile Ala Leu Ala Tyr Gly Gly Asp Val Asp Leu Ala Pro  
                   85                                  90                                  95

Arg Pro Val His Gly Glu Val Ser Gln Ile Thr His Asp Gly Ser Gly  
                   100                                  105                                  110

Leu Phe Ala Gly Ile Pro Glu Thr Phe Glu Ala Val Arg Tyr His Ser  
           115                                  120                                  125

Met Val Ala Thr Arg Leu Pro Glu Ser Leu Lys Ala Thr Ala Thr Ser  
   130                                  135                                  140

Asp Asp Gly Leu Ile Met Ala Leu Ala His Glu Val Leu Pro Gln Trp  
 145                                  150                                  155                                  160

Gly Val Gln Phe His Pro Glu Ser Ile Gly Gly Gln Phe Gly His Gln  
                   165                                  170                                  175

Ile Ile Lys Asn Phe Leu Asn Leu Ala Arg Thr Tyr Arg Trp Gln Leu  
                   180                                  185                                  190

Thr Glu Lys Thr Ile Pro Leu Ser Val Asp Ser Ala Ala Val Phe Glu  
           195                                  200                                  205

Thr	Phe	Phe	Ala	His	Ser	Ser	His	Ala	Phe	Trp	Leu	Asp	Asp	Ala	Gln
210						215					220				
Gly	Thr	Ser	Tyr	Leu	Gly	Asp	Ala	Ser	Gly	Pro	Leu	Ala	Arg	Thr	Lys
225					230					235					240
Thr	His	Asn	Val	Gly	Glu	Gly	Asp	Phe	Phe	Thr	Trp	Leu	Lys	Glu	Asp
				245					250					255	
Leu	Ala	Ala	Asn	Ser	Val	Ala	Pro	Gly	Gln	Gly	Phe	Arg	Leu	Gly	Trp
			260					265					270		
Val	Gly	Tyr	Val	Gly	Tyr	Glu	Leu	Lys	Ala	Glu	Ala	Gly	Ala	Arg	Ala
		275					280					285			
Ala	His	Thr	Ser	Ser	Leu	Pro	Asp	Ala	His	Leu	Ile	Phe	Ala	Asp	Arg
	290					295					300				
Ala	Ile	Ala	Val	Glu	Ser	Asp	Gln	Val	Arg	Leu	Leu	Ala	Leu	Gly	Glu
305					310					315					320
Gln	Asp	Glu	Trp	Phe	Glu	Glu	Thr	Ile	Lys	Lys	Leu	His	Asn	Leu	Val
				325					330					335	
Ala	Pro	Arg	Ile	Pro	Ala	Ser	Gly	His	Leu	Ala	Leu	Gln	Val	Arg	Asp
			340					345					350		
Ser	Lys	Asp	Glu	Tyr	Leu	Asp	Lys	Ile	Arg	Arg	Ala	Gln	Glu	Leu	Ile
		355					360					365			
Thr	Arg	Gly	Glu	Ser	Tyr	Glu	Ile	Cys	Leu	Thr	Thr	Lys	Leu	Gln	Gly
	370					375					380				
Thr	Thr	Asp	Val	Ala	Pro	Leu	Ala	Ala	Tyr	Leu	Ala	Leu	Arg	Gly	Ala
385					390					395					400
Asn	Pro	Thr	Ala	Tyr	Gly	Ala	Tyr	Leu	Gln	Leu	Gly	Asp	Thr	Ser	Ile
			405						410					415	
Leu	Ser	Ser	Ser	Pro	Glu	Arg	Phe	Ile	Thr	Ile	Asp	Ser	Ala	Gly	Tyr
			420					425					430		
Val	Glu	Ser	Lys	Pro	Ile	Lys	Gly	Thr	Arg	Pro	Arg	Gly	Arg	Thr	Ala
		435					440					445			
Gln	Glu	Asp	Gln	Glu	Ile	Ile	Ala	Glu	Leu	Arg	Ser	Asn	Pro	Lys	Asp
	450					455					460				
Arg	Ala	Glu	Asn	Leu	Met	Ile	Val	Asp	Leu	Val	Arg	Asn	Asp	Leu	Ala
465					470					475					480
Arg	Gly	Ala	Leu	Pro	Thr	Thr	Val	Lys	Thr	Ser	Lys	Leu	Phe	Asp	Val
				485					490					495	
Glu	Thr	Tyr	Ala	Thr	Val	His	Gln	Leu	Val	Ser	Thr	Val	Ser	Ala	Glu
			500					505					510		
Leu	Gly	Pro	Arg	Ser	Pro	Ile	Glu	Cys	Val	Arg	Ala	Ala	Phe	Pro	Gly
		515					520					525			

Gly Ser Met Thr Gly Ala Pro Lys Leu Arg Thr Met Glu Ile Ile Asp  
 530 535 540

Glu Leu Glu Ala Ala Pro Arg Gly Ile Tyr Ser Gly Gly Leu Gly Tyr  
 545 550 555 560

Phe Ser Leu Asp Gly Ala Val Asp Leu Ser Met Val Ile Arg Thr Leu  
 565 570 575

Val Ile Gln Asn Asn His Val Glu Tyr Gly Val Gly Gly Ala Leu Leu  
 580 585 590

Ala Leu Ser Asp Pro Glu Ala Glu Trp Glu Glu Ile Arg Val Lys Ser  
 595 600 605

Arg Pro Leu Leu Asn Leu Phe Gly Val Glu Phe Pro  
 610 615 620

&lt;210&gt; 461

&lt;211&gt; 747

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(724)

&lt;223&gt; RXA00958

&lt;400&gt; 461

attctaattcc tcaatctgaa gccgatgaga cgttgcacaa ggcgtatgcc gtgttgaatg 60

ccattgcgct tgctgctggt tccactttgg aggtcatccg atg aca cac gtt gtt 115  
 Met Thr His Val Val  
 1 5

ctc att gat aat cac gat tct ttt gtc tac aac ctg gtg gat gcg ttc 163  
 Leu Ile Asp Asn His Asp Ser Phe Val Tyr Asn Leu Val Asp Ala Phe  
 10 15 20

gcc gtg gcc ggt tat aag tgc acg gtg ttc cgc aat acg gtg cca gtg 211  
 Ala Val Ala Gly Tyr Lys Cys Thr Val Phe Arg Asn Thr Val Pro Val  
 25 30 35

gaa acc att ttg gca gcc aac ccg gac ctg atc tgc ctt tca cct gga 259  
 Glu Thr Ile Leu Ala Ala Asn Pro Asp Leu Ile Cys Leu Ser Pro Gly  
 40 45 50

cct ggt tac cct gcc gat gcg ggc aac atg atg gcg ctg atc gag cgc 307  
 Pro Gly Tyr Pro Ala Asp Ala Gly Asn Met Met Ala Leu Ile Glu Arg  
 55 60 65

aca ctc ggc cag att cct tta ctg ggt att tgc ctc ggc tac cag gca 355  
 Thr Leu Gly Gln Ile Pro Leu Leu Gly Ile Cys Leu Gly Tyr Gln Ala  
 70 75 80 85

ctc atc gaa tac cac ggc ggc aag gtt gag cct tgt ggc cct gtg cac 403  
 Leu Ile Glu Tyr His Gly Gly Lys Val Glu Pro Cys Gly Pro Val His  
 90 95 100

ggc acc acc gac aac atg atc ctt act gat gca ggt gtg cag agc cct 451

Gly Thr Thr Asp Asn Met Ile Leu Thr Asp Ala Gly Val Gln Ser Pro  
 105 110 115

gtt ttt gca ggt ctt gcc act gat gtt gag cct gat cat cca gaa atc 499  
 Val Phe Ala Gly Leu Ala Thr Asp Val Glu Pro Asp His Pro Glu Ile  
 120 125 130

cca ggc cgc aag gtt cca att ggc cgt tat cac tca ctg ggc tgc gtg 547  
 Pro Gly Arg Lys Val Pro Ile Gly Arg Tyr His Ser Leu Gly Cys Val  
 135 140 145

gtt gcc cca gac ggt att gaa tca cta ggt acc tgt tcc tcg gag att 595  
 Val Ala Pro Asp Gly Ile Glu Ser Leu Gly Thr Cys Ser Ser Glu Ile  
 150 155 160 165

ggt gat gtc atc atg gcg gca cgc acc acc gat gga aag gcc att ggc 643  
 Gly Asp Val Ile Met Ala Ala Arg Thr Thr Asp Gly Lys Ala Ile Gly  
 170 175 180

ctg cag ttt cac cct gag tca gtg cta agc cca acg ggt cct gtc att 691  
 Leu Gln Phe His Pro Glu Ser Val Leu Ser Pro Thr Gly Pro Val Ile  
 185 190 195

ttg tcc cgc tgt gtc gaa cag ctt ctc gcg aac taataaaaaa aggatttgat 744  
 Leu Ser Arg Cys Val Glu Gln Leu Leu Ala Asn  
 200 205

tca 747

<210> 462

<211> 208

<212> PRT

<213> Corynebacterium glutamicum

<400> 462

Met Thr His Val Val Leu Ile Asp Asn His Asp Ser Phe Val Tyr Asn  
 1 5 10 15

Leu Val Asp Ala Phe Ala Val Ala Gly Tyr Lys Cys Thr Val Phe Arg  
 20 25 30

Asn Thr Val Pro Val Glu Thr Ile Leu Ala Ala Asn Pro Asp Leu Ile  
 35 40 45

Cys Leu Ser Pro Gly Pro Gly Tyr Pro Ala Asp Ala Gly Asn Met Met  
 50 55 60

Ala Leu Ile Glu Arg Thr Leu Gly Gln Ile Pro Leu Leu Gly Ile Cys  
 65 70 75 80

Leu Gly Tyr Gln Ala Leu Ile Glu Tyr His Gly Gly Lys Val Glu Pro  
 85 90 95

Cys Gly Pro Val His Gly Thr Thr Asp Asn Met Ile Leu Thr Asp Ala  
 100 105 110

Gly Val Gln Ser Pro Val Phe Ala Gly Leu Ala Thr Asp Val Glu Pro  
 115 120 125

Asp His Pro Glu Ile Pro Gly Arg Lys Val Pro Ile Gly Arg Tyr His

130	135	140
Ser Leu Gly Cys Val Val Ala Pro Asp Gly Ile Glu Ser Leu Gly Thr		
145	150	155 160
Cys Ser Ser Glu Ile Gly Asp Val Ile Met Ala Ala Arg Thr Thr Asp		
	165	170 175
Gly Lys Ala Ile Gly Leu Gln Phe His Pro Glu Ser Val Leu Ser Pro		
	180	185 190
Thr Gly Pro Val Ile Leu Ser Arg Cys Val Glu Gln Leu Leu Ala Asn		
	195	200 205

&lt;210&gt; 463

&lt;211&gt; 469

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(469)

&lt;223&gt; RXN03007

&lt;400&gt; 463

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gaacagcttc tcgcgaacta ataaaaaaag gatttgattc atg act tct cca gca	115
Met Thr Ser Pro Ala	
1 5	

aca ctg aaa gtt ctc aac gcc tac ttg gat aac ccc act cca acc ctg	163
Thr Leu Lys Val Leu Asn Ala Tyr Leu Asp Asn Pro Thr Pro Thr Leu	
10 15 20	

gag gag gca att gag gtg ttc acc ccg ctg acc gtg ggt gaa tac gat	211
Glu Glu Ala Ile Glu Val Phe Thr Pro Leu Thr Val Gly Glu Tyr Asp	
25 30 35	

gac gtg cac atc gca gcg ctg ctt gcc acc atc cgt act cgc ggt gag	259
Asp Val His Ile Ala Ala Leu Leu Ala Thr Ile Arg Thr Arg Gly Glu	
40 45 50	

cag ttc gct gat att gcc ggc gct gcc aag gcg ttc ctc gcg gcg gct	307
Gln Phe Ala Asp Ile Ala Gly Ala Ala Lys Ala Phe Leu Ala Ala Ala	
55 60 65	

cgt ccg ttc ccg att act ggc gca ggt ttg cta gat tcc gct ggt act	355
Arg Pro Phe Pro Ile Thr Gly Ala Gly Leu Leu Asp Ser Ala Gly Thr	
70 75 80 85	

ggt ggc gac ggt gcc aac acc atc aac atc acc acc ggc gca tcc ctg	403
Gly Gly Asp Gly Ala Asn Thr Ile Asn Ile Thr Thr Gly Ala Ser Leu	
90 95 100	

atc gca gca tcc ggt gga gtg aag ctg gtt aag cac ggc aac cgt tcg	451
Ile Ala Ala Ser Gly Gly Val Lys Leu Val Lys His Gly Asn Arg Ser	

105 110 115 469

gtg agc tcc aag tcc ggc  
Val Ser Ser Lys Ser Gly  
120

<210> 464  
<211> 123  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 464  
Met Thr Ser Pro Ala Thr Leu Lys Val Leu Asn Ala Tyr Leu Asp Asn  
1 5 10 15  
Pro Thr Pro Thr Leu Glu Glu Ala Ile Glu Val Phe Thr Pro Leu Thr  
20 25 30  
Val Gly Glu Tyr Asp Asp Val His Ile Ala Ala Leu Leu Ala Thr Ile  
35 40 45  
Arg Thr Arg Gly Glu Gln Phe Ala Asp Ile Ala Gly Ala Ala Lys Ala  
50 55 60  
Phe Leu Ala Ala Ala Arg Pro Phe Pro Ile Thr Gly Ala Gly Leu Leu  
65 70 75 80  
Asp Ser Ala Gly Thr Gly Gly Asp Gly Ala Asn Thr Ile Asn Ile Thr  
85 90 95  
Thr Gly Ala Ser Leu Ile Ala Ala Ser Gly Gly Val Lys Leu Val Lys  
100 105 110  
His Gly Asn Arg Ser Val Ser Ser Lys Ser Gly  
115 120

<210> 465  
<211> 564  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(541)  
<223> RXN02918

<400> 465  
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tgattctatt attgccaaat cagaaagcag gagagacccg atg agc gaa atc cta 115  
Met Ser Glu Ile Leu  
1 5  
gaa acc tat tgg gca ccc cac ttt gga aaa acc gaa gaa gcc aca gca 163  
Glu Thr Tyr Trp Ala Pro His Phe Gly Lys Thr Glu Glu Ala Thr Ala  
10 15 20  
ctc gtt tca tac ctg gca caa gct tcc ggc gat ccc att gag gtt cac 211  
Leu Val Ser Tyr Leu Ala Gln Ala Ser Gly Asp Pro Ile Glu Val His



25								30					35					
acc	ctg	ttc	ggg	gat	tta	ggt	tta	gac	gga	ctc	tct	gga	aac	tac	acc	259		
Thr	Leu	Phe	Gly	Asp	Leu	Gly	Leu	Asp	Gly	Leu	Ser	Gly	Asn	Tyr	Thr			
		40					45					50						
gac	act	gag	att	gac	ggc	tac	ggc	gac	gca	ttc	ctg	ctg	gtt	gca	gcg	307		
Asp	Thr	Glu	Ile	Asp	Gly	Tyr	Gly	Asp	Ala	Phe	Leu	Leu	Val	Ala	Ala			
	55					60					65							
cta	tcc	gtg	ttg	atg	gct	gaa	aac	aaa	gca	aca	ggt	ggc	gtg	aat	ctg	355		
Leu	Ser	Val	Leu	Met	Ala	Glu	Asn	Lys	Ala	Thr	Gly	Gly	Val	Asn	Leu			
70					75				80						85			
ggt	gag	ctt	ggg	gga	gct	gat	aaa	tcg	atc	cgg	ctg	cat	gtt	gaa	tcc	403		
Gly	Glu	Leu	Gly	Gly	Ala	Asp	Lys	Ser	Ile	Arg	Leu	His	Val	Glu	Ser			
				90				95					100					
aag	gag	aac	acc	caa	atc	aac	acc	gca	ttg	aag	tat	ttt	gcg	ctc	tcc	451		
Lys	Glu	Asn	Thr	Gln	Ile	Asn	Thr	Ala	Leu	Lys	Tyr	Phe	Ala	Leu	Ser			
			105					110					115					
cca	gaa	gac	cac	gca	gca	gca	gat	cgc	ttc	gat	gag	gat	gac	ctg	tct	499		
Pro	Glu	Asp	His	Ala	Ala	Ala	Asp	Arg	Phe	Asp	Glu	Asp	Asp	Leu	Ser			
		120					125					130						
gag	ctt	gcc	aac	ttg	agt	gaa	gag	ctg	cgc	gga	cag	ctg	gac			541		
Glu	Leu	Ala	Asn	Leu	Ser	Glu	Glu	Leu	Arg	Gly	Gln	Leu	Asp					
	135					140					145							
taattgtctc	ccatttaagg	agt														564		

&lt;210&gt; 466

&lt;211&gt; 147

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 466

Met	Ser	Glu	Ile	Leu	Glu	Thr	Tyr	Trp	Ala	Pro	His	Phe	Gly	Lys	Thr
1				5					10					15	
Glu	Glu	Ala	Thr	Ala	Leu	Val	Ser	Tyr	Leu	Ala	Gln	Ala	Ser	Gly	Asp
			20					25					30		
Pro	Ile	Glu	Val	His	Thr	Leu	Phe	Gly	Asp	Leu	Gly	Leu	Asp	Gly	Leu
		35					40					45			
Ser	Gly	Asn	Tyr	Thr	Asp	Thr	Glu	Ile	Asp	Gly	Tyr	Gly	Asp	Ala	Phe
	50				55					60					
Leu	Leu	Val	Ala	Ala	Leu	Ser	Val	Leu	Met	Ala	Glu	Asn	Lys	Ala	Thr
65					70				75						80
Gly	Gly	Val	Asn	Leu	Gly	Glu	Leu	Gly	Gly	Ala	Asp	Lys	Ser	Ile	Arg
			85					90						95	
Leu	His	Val	Glu	Ser	Lys	Glu	Asn	Thr	Gln	Ile	Asn	Thr	Ala	Leu	Lys
			100				105						110		
Tyr	Phe	Ala	Leu	Ser	Pro	Glu	Asp	His	Ala	Ala	Ala	Asp	Arg	Phe	Asp

115	120	125	
Glu Asp Asp Leu Ser Glu Leu Ala Asn Leu Ser Glu Glu Leu Arg Gly			
130	135	140	
Gln Leu Asp			
145			
<210> 467			
<211> 735			
<212> DNA			
<213> Corynebacterium glutamicum			
<220>			
<221> CDS			
<222> (101)..(712)			
<223> RXN01116			
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acaggacggt gtctaactaa tgacttggga tcataaccaa atg gca gcc cgc gtt			115
		Met Ala Ala Arg Val	5
		1	
gcc cag gaa ctt gaa gac ggc cag tac gtc aac ctc ggc atc ggc atg			163
Ala Gln Glu Leu Glu Asp Gly Gln Tyr Val Asn Leu Gly Ile Gly Met			
10	15	20	
cct aca ctt atc ccc ggc tac ctg cct gag gga cta gag gtt atc ctt			211
Pro Thr Leu Ile Pro Gly Tyr Leu Pro Glu Gly Leu Glu Val Ile Leu			
25	30	35	
cac tcc gaa aac ggt gtg ctg ggc gtt gga cct tac cca act gaa gag			259
His Ser Glu Asn Gly Val Leu Gly Val Gly Pro Tyr Pro Thr Glu Glu			
40	45	50	
gaa ctt gat cct gag ctg atc aac gcc ggc aag gaa acc atc acg gtt			307
Glu Leu Asp Pro Glu Leu Ile Asn Ala Gly Lys Glu Thr Ile Thr Val			
55	60	65	
gca cct ggc gca tcc tac ttc tcc tct tct gat tct ttc gcc atg atc			355
Ala Pro Gly Ala Ser Tyr Phe Ser Ser Ser Asp Ser Phe Ala Met Ile			
70	75	80	85
cgc tcc aag tct gtc gac gtt gca gtc ttg ggc gtt atg gaa gtc tcc			403
Arg Ser Lys Ser Val Asp Val Ala Val Leu Gly Val Met Glu Val Ser			
90	95	100	
cag tac ggc gac ctg gcc aac tgg atg att ccc ggc aag ctg gtc aag			451
Gln Tyr Gly Asp Leu Ala Asn Trp Met Ile Pro Gly Lys Leu Val Lys			
105	110	115	
ggt atg ggt ggc gca atg gat ctg gtg cac ggc gca tcc aag atc atc			499
Gly Met Gly Gly Ala Met Asp Leu Val His Gly Ala Ser Lys Ile Ile			
120	125	130	
gcc atg acc gat cac atc acc aag aag ggc gct ccg aag atc ctt aag			547
Ala Met Thr Asp His Ile Thr Lys Lys Gly Ala Pro Lys Ile Leu Lys			
135	140	145	

gag tgt cgc ctc cca ctg act ggc gcg aag tgc gtg gac atg att gtc 595  
 Glu Cys Arg Leu Pro Leu Thr Gly Ala Lys Cys Val Asp Met Ile Val  
 150 155 160 165

acc acc cac gct gtg ttc tct gtg gac cct gaa gaa ggc ctc acg ctc 643  
 Thr Thr His Ala Val Phe Ser Val Asp Pro Glu Glu Gly Leu Thr Leu  
 170 175 180

atc gag tgc gcc gac ggt gtc acc gtt gag gaa ctc cgc gaa atc acc 691  
 Ile Glu Cys Ala Asp Gly Val Thr Val Glu Glu Leu Arg Glu Ile Thr  
 185 190 195

gaa gcc gat ttc aaa gtt gct taagcaaacg ctgcgcaatt aag 735  
 Glu Ala Asp Phe Lys Val Ala  
 200

<210> 468

<211> 204

<212> PRT

<213> Corynebacterium glutamicum

<400> 468

Met Ala Ala Arg Val Ala Gln Glu Leu Glu Asp Gly Gln Tyr Val Asn  
 1 5 10 15

Leu Gly Ile Gly Met Pro Thr Leu Ile Pro Gly Tyr Leu Pro Glu Gly  
 20 25 30

Leu Glu Val Ile Leu His Ser Glu Asn Gly Val Leu Gly Val Gly Pro  
 35 40 45

Tyr Pro Thr Glu Glu Glu Leu Asp Pro Glu Leu Ile Asn Ala Gly Lys  
 50 55 60

Glu Thr Ile Thr Val Ala Pro Gly Ala Ser Tyr Phe Ser Ser Ser Asp  
 65 70 75 80

Ser Phe Ala Met Ile Arg Ser Lys Ser Val Asp Val Ala Val Leu Gly  
 85 90 95

Val Met Glu Val Ser Gln Tyr Gly Asp Leu Ala Asn Trp Met Ile Pro  
 100 105 110

Gly Lys Leu Val Lys Gly Met Gly Gly Ala Met Asp Leu Val His Gly  
 115 120 125

Ala Ser Lys Ile Ile Ala Met Thr Asp His Ile Thr Lys Lys Gly Ala  
 130 135 140

Pro Lys Ile Leu Lys Glu Cys Arg Leu Pro Leu Thr Gly Ala Lys Cys  
 145 150 155 160

Val Asp Met Ile Val Thr Thr His Ala Val Phe Ser Val Asp Pro Glu  
 165 170 175

Glu Gly Leu Thr Leu Ile Glu Cys Ala Asp Gly Val Thr Val Glu Glu  
 180 185 190

Leu Arg Glu Ile Thr Glu Ala Asp Phe Lys Val Ala

195

200

&lt;210&gt; 469

&lt;211&gt; 876

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(853)

&lt;223&gt; RXN01115

&lt;400&gt; 469

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gccagggtct tgcagctgtc tttgaaaagg agaactaaaa atg gct att ttg cac 115  
 Met Ala Ile Leu His  
 1 5

agc gtt tcc tac gga act tcc gac aac acc ttg gtg ttc att ggc tcg 163  
 Ser Val Ser Tyr Gly Thr Ser Asp Asn Thr Leu Val Phe Ile Gly Ser  
 10 15 20

ttg ggt tcc acc acc gac atg tgg ctg cca cag ctg gat gcc ttg cat 211  
 Leu Gly Ser Thr Thr Asp Met Trp Leu Pro Gln Leu Asp Ala Leu His  
 25 30 35

aag gat ttc cgc gtc atc gct gtt gat cac cgc gga cat ggt ctg tct 259  
 Lys Asp Phe Arg Val Ile Ala Val Asp His Arg Gly His Gly Leu Ser  
 40 45 50

gaa ctc atc gaa ggc acc ccc act gtg gcg gat ctg gcg cag gat gtg 307  
 Glu Leu Ile Glu Gly Thr Pro Thr Val Ala Asp Leu Ala Gln Asp Val  
 55 60 65

ctg gat acc ctc gat gac ctg ggt gtc gga aac ttc ggc gtc atc gga 355  
 Leu Asp Thr Leu Asp Asp Leu Gly Val Gly Asn Phe Gly Val Ile Gly  
 70 75 80 85

cta tct ctc ggc gga gcg gtt gca caa tac ttg gcg gcc acc tct gat 403  
 Leu Ser Leu Gly Gly Ala Val Ala Gln Tyr Leu Ala Ala Thr Ser Asp  
 90 95 100

cgt gtc acc aag gca gca ttc atg tgt acc gct gca aaa ttc ggc gag 451  
 Arg Val Thr Lys Ala Ala Phe Met Cys Thr Ala Ala Lys Phe Gly Glu  
 105 110 115

ccc cag ggc tgg cta gat cgc gcc gca gcg tgc cgc gaa aac ggc act 499  
 Pro Gln Gly Trp Leu Asp Arg Ala Ala Ala Cys Arg Glu Asn Gly Thr  
 120 125 130

ggt tct ctg tcc gaa gct gtg atc cag cgc tgg ttc tcc ccc act tgg 547  
 Gly Ser Leu Ser Glu Ala Val Ile Gln Arg Trp Phe Ser Pro Thr Trp  
 135 140 145

ttg gag aac aac cca gcg tcc cgc gag cac ttc gaa gcc atg gtt gcc 595  
 Leu Glu Asn Asn Pro Ala Ser Arg Glu His Phe Glu Ala Met Val Ala  
 150 155 160 165

ggc acc cca tct gag ggt tac gcg ctg tgc tgc gag gcg ttg gca acc 643

Gly	Thr	Pro	Ser	Glu	Gly	Tyr	Ala	Leu	Cys	Cys	Glu	Ala	Leu	Ala	Thr		
				170					175					180			
tgg	gat	ttc	acc	gat	cgc	ctg	gga	gaa	atc	acc	gtg	cca	gtg	ctc	acc	691	
Trp	Asp	Phe	Thr	Asp	Arg	Leu	Gly	Glu	Ile	Thr	Val	Pro	Val	Leu	Thr		
			185					190					195				
atc	gca	ggt	gcc	gat	gac	ccc	tcc	act	cct	cca	gca	acc	gtg	cag	atc	739	
Ile	Ala	Gly	Ala	Asp	Asp	Pro	Ser	Thr	Pro	Pro	Ala	Thr	Val	Gln	Ile		
		200					205					210					
att	gcc	gat	ggc	gtt	ggc	ggc	gag	tcc	cgc	gca	gag	gtc	cta	agc	cca	787	
Ile	Ala	Asp	Gly	Val	Gly	Gly	Glu	Ser	Arg	Ala	Glu	Val	Leu	Ser	Pro		
	215					220					225						
gcc	gcg	cac	gta	cca	acc	gtg	gaa	cgt	cca	aac	gag	gta	aat	gaa	ctg	835	
Ala	Ala	His	Val	Pro	Thr	Val	Glu	Arg	Pro	Asn	Glu	Val	Asn	Glu	Leu		
230					235					240				245			
cta	gca	cag	cat	ttc	gct	taatgttgta	ggcatgtttca	caa								876	
Leu	Ala	Gln	His	Phe	Ala												
				250													

&lt;210&gt; 470

&lt;211&gt; 251

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 470

Met	Ala	Ile	Leu	His	Ser	Val	Ser	Tyr	Gly	Thr	Ser	Asp	Asn	Thr	Leu		
1				5					10					15			
Val	Phe	Ile	Gly	Ser	Leu	Gly	Ser	Thr	Thr	Asp	Met	Trp	Leu	Pro	Gln		
			20					25					30				
Leu	Asp	Ala	Leu	His	Lys	Asp	Phe	Arg	Val	Ile	Ala	Val	Asp	His	Arg		
		35					40					45					
Gly	His	Gly	Leu	Ser	Glu	Leu	Ile	Glu	Gly	Thr	Pro	Thr	Val	Ala	Asp		
	50					55					60						
Leu	Ala	Gln	Asp	Val	Leu	Asp	Thr	Leu	Asp	Asp	Leu	Gly	Val	Gly	Asn		
	65				70					75					80		
Phe	Gly	Val	Ile	Gly	Leu	Ser	Leu	Gly	Gly	Ala	Val	Ala	Gln	Tyr	Leu		
				85					90					95			
Ala	Ala	Thr	Ser	Asp	Arg	Val	Thr	Lys	Ala	Ala	Phe	Met	Cys	Thr	Ala		
			100					105					110				
Ala	Lys	Phe	Gly	Glu	Pro	Gln	Gly	Trp	Leu	Asp	Arg	Ala	Ala	Ala	Cys		
		115					120					125					
Arg	Glu	Asn	Gly	Thr	Gly	Ser	Leu	Ser	Glu	Ala	Val	Ile	Gln	Arg	Trp		
	130					135						140					
Phe	Ser	Pro	Thr	Trp	Leu	Glu	Asn	Asn	Pro	Ala	Ser	Arg	Glu	His	Phe		
145					150					155					160		
Glu	Ala	Met	Val	Ala	Gly	Thr	Pro	Ser	Glu	Gly	Tyr	Ala	Leu	Cys	Cys		

	165		170		175										
Glu	Ala	Leu	Ala	Thr	Trp	Asp	Phe	Thr	Asp	Arg	Leu	Gly	Glu	Ile	Thr
			180					185					190		
Val	Pro	Val	Leu	Thr	Ile	Ala	Gly	Ala	Asp	Asp	Pro	Ser	Thr	Pro	Pro
			195				200					205			
Ala	Thr	Val	Gln	Ile	Ile	Ala	Asp	Gly	Val	Gly	Gly	Glu	Ser	Arg	Ala
	210					215					220				
Glu	Val	Leu	Ser	Pro	Ala	Ala	His	Val	Pro	Thr	Val	Glu	Arg	Pro	Asn
225					230					235					240
Glu	Val	Asn	Glu	Leu	Leu	Ala	Gln	His	Phe	Ala					
				245					250						

&lt;210&gt; 471

&lt;211&gt; 1284

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1261)

&lt;223&gt; RXS00116

&lt;400&gt; 471

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tttgcgcacc	aatcaatggg	ggatcaaata	tagtagctgc	atg	agt	aat	gac	ttc		115
				Met	Ser	Asn	Asp	Phe		
				1				5		

gtc	gtt	tct	agg	ctt	aga	ccc	ttt	ggt	gaa	acg	att	ttt	gca	acc	atg	163
Val	Val	Ser	Arg	Leu	Arg	Pro	Phe	Gly	Glu	Thr	Ile	Phe	Ala	Thr	Met	
				10					15					20		

acc	cag	cga	gct	gtt	gag	gcg	ggt	gca	atc	aat	ctt	ggt	cag	ggc	ttt	211
Thr	Gln	Arg	Ala	Val	Glu	Ala	Gly	Ala	Ile	Asn	Leu	Gly	Gln	Gly	Phe	
			25				30						35			

cct	gat	gag	gat	ggt	cct	cgt	cgg	atg	tta	gag	atc	gcg	tcg	gag	cag	259
Pro	Asp	Glu	Asp	Gly	Pro	Arg	Arg	Met	Leu	Glu	Ile	Ala	Ser	Glu	Gln	
		40				45						50				

att	ctc	ggg	gga	aat	aat	cag	tat	tcg	gcg	ggg	cgt	ggg	gat	gct	tcg	307
Ile	Leu	Gly	Gly	Asn	Asn	Gln	Tyr	Ser	Ala	Gly	Arg	Gly	Asp	Ala	Ser	
	55					60					65					

ttg	agg	gca	gct	gtg	gct	cgt	gat	cat	ttg	gag	agg	ttt	gat	ctg	gag	355
Leu	Arg	Ala	Ala	Val	Ala	Arg	Asp	His	Leu	Glu	Arg	Phe	Asp	Leu	Glu	
70					75					80					85	

tac	aac	cct	gat	tcg	gag	gtg	ttg	atc	acg	gtg	ggg	gcc	act	gag	gcg	403
Tyr	Asn	Pro	Asp	Ser	Glu	Val	Leu	Ile	Thr	Val	Gly	Ala	Thr	Glu	Ala	
				90					95					100		

att	acg	gcg	act	gtg	ttg	ggt	ttg	gtg	gag	cct	ggg	gat	gaa	gtg	atc	451
Ile	Thr	Ala	Thr	Val	Leu	Gly	Leu	Val	Glu	Pro	Gly	Asp	Glu	Val	Ile	

105						110						115						
gtt	ttg	gaa	ccg	tat	tac	gat	gcg	tat	gcg	gcg	gct	att	gcg	ttg	gcg	499		
Val	Leu	Glu	Pro	Tyr	Tyr	Asp	Ala	Tyr	Ala	Ala	Ala	Ile	Ala	Leu	Ala			
		120					125					130						
ggg	gcg	acg	cgg	gtg	gcg	gtt	cct	ttg	cag	gag	gtg	gag	aac	tcg	tgg	547		
Gly	Ala	Thr	Arg	Val	Ala	Val	Pro	Leu	Gln	Glu	Val	Glu	Asn	Ser	Trp			
	135					140					145							
gat	gtg	gat	gtc	gat	aag	ttg	cat	gcg	gcg	gtg	act	aag	aag	acg	cgg	595		
Asp	Val	Asp	Val	Asp	Lys	Leu	His	Ala	Ala	Val	Thr	Lys	Lys	Thr	Arg			
150					155					160					165			
atg	att	atc	gtt	aat	tcg	ccg	cat	aat	ccg	acg	ggt	tcg	gtg	ttt	tct	643		
Met	Ile	Ile	Val	Asn	Ser	Pro	His	Asn	Pro	Thr	Gly	Ser	Val	Phe	Ser			
				170					175					180				
aag	aag	gcg	ttg	aag	cag	ttg	gcg	ggt	gtt	gct	cgt	gcg	tat	gac	ttg	691		
Lys	Lys	Ala	Leu	Lys	Gln	Leu	Ala	Gly	Val	Ala	Arg	Ala	Tyr	Asp	Leu			
			185					190					195					
ttg	gtg	ttg	tca	gat	gag	gtg	tat	gag	cat	ctt	gtt	ttt	gat	gat	cag	739		
Leu	Val	Leu	Ser	Asp	Glu	Val	Tyr	Glu	His	Leu	Val	Phe	Asp	Asp	Gln			
		200					205					210						
aag	cat	gtg	agt	gtc	gcg	aag	ctg	ccc	ggt	atg	tgg	gat	cgc	acg	gtg	787		
Lys	His	Val	Ser	Val	Ala	Lys	Leu	Pro	Gly	Met	Trp	Asp	Arg	Thr	Val			
	215					220					225							
acg	gtg	tcg	tcg	gcg	gcg	aaa	acg	ttc	aat	gtg	act	ggt	tgg	aag	acg	835		
Thr	Val	Ser	Ser	Ala	Ala	Lys	Thr	Phe	Asn	Val	Thr	Gly	Trp	Lys	Thr			
230					235					240					245			
ggg	tgg	gcg	ttg	gca	ccg	gag	ccg	ttg	ttg	gag	gcg	gtg	ttg	aag	gcg	883		
Gly	Trp	Ala	Leu	Ala	Pro	Glu	Pro	Leu	Leu	Glu	Ala	Val	Leu	Lys	Ala			
				250				255					260					
aag	cag	ttt	atg	tct	tat	gtg	ggg	gct	aca	cct	ttt	cag	ccg	gct	gtg	931		
Lys	Gln	Phe	Met	Ser	Tyr	Val	Gly	Ala	Thr	Pro	Phe	Gln	Pro	Ala	Val			
			265					270					275					
gcg	cat	gcg	att	gaa	cat	gag	cag	aag	tgg	gtg	tca	aag	atg	tct	aag	979		
Ala	His	Ala	Ile	Glu	His	Glu	Gln	Lys	Trp	Val	Ser	Lys	Met	Ser	Lys			
			280				285					290						
ggg	ctt	gag	ctc	aag	cgg	gat	att	ttg	cgt	act	gcg	tta	gat	aag	gcg			
1027																		
Gly	Leu	Glu	Leu	Lys	Arg	Asp	Ile	Leu	Arg	Thr	Ala	Leu	Asp	Lys	Ala			
	295					300					305							
ggg	ctg	aag	act	cat	gac	agt	atg	ggc	acg	tat	ttc	atc	gtt	gcg	gat			
1075																		
Gly	Leu	Lys	Thr	His	Asp	Ser	Met	Gly	Thr	Tyr	Phe	Ile	Val	Ala	Asp			
310					315					320					325			
att	ggg	gat	cgt	gat	ggt	gcg	gag	ttc	tgt	ttt	gag	ttg	att	gag	aag			
1123																		
Ile	Gly	Asp	Arg	Asp	Gly	Ala	Glu	Phe	Cys	Phe	Glu	Leu	Ile	Glu	Lys			
				330					335					340				

gtt ggg gtg gcg gcg att ccg gtg cag gcg ttt gtg gat cat ccg aag  
 1171  
 Val Gly Val Ala Ala Ile Pro Val Gln Ala Phe Val Asp His Pro Lys  
                   345                  350                  355

aag tgg tcg tcg aag gtt cgt ttt gcg ttt tgc aaa aaa gaa gag acg  
 1219  
 Lys Trp Ser Ser Lys Val Arg Phe Ala Phe Cys Lys Lys Glu Glu Thr  
           360                  365                  370

ctc cgc gaa gct gcg gag cgt ctc aag ggg att aag aaa cta  
 1261  
 Leu Arg Glu Ala Ala Glu Arg Leu Lys Gly Ile Lys Lys Leu  
           375                  380                  385

tagtttgaac aggttggttg ggg  
 1284

<210> 472  
 <211> 387  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 472  
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   1                  5                  10                  15  
 Ile Phe Ala Thr Met Thr Gln Arg Ala Val Glu Ala Gly Ala Ile Asn  
                   20                  25                  30  
 Leu Gly Gln Gly Phe Pro Asp Glu Asp Gly Pro Arg Arg Met Leu Glu  
           35                  40                  45  
 Ile Ala Ser Glu Gln Ile Leu Gly Gly Asn Asn Gln Tyr Ser Ala Gly  
           50                  55                  60  
 Arg Gly Asp Ala Ser Leu Arg Ala Ala Val Ala Arg Asp His Leu Glu  
   65                  70                  75                  80  
 Arg Phe Asp Leu Glu Tyr Asn Pro Asp Ser Glu Val Leu Ile Thr Val  
                   85                  90                  95  
 Gly Ala Thr Glu Ala Ile Thr Ala Thr Val Leu Gly Leu Val Glu Pro  
           100                  105                  110  
 Gly Asp Glu Val Ile Val Leu Glu Pro Tyr Tyr Asp Ala Tyr Ala Ala  
           115                  120                  125  
 Ala Ile Ala Leu Ala Gly Ala Thr Arg Val Ala Val Pro Leu Gln Glu  
           130                  135                  140  
 Val Glu Asn Ser Trp Asp Val Asp Val Asp Lys Leu His Ala Ala Val  
   145                  150                  155                  160  
 Thr Lys Lys Thr Arg Met Ile Ile Val Asn Ser Pro His Asn Pro Thr  
                   165                  170                  175  
 Gly Ser Val Phe Ser Lys Lys Ala Leu Lys Gln Leu Ala Gly Val Ala  
                   180                  185                  190



Arg Ala Tyr Asp Leu Leu Val Leu Ser Asp Glu Val Tyr Glu His Leu  
 195 200 205  
 Val Phe Asp Asp Gln Lys His Val Ser Val Ala Lys Leu Pro Gly Met  
 210 215 220  
 Trp Asp Arg Thr Val Thr Val Ser Ser Ala Ala Lys Thr Phe Asn Val  
 225 230 235 240  
 Thr Gly Trp Lys Thr Gly Trp Ala Leu Ala Pro Glu Pro Leu Leu Glu  
 245 250 255  
 Ala Val Leu Lys Ala Lys Gln Phe Met Ser Tyr Val Gly Ala Thr Pro  
 260 265 270  
 Phe Gln Pro Ala Val Ala His Ala Ile Glu His Glu Gln Lys Trp Val  
 275 280 285  
 Ser Lys Met Ser Lys Gly Leu Glu Leu Lys Arg Asp Ile Leu Arg Thr  
 290 295 300  
 Ala Leu Asp Lys Ala Gly Leu Lys Thr His Asp Ser Met Gly Thr Tyr  
 305 310 315 320  
 Phe Ile Val Ala Asp Ile Gly Asp Arg Asp Gly Ala Glu Phe Cys Phe  
 325 330 335  
 Glu Leu Ile Glu Lys Val Gly Val Ala Ala Ile Pro Val Gln Ala Phe  
 340 345 350  
 Val Asp His Pro Lys Lys Trp Ser Ser Lys Val Arg Phe Ala Phe Cys  
 355 360 365  
 Lys Lys Glu Glu Thr Leu Arg Glu Ala Ala Glu Arg Leu Lys Gly Ile  
 370 375 380  
 Lys Lys Leu  
 385

&lt;210&gt; 473

&lt;211&gt; 607

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(607)

&lt;223&gt; FRXA00116

&lt;400&gt; 473

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 ttctaggctt agaccctttg gtgaaacgat ttttgcaacc atg acc cag cga gct 115  
 Met Thr Gln Arg Ala  
 1 5

 gtt gag gcg ggt gca atc aat ctt ggt cag ggc ttt cct gat gag gat 163  
 Val Glu Ala Gly Ala Ile Asn Leu Gly Gln Gly Phe Pro Asp Glu Asp  
 10 15 20

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ggt cct cgt cgg atg tta gag atc gcg tcg gag cag att ctc ggg gga 211
Gly Pro Arg Arg Met Leu Glu Ile Ala Ser Glu Gln Ile Leu Gly Gly
      25                      30                      35

aat aat cag tat tcg gcg ggg cgt ggg gat gct tcg ttg agg gca gct 259
Asn Asn Gln Tyr Ser Ala Gly Arg Gly Asp Ala Ser Leu Arg Ala Ala
      40                      45                      50

gtg gct cgt gat cat ttg gag agg ttt gat ctg gag tac aac cct gat 307
Val Ala Arg Asp His Leu Glu Arg Phe Asp Leu Glu Tyr Asn Pro Asp
      55                      60                      65

tcg gag gtg ttg atc acg gtg ggg gcc act gag gcg att acg gcg act 355
Ser Glu Val Leu Ile Thr Val Gly Ala Thr Glu Ala Ile Thr Ala Thr
      70                      75                      80                      85

gtg ttg ggt ttg gtg gag cct ggg gat gaa gtg atc gtt ttg gaa ccg 403
Val Leu Gly Leu Val Glu Pro Gly Asp Glu Val Ile Val Leu Glu Pro
      90                      95                      100

tat tac gat gcg tat gcg gcg gct att gcg ttg gcg ggg gcg acg cgg 451
Tyr Tyr Asp Ala Tyr Ala Ala Ala Ile Ala Leu Ala Gly Ala Thr Arg
      105                      110                      115

gtg gcg gtt cct ttg cag gag gtg gag aac tcg tgg gat gtg gat gtc 499
Val Ala Val Pro Leu Gln Glu Val Glu Asn Ser Trp Asp Val Asp Val
      120                      125                      130

gat aag ttg cat gcg gcg gtg act aag aag acg cgg atg att atc gtt 547
Asp Lys Leu His Ala Ala Val Thr Lys Lys Thr Arg Met Ile Ile Val
      135                      140                      145

aat tcg ccg cat aat ccg acg ggt tcg gtg ttt tct aag aag gcg ttg 595
Asn Ser Pro His Asn Pro Thr Gly Ser Val Phe Ser Lys Lys Ala Leu
      150                      155                      160                      165

aag cag ttg gcg
Lys Gln Leu Ala 607

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&lt;210&gt; 474

&lt;211&gt; 169

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 474

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Met Thr Gln Arg Ala Val Glu Ala Gly Ala Ile Asn Leu Gly Gln Gly
  1                      5                      10                      15

Phe Pro Asp Glu Asp Gly Pro Arg Arg Met Leu Glu Ile Ala Ser Glu
      20                      25                      30

Gln Ile Leu Gly Gly Asn Asn Gln Tyr Ser Ala Gly Arg Gly Asp Ala
      35                      40                      45

Ser Leu Arg Ala Ala Val Ala Arg Asp His Leu Glu Arg Phe Asp Leu
      50                      55                      60

Glu Tyr Asn Pro Asp Ser Glu Val Leu Ile Thr Val Gly Ala Thr Glu
      65                      70                      75                      80

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Ala Ile Thr Ala Thr Val Leu Gly Leu Val Glu Pro Gly Asp Glu Val  
85 90 95

Ile Val Leu Glu Pro Tyr Tyr Asp Ala Tyr Ala Ala Ala Ile Ala Leu  
100 105 110

Ala Gly Ala Thr Arg Val Ala Val Pro Leu Gln Glu Val Glu Asn Ser  
115 120 125

Trp Asp Val Asp Val Asp Lys Leu His Ala Ala Val Thr Lys Lys Thr  
130 135 140

Arg Met Ile Ile Val Asn Ser Pro His Asn Pro Thr Gly Ser Val Phe  
145 150 155 160

Ser Lys Lys Ala Leu Lys Gln Leu Ala  
165

**<210> 475**

**<211> 843**

**<212> DNA**

<213> Corynebacterium glutamicum

**<220>**

**<221> CDS**

**<222> (101) . . (820)**

<223> RXS00391

<400> 475

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Leu Leu Arg Asp Ser  
1 5

caa cga gtt ggc ctc gcc atc gat cct tcg atc gct ttg gtg atg gcc 163  
Gln Arg Val Gly Leu Ala Ile Asp Pro Ser Ile Ala Leu Val Met Ala  
10 15 20

act tct ggt tct aca ggt acc ccg aag ggc gct cag ctc act ccg ttg 211  
Thr Ser Gly Ser Thr Gly Thr Pro Lys Gly Ala Gln Leu Thr Pro Leu  
25 30 35

aat ttg gtg agt tcc gcc gat gct acg cat cag ttt tta ggt ggc gaa 259  
Asn Leu Val Ser Ser Ala Asp Ala Thr His Gln Phe Leu Gly Gly Glu  
40 45 50

ggc cag tgg ttg ctt gcc atg cca gca cac cac att gca ggc atg cag 307  
Gly Gln Trp Leu Leu Ala Met Pro Ala His His Ile Ala Gly Met Gln  
55 60 65

gtg	ctt	ctt	cga	agc	ctc	att	gct	gga	gtt	gag	cca	cta	gct	att	gat	355
Val	Leu	Leu	Arg	Ser	Leu	Ile	Ala	Gly	Val	Glu	Pro	Leu	Ala	Ile	Asp	
70					75					80					85	

ctc agc aca ggt ttt cac att gac gct ttc gca ggc gcc gcg gca gaa 403  
Leu Ser Thr Gly Phe His Ile Asp Ala Phe Ala Gly Ala Ala Ala Glu  
90 95 100

ctg aaa aat acc ggc gac cgc gtc tat aca tcc ttg act cca atg cag 451  
 Leu Lys Asn Thr Gly Asp Arg Val Tyr Thr Ser Leu Thr Pro Met Gln  
 105 110 115  
  
 tta ctt aaa gca atg gac tcc ttg caa ggc att gaa gcc ctg aaa ctt 499  
 Leu Leu Lys Ala Met Asp Ser Leu Gln Gly Ile Glu Ala Leu Lys Leu  
 120 125 130  
  
 ttt gat gtc att ctt gtt ggc ggt gct gca ttg tct aag cag gcc cga 547  
 Phe Asp Val Ile Leu Val Gly Gly Ala Ala Leu Ser Lys Gln Ala Arg  
 135 140 145  
  
 att tct gcg gag cag cta gac atc aac att gtc acc acc tac ggc tcc 595  
 Ile Ser Ala Glu Gln Leu Asp Ile Asn Ile Val Thr Thr Tyr Gly Ser  
 150 155 160 165  
  
 tca gag act tca ggt ggc tgc gtt tat gat ggc aag ccc att ccc ggc 643  
 Ser Glu Thr Ser Gly Gly Cys Val Tyr Asp Gly Lys Pro Ile Pro Gly  
 170 175 180  
  
 gcg aaa gtc cgt att tcg gat gag cgc att gag ttg ggt ggc ccg atg 691  
 Ala Lys Val Arg Ile Ser Asp Glu Arg Ile Glu Leu Gly Gly Pro Met  
 185 190 195  
  
 att gcg cag ggc tac aga aat gca cct gaa cat ccg gat ttc gcc aac 739  
 Ile Ala Gln Gly Tyr Arg Asn Ala Pro Glu His Pro Asp Phe Ala Asn  
 200 205 210  
  
 gag ggt tgg ttt acc acc tct gat tca ggt gaa ctc cac gac ggg att 787  
 Glu Gly Trp Phe Thr Thr Ser Asp Ser Gly Glu Leu His Asp Gly Ile  
 215 220 225  
  
 ctc acc gtg act ggt cgc gtg gat acc cgt cat tgattccggt ggattgaagt 840  
 Leu Thr Val Thr Gly Arg Val Asp Thr Arg His  
 230 235 240  
  
 tgc 843

&lt;210&gt; 476

&lt;211&gt; 240

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 476

Leu Leu Arg Asp Ser Gln Arg Val Gly Leu Ala Ile Asp Pro Ser Ile  
 1 5 10 15  
  
 Ala Leu Val Met Ala Thr Ser Gly Ser Thr Gly Thr Pro Lys Gly Ala  
 20 25 30  
  
 Gln Leu Thr Pro Leu Asn Leu Val Ser Ser Ala Asp Ala Thr His Gln  
 35 40 45  
  
 Phe Leu Gly Gly Glu Gly Gln Trp Leu Leu Ala Met Pro Ala His His  
 50 55 60  
  
 Ile Ala Gly Met Gln Val Leu Leu Arg Ser Leu Ile Ala Gly Val Glu  
 65 70 75 80  
  
 Pro Leu Ala Ile Asp Leu Ser Thr Gly Phe His Ile Asp Ala Phe Ala

85								90				95			
Gly	Ala	Ala	Ala	Glu	Leu	Lys	Asn	Thr	Gly	Asp	Arg	Val	Tyr	Thr	Ser
100								105				110			
Leu	Thr	Pro	Met	Gln	Leu	Leu	Lys	Ala	Met	Asp	Ser	Leu	Gln	Gly	Ile
115								120				125			
Glu	Ala	Leu	Lys	Leu	Phe	Asp	Val	Ile	Leu	Val	Gly	Gly	Ala	Ala	Leu
130								135				140			
Ser	Lys	Gln	Ala	Arg	Ile	Ser	Ala	Glu	Gln	Leu	Asp	Ile	Asn	Ile	Val
145								150				155			
Thr	Thr	Tyr	Gly	Ser	Ser	Glu	Thr	Ser	Gly	Gly	Cys	Val	Tyr	Asp	Gly
165								170				175			
Lys	Pro	Ile	Pro	Gly	Ala	Lys	Val	Arg	Ile	Ser	Asp	Glu	Arg	Ile	Glu
180								185				190			
Leu	Gly	Gly	Pro	Met	Ile	Ala	Gln	Gly	Tyr	Arg	Asn	Ala	Pro	Glu	His
195								200				205			
Pro	Asp	Phe	Ala	Asn	Glu	Gly	Trp	Phe	Thr	Thr	Ser	Asp	Ser	Gly	Glu
210								215				220			
Leu	His	Asp	Gly	Ile	Leu	Thr	Val	Thr	Gly	Arg	Val	Asp	Thr	Arg	His
225								230				235			

&lt;210&gt; 477

&lt;211&gt; 1017

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(994)

&lt;223&gt; RXS00393

&lt;400&gt; 477

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aattgcgcga	tcgagtatgt	gatggggaaa	gatagagggt	atg	tct	cac	acg	gaa	115
				Met	Ser	His	Thr	Glu	
				1				5	

ccc	cag	ccg	aat	tct	gta	act	ttg	tcc	gat	tgg	att	caa	ggc	gca	cgc	163
Pro	Gln	Pro	Asn	Ser	Val	Thr	Leu	Ser	Asp	Trp	Ile	Gln	Gly	Ala	Arg	
				10					15					20		

ccg	cgt	acc	tgg	gca	aat	gcg	ttc	gcg	cct	gtc	att	gcc	ggg	tca	ggg	211
Pro	Arg	Thr	Trp	Ala	Asn	Ala	Phe	Ala	Pro	Val	Ile	Ala	Gly	Ser	Gly	
			25				30						35			

gtc	gcc	gct	ttt	cat	gat	ggg	ttt	gtg	tgg	tgg	aag	gcc	ttg	ctg	gcg	259
Val	Ala	Ala	Phe	His	Asp	Gly	Phe	Val	Trp	Trp	Lys	Ala	Leu	Leu	Ala	
			40				45					50				

ctt gtc gtg gcg tgg gct ttg atc atc ggt gtg aat tac gcc aat gat	307
Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val Asn Tyr Ala Asn Asp	
55 60 65	
tac tct gat ggc att cgt ggc acc gat gaa gac cgc acc ggt cct ctg	355
Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp Arg Thr Gly Pro Leu	
70 75 80 85	
cga ctc act ggt tct ggg ttg gct gag ccg aag aaa gtg aaa gct gcg	403
Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys Lys Val Lys Ala Ala	
90 95 100	
gcg ttt att tct ttc ggt atc gca ggt gtc gcc ggc acc gcg ctg agc	451
Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala Gly Thr Ala Leu Ser	
105 110 115	
ctg ttg agc gcg tgg tgg ctg atc ctc atc ggc atc ctg tgt gtg ctg	499
Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly Ile Leu Cys Val Leu	
120 125 130	
ggc gcg tgg ttc tac acc ggc ggt aaa aat cct tat ggt tac cgc ggc	547
Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro Tyr Gly Tyr Arg Gly	
135 140 145	
ctc ggc gag att gct gtg ttc atc ttc ttc ggc ctc gtc gcg gtc atg	595
Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly Leu Val Ala Val Met	
150 155 160 165	
gga acg cag ttc acc caa acc ggt tcc gtc agc tgg gcc ggt ttg gcc	643
Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser Trp Ala Gly Leu Ala	
170 175 180	
gcc gca gtt ggc gtg ggg tcg atg tct gct ggc gtg aac ttg gcc aac	691
Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly Val Asn Leu Ala Asn	
185 190 195	
aat att cgc gat att cca acc gat agc aag acc gga aaa att acc ctc	739
Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr Gly Lys Ile Thr Leu	
200 205 210	
gcg gtc cgc ctg ggc gat gcg ggt gct cgt aag ctg ttc ctc gcg ctg	787
Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys Leu Phe Leu Ala Leu	
215 220 225	
att tcc acg ccg ttc atc atg tcc atc tgc ctg gcg ttt gtc gcc tgg	835
Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu Ala Phe Val Ala Trp	
230 235 240 245	
cca gcg ctg atc gcg atc atc gtt ttc ccg ctg gca ctg aaa gcc gca	883
Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu Ala Leu Lys Ala Ala	
250 255 260	
ggg ccg atc cgc aac aac gcc acc ggc aag gat ctc atc ccc gtc atc	931
Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp Leu Ile Pro Val Ile	
265 270 275	
ggc tca aca ggg cgc gcc atg gcg ttg tgg gcc gtg ctc acg ggc ctg	979
Gly Ser Thr Gly Arg Ala Met Ala Leu Trp Ala Val Leu Thr Gly Leu	
280 285 290	

gca tta gcg ttt agc taaaacgctt ttcgacgctc ccc  
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 Ala Leu Ala Phe Ser  
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<210> 478

<211> 298

<212> PRT

<213> Corynebacterium glutamicum

<400> 478

Met Ser His Thr Glu Pro Gln Pro Asn Ser Val Thr Leu Ser Asp Trp  
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Ile Gln Gly Ala Arg Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val  
 20 25 30

Ile Ala Gly Ser Gly Val Ala Ala Phe His Asp Gly Phe Val Trp Trp  
 35 40 45

Lys Ala Leu Leu Ala Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val  
 50 55 60

Asn Tyr Ala Asn Asp Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp  
 65 70 75 80

Arg Thr Gly Pro Leu Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys  
 85 90 95

Lys Val Lys Ala Ala Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala  
 100 105 110

Gly Thr Ala Leu Ser Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly  
 115 120 125

Ile Leu Cys Val Leu Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro  
 130 135 140

Tyr Gly Tyr Arg Gly Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly  
 145 150 155 160

Leu Val Ala Val Met Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser  
 165 170 175

Trp Ala Gly Leu Ala Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly  
 180 185 190

Val Asn Leu Ala Asn Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr  
 195 200 205

Gly Lys Ile Thr Leu Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys  
 210 215 220

Leu Phe Leu Ala Leu Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu  
 225 230 235 240

Ala Phe Val Ala Trp Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu  
 245 250 255

Ala Leu Lys Ala Ala Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp

260								265				270			
Leu	Ile	Pro	Val	Ile	Gly	Ser	Thr	Gly	Arg	Ala	Met	Ala	Leu	Trp	Ala
		275					280					285			
.															
Val	Leu	Thr	Gly	Leu	Ala	Leu	Ala	Phe	Ser						
	290					295									

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<210> 479
<211> 1005
<212> DNA
<213> Corynebacterium glutamicum
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<221> CDS
<222> (101)..(982)
<223> FRXA00393
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aattgcgcgga tcgagtatgt gatggggaaa gatagagggtt atg tct cac acg gaa 115  
Met Ser His Thr Glu  
1 5

ccc cag ccg aat tct gta act ttg tcc gat tgg att caa ggc gca cgc 163  
Pro Gln Pro Asn Ser Val Thr Leu Ser Asp Trp Ile Gln Gly Ala Arg  
10 15 20

ccg cgt acc tgg gca aat gcg ttc gcg cct gtc att gcc ggt tca ggt 211  
Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val Ile Ala Gly Ser Gly  
25 30 35

gtc gcc gct ttt cat gat ggt ttt gtg tgg tgg aag gcc ttg ctg gcg 259  
Val Ala Ala Phe His Asp Gly Phe Val Trp Trp Lys Ala Leu Leu Ala  
40 45 50

ctt gtc gtg gcg tgg gct ttg atc atc ggt gtg aat tac gcc aat gat 307  
Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val Asn Tyr Ala Asn Asp  
55 60 65

tac tct gat ggc att cgt ggc acc gat gaa gac cgc acc ggt cct ctg 355  
Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp Arg Thr Gly Pro Leu  
70 75 80 85

cga ctc act ggt tct ggg ttg gct gag ccg aag aaa gtg aaa gct gcg 403  
Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys Lys Val Lys Ala Ala  
90 95 100

gcg ttt att tct ttc ggt atc gca ggt gtc gcc ggc acc gcg ctg agc 451  
Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala Gly Thr Ala Leu Ser  
105 110 115

ctg ttg agc gcg tgg tgg ctg atc ctc atc ggc atc ctg tgt gtg ctg 499  
Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly Ile Leu Cys Val Leu  
120 125 130

ggc gcg tgg ttc tac acc ggc ggt aaa aat cct tat ggt tac cgc ggg 547  
Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro Tyr Gly Tyr Arg Gly  
135 140 145



ctc ggc gag att gct gtg ttc atc ttc ttc ggc ctc gtc gcg gtc atg 595  
 Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly Leu Val Ala Val Met 165  
 150 155 160

gga acg cag ttc acc caa acc ggt tcc gtc agc tgg gcc ggt ttg gcc 643  
 Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser Trp Ala Gly Leu Ala 180  
 170 175

gcc gca gtt ggc gtg ggg tcg atg tct gct ggc gtg aac ttg gcc aac 691  
 Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly Val Asn Leu Ala Asn 195  
 185 190

aat att cgc gat att cca acc gat agc aag acc gga aaa att acc ctc 739  
 Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr Gly Lys Ile Thr Leu 210  
 200 205

gcg gtc cgc ctg ggc gat gcg ggt gct cgt aag ctg ttc ctc gcg ctg 787  
 Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys Leu Phe Leu Ala Leu 225  
 215 220

att tcc acg ccg ttc atc atg tcc atc tgc ctg gcg ttt gtc gcc tgg 835  
 Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu Ala Phe Val Ala Trp 245  
 230 235 240

cca gcg ctg atc gcg atc atc gtt ttc ccg ctg gca ctg aaa gcc gca 883  
 Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu Ala Leu Lys Ala Ala 260  
 250 255

ggg ccg atc cgc aac aac gcc acc ggc aag gat ctc atc ccg tca tcg 931  
 Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp Leu Ile Pro Ser Ser 275  
 265 270

gct caa cag ggc gcg cca tgg cgt tgt ggg ccg tgc tca cgg gcc tgg 979  
 Ala Gln Gln Gly Ala Pro Trp Arg Cys Gly Pro Cys Ser Arg Ala Trp 290  
 280 285

cat tagcggttag ctaaaacgct ttt  
 1005  
 His

<210> 480  
 <211> 294  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 480  
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 20 25 30  
 Ile Ala Gly Ser Gly Val Ala Ala Phe His Asp Gly Phe Val Trp Trp  
 35 40 45  
 Lys Ala Leu Leu Ala Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val  
 50 55 60

Asn Tyr Ala Asn Asp Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp  
 65 70 75 80  
 Arg Thr Gly Pro Leu Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys  
 85 90 95  
 Lys Val Lys Ala Ala Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala  
 100 105 110  
 Gly Thr Ala Leu Ser Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly  
 115 120 125  
 Ile Leu Cys Val Leu Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro  
 130 135 140  
 Tyr Gly Tyr Arg Gly Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly  
 145 150 155 160  
 Leu Val Ala Val Met Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser  
 165 170 175  
 Trp Ala Gly Leu Ala Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly  
 180 185 190  
 Val Asn Leu Ala Asn Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr  
 195 200 205  
 Gly Lys Ile Thr Leu Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys  
 210 215 220  
 Leu Phe Leu Ala Leu Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu  
 225 230 235 240  
 Ala Phe Val Ala Trp Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu  
 245 250 255  
 Ala Leu Lys Ala Ala Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp  
 260 265 270  
 Leu Ile Pro Ser Ser Ala Gln Gln Gly Ala Pro Trp Arg Cys Gly Pro  
 275 280 285  
 Cys Ser Arg Ala Trp His  
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<210> 481  
 <211> 987  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(964)  
 <223> RXS00446

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 ggtgacggag gctacttggg gggctaatacg gtaccgggat atg ggt gcg gtt gag 115  
 Met Gly Ala Val Glu

ctc	cgt	gag	gct	ctt	gca	gag	cat	tta	gag	gtt	gag	ttt	gac	cag	gtc	163
Leu	Arg	Glu	Ala	Leu	Ala	Glu	His	Leu	Glu	Val	Glu	Phe	Asp	Gln	Val	
				10					15					20		
acg	gta	ggc	tgc	ggc	tcg	tct	gcg	ctg	tgt	caa	cag	ctg	gtt	cag	gca	211
Thr	Val	Gly	Cys	Gly	Ser	Ser	Ala	Leu	Cys	Gln	Gln	Leu	Val	Gln	Ala	
				25					30					35		
acg	tgc	gct	cag	ggc	gat	gag	gtc	att	ttt	cca	tgg	cgc	agc	ttt	gag	259
Thr	Cys	Ala	Gln	Gly	Asp	Glu	Val	Ile	Phe	Pro	Trp	Arg	Ser	Phe	Glu	
				40					45					50		
gct	tat	cca	att	ttc	gcg	cag	gtc	gcg	ggc	gcc	act	cct	gtt	gcc	att	307
Ala	Tyr	Pro	Ile	Phe	Ala	Gln	Val	Ala	Gly	Ala	Thr	Pro	Val	Ala	Ile	
				55					60					65		
ccg	ctg	act	gct	gat	cag	aat	cat	gat	ctt	gat	gcg	atg	gca	gcc	gcg	355
Pro	Leu	Thr	Ala	Asp	Gln	Asn	His	Asp	Leu	Asp	Ala	Met	Ala	Ala	Ala	
				70					75					80		
atc	act	gat	aag	acc	cgc	ctc	att	ttc	atc	tgc	aac	ccc	aac	aat	cct	403
Ile	Thr	Asp	Lys	Thr	Arg	Leu	Ile	Phe	Ile	Cys	Asn	Pro	Asn	Asn	Pro	
				90					95					100		
tcg	ggc	acc	acc	atc	acc	cag	gcg	cag	ttt	gat	aat	ttc	atg	gaa	aag	451
Ser	Gly	Thr	Thr	Ile	Thr	Gln	Ala	Gln	Phe	Asp	Asn	Phe	Met	Glu	Lys	
				105					110					115		
gtt	cca	aac	gat	gtc	gtt	gtt	ggg	ctg	gat	gag	gct	tat	ttt	gag	ttc	499
Val	Pro	Asn	Asp	Val	Val	Val	Gly	Leu	Asp	Glu	Ala	Tyr	Phe	Glu	Phe	
				120					125					130		
aac	cgc	gcg	gac	gac	acc	cca	gtt	gcc	act	gag	gaa	atc	cac	cgc	cac	547
Asn	Arg	Ala	Asp	Asp	Thr	Pro	Val	Ala	Thr	Glu	Glu	Ile	His	Arg	His	
				135					140					145		
gac	aac	gtg	att	ggc	ttg	cgc	acg	ttc	tcc	aag	gcg	tat	ggc	ctg	gcg	595
Asp	Asn	Val	Ile	Gly	Leu	Arg	Thr	Phe	Ser	Lys	Ala	Tyr	Gly	Leu	Ala	
				150					155					160		
ggc	ttg	cgt	gtt	ggc	tac	gcc	ttc	gga	aac	gca	gag	atc	atc	gca	gcg	643
Gly	Leu	Arg	Val	Gly	Tyr	Ala	Phe	Gly	Asn	Ala	Glu	Ile	Ile	Ala	Ala	
				170					175					180		
atg	aat	aag	gtg	gct	att	cct	ttc	gcg	gtg	aat	tca	gca	gct	cag	gcg	691
Met	Asn	Lys	Val	Ala	Ile	Pro	Phe	Ala	Val	Asn	Ser	Ala	Ala	Gln	Ala	
				185					190					195		
gca	gcg	ctt	gcg	agt	ttg	aat	tct	gcc	gat	gag	ttg	atg	gaa	cgg	gtg	739
Ala	Ala	Leu	Ala	Ser	Leu	Asn	Ser	Ala	Asp	Glu	Leu	Met	Glu	Arg	Val	
				200					205					210		
gag	gaa	acc	gtc	gaa	aag	cgt	gat	gct	gtg	gtg	tca	gcg	ctt	ggc	gct	787
Glu	Glu	Thr	Val	Glu	Lys	Arg	Asp	Ala	Val	Val	Ser	Ala	Leu	Gly	Ala	
				215					220					225		
gcg	ccg	acg	cag	gcc	aat	ttc	gtc	tgg	ctg	ccg	ggc	gag	ggc	gcc	gct	835
Ala	Pro	Thr	Gln	Ala	Asn	Phe	Val	Trp	Leu	Pro	Gly	Glu	Gly	Ala	Ala	
				230					235					240		
														245		

gag ttg gcg gct aaa ttg gcc gag cac ggc atc gtg att cgc gcg ttc 883  
 Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile Arg Ala Phe  
                   250                  255                  260

ccc gag ggt gcg cgc att tcg gtg acc aac gcc gag gaa act gac aag 931  
 Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu Thr Asp Lys  
                   265                  270                  275

ctg ctg cgc gcg tgg gag gcc atc aat gct ggg tagtctttgg cgttttgagg 984  
 Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly  
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tgc 987

<210> 482

<211> 288

<212> PRT

<213> Corynebacterium glutamicum

<400> 482

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Glu Phe Asp Gln Val Thr Val Gly Cys Gly Ser Ser Ala Leu Cys Gln  
                   20                  25                  30

Gln Leu Val Gln Ala Thr Cys Ala Gln Gly Asp Glu Val Ile Phe Pro  
                   35                  40                  45

Trp Arg Ser Phe Glu Ala Tyr Pro Ile Phe Ala Gln Val Ala Gly Ala  
                   50                  55                  60

Thr Pro Val Ala Ile Pro Leu Thr Ala Asp Gln Asn His Asp Leu Asp  
   65                  70                  75                  80

Ala Met Ala Ala Ala Ile Thr Asp Lys Thr Arg Leu Ile Phe Ile Cys  
                   85                  90                  95

Asn Pro Asn Asn Pro Ser Gly Thr Thr Ile Thr Gln Ala Gln Phe Asp  
                   100                  105                  110

Asn Phe Met Glu Lys Val Pro Asn Asp Val Val Val Gly Leu Asp Glu  
                   115                  120                  125

Ala Tyr Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu  
                   130                  135                  140

Glu Ile His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys  
   145                  150                  155                  160

Ala Tyr Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala  
                   165                  170                  175

Glu Ile Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn  
                   180                  185                  190

Ser Ala Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu  
                   195                  200                  205

Leu Met Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val  
 210 215 220  
 Ser Ala Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro  
 225 230 235 240  
 Gly Glu Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile  
 245 250 255  
 Val Ile Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala  
 260 265 270  
 Glu Glu Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly  
 275 280 285

&lt;210&gt; 483

&lt;211&gt; 545

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(522)

&lt;223&gt; FRXA00446

&lt;400&gt; 483

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Met Glu Lys Val Pro Asn Asp Val Val Val Gly Leu Asp Glu Ala Tyr	
1 5 10 15	
ttt gag ttc aac cgc gcg gac gac acc cca gtt gcc act gag gaa atc	96
Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu Glu Ile	
20 25 30	
cac cgc cac gac aac gtg att ggt ttg cgc acg ttc tcc aag gcg tat	144
His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys Ala Tyr	
35 40 45	
ggc ctg gcg ggc ttg cgt gtt ggt tac gcc ttc gga aac gca gag atc	192
Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala Glu Ile	
50 55 60	
atc gca gcg atg aat aag gtg gct att cct ttc gcg gtg aat tca gca	240
Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala	
65 70 75 80	
gct cag gcg gca gcg ctt gcg agt ttg aat tct gcc gat gag ttg atg	288
Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met	
85 90 95	
gaa cgg gtg gag gaa acc gtc gaa aag cgt gat gct gtg gtg tca gcg	336
Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala	
100 105 110	
ctt ggt gct gcg ccg acg cag gcc aat ttc gtc tgg ctg ccg ggc gag	384
Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu	
115 120 125	

ggc gcc gct gag ttg gcg gct aaa ttg gcc gag cac ggc atc gtg att 432  
 Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile  
 130 135 140

cgc gcg ttc ccc gag ggt gcg cgc att tcg gtg acc aac gcc gag gaa 480  
 Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu  
 145 150 155 160

act gac aag ctg ctg cgc gcg tgg gag gcc atc aat gct ggg 522  
 Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly  
 165 170

tagtctttgg cgttttgcgg tgc 545

<210> 484

<211> 174

<212> PRT

<213> Corynebacterium glutamicum

<400> 484

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Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu Glu Ile  
 20 25 30

His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys Ala Tyr  
 35 40 45

Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala Glu Ile  
 50 55 60

Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala  
 65 70 75 80

Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met  
 85 90 95

Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala  
 100 105 110

Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu  
 115 120 125

Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile  
 130 135 140

Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu  
 145 150 155 160

Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly  
 165 170

<210> 485

<211> 1230

<212> DNA

<213> Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1207)

&lt;223&gt; RXS00618

&lt;400&gt; 485

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                                         Met Gln Met Leu Asp
                                         1                               5

cga gtc cac cgt cgc agg cgc gaa ggc aaa gac acc tta atg ttc tgc 163
Arg Val His Arg Arg Arg Glu Gly Lys Asp Thr Leu Met Phe Cys
                               10                               15                               20

gct ggc cag ccg tca act ggt gcg cca gaa gca gtc atc gaa gaa gca 211
Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala Val Ile Glu Glu Ala
                               25                               30                               35

gag atc gct ctt cgc tcg ggt cct ttg gga tac acc gag gtg att ggt 259
Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr Thr Glu Val Ile Gly
                               40                               45                               50

gat cgt gag ttc cgt gaa cgc atc gcc gat tgg cac tct gct act tat 307
Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp His Ser Ala Thr Tyr
                               55                               60                               65

gac gta gac acc aac cct gac aat gtt att gtc acc acc ggt tct tca 355
Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val Thr Thr Gly Ser Ser
                               70                               75                               80                               85

ggg gga ttc gtg gca tcg ttt atc gcc acc ttg gat cac ggg gat tat 403
Gly Gly Phe Val Ala Ser Phe Ile Ala Thr Leu Asp His Gly Asp Tyr
                               90                               95                               100

gtg gca atg cct acc ccg ggg tac ccg gca tat cgc aat att ctg gaa 451
Val Ala Met Pro Thr Pro Gly Tyr Pro Ala Tyr Arg Asn Ile Leu Glu
                               105                               110                               115

tct ttg ggg gcg aag gtt ctg aac ctg cgc tgt act gca gag act cgt 499
Ser Leu Gly Ala Lys Val Leu Asn Leu Arg Cys Thr Ala Glu Thr Arg
                               120                               125                               130

ttc cag cca acc gct caa atg ttg gag gaa ctg cca cac aag ccg aag 547
Phe Gln Pro Thr Ala Gln Met Leu Glu Glu Leu Pro His Lys Pro Lys
                               135                               140                               145

gct gtt att gtc acc agc cca gga aac cca acg ggc acc atc att gat 595
Ala Val Ile Val Thr Ser Pro Gly Asn Pro Thr Gly Thr Ile Ile Asp
                               150                               155                               160                               165

ccg gaa gag cta gag cgc atc gcc aag tgg tgc gat gac aat gat gct 643
Pro Glu Glu Leu Glu Arg Ile Ala Lys Trp Cys Asp Asp Asn Asp Ala
                               170                               175                               180

gtt ctt atc tct gat gag gac tac cac ggc atg agc ttt ggt cgt ccg 691
Val Leu Ile Ser Asp Glu Asp Tyr His Gly Met Ser Phe Gly Arg Pro
                               185                               190                               195

ctg gca act gcg cat cag ttt tcc aag aac gcc atc gtg gtg ggt acc 739

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Leu Ala Thr Ala His Gln Phe Ser Lys Asn Ala Ile Val Val Gly Thr  
 200 205 210  
 ttg tcc aag tac ttc tcc atg acg ggt tgg cgc gtg ggt tgg atc atc 787  
 Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp Arg Val Gly Trp Ile Ile  
 215 220 225  
 gtt cca gat gag ctg gtc aca ccg att gaa aac ctg cag gct tct ctt 835  
 Val Pro Asp Glu Leu Val Thr Pro Ile Glu Asn Leu Gln Ala Ser Leu  
 230 235 240 245  
 tcc ttg tgt gct cct gcc atc ggg cag gct gcg gga cgc gca gcc ttc 883  
 Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala Ala Gly Arg Ala Ala Phe  
 250 255 260  
 act ttg gag gct ggg gcc gaa ctt gat gcc cac gtt gaa gcg tat cgc 931  
 Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala His Val Glu Ala Tyr Arg  
 265 270 275  
 gag gcc cgg gag gtg ttc gtc gat aag ctc cct gaa atc ggg ctt ggc 979  
 Glu Ala Arg Glu Val Phe Val Asp Lys Leu Pro Glu Ile Gly Leu Gly  
 280 285 290  
 act ttc gcc gac ccg gat ggc ggc ctg tat ttg tgg gtc gat gtt tct  
 1027  
 Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr Leu Trp Val Asp Val Ser  
 295 300 305  
 gca tac acc gat gat tca gag gaa tgg gca ttg cgt ttg ctc gat gaa  
 1075  
 Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala Leu Arg Leu Leu Asp Glu  
 310 315 320 325  
 gcg ggc gtg gcc gtc gcg ccg ggt gtt gat ttt gat cct gag gaa ggc  
 1123  
 Ala Gly Val Ala Val Ala Pro Gly Val Asp Phe Asp Pro Glu Glu Gly  
 330 335 340  
 cac aag tgg att cgt ttg agc ctg tgc gcg tca aag gaa gac acc att  
 1171  
 His Lys Trp Ile Arg Leu Ser Leu Cys Ala Ser Lys Glu Asp Thr Ile  
 345 350 355  
 gaa ggt gtg cgc aaa atc gga gaa ttc atc aaa aaa tagcagcgac  
 1217  
 Glu Gly Val Arg Lys Ile Gly Glu Phe Ile Lys Lys  
 360 365  
 taggttagtt tcg  
 1230

&lt;210&gt; 486

&lt;211&gt; 369

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 486

Met Gln Met Leu Asp Arg Val His Arg Arg Arg Arg Glu Gly Lys Asp  
 1 5 10 15



Thr Leu Met Phe Cys Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala  
 20 25 30  
 Val Ile Glu Glu Ala Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr  
 35 40 45  
 Thr Glu Val Ile Gly Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp  
 50 55 60  
 His Ser Ala Thr Tyr Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val  
 65 70 75 80  
 Thr Thr Gly Ser Ser Gly Gly Phe Val Ala Ser Phe Ile Ala Thr Leu  
 85 90 95  
 Asp His Gly Asp Tyr Val Ala Met Pro Thr Pro Gly Tyr Pro Ala Tyr  
 100 105 110  
 Arg Asn Ile Leu Glu Ser Leu Gly Ala Lys Val Leu Asn Leu Arg Cys  
 115 120 125  
 Thr Ala Glu Thr Arg Phe Gln Pro Thr Ala Gln Met Leu Glu Glu Leu  
 130 135 140  
 Pro His Lys Pro Lys Ala Val Ile Val Thr Ser Pro Gly Asn Pro Thr  
 145 150 155 160  
 Gly Thr Ile Ile Asp Pro Glu Glu Leu Glu Arg Ile Ala Lys Trp Cys  
 165 170 175  
 Asp Asp Asn Asp Ala Val Leu Ile Ser Asp Glu Asp Tyr His Gly Met  
 180 185 190  
 Ser Phe Gly Arg Pro Leu Ala Thr Ala His Gln Phe Ser Lys Asn Ala  
 195 200 205  
 Ile Val Val Gly Thr Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp Arg  
 210 215 220  
 Val Gly Trp Ile Ile Val Pro Asp Glu Leu Val Thr Pro Ile Glu Asn  
 225 230 235 240  
 Leu Gln Ala Ser Leu Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala Ala  
 245 250 255  
 Gly Arg Ala Ala Phe Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala His  
 260 265 270  
 Val Glu Ala Tyr Arg Glu Ala Arg Glu Val Phe Val Asp Lys Leu Pro  
 275 280 285  
 Glu Ile Gly Leu Gly Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr Leu  
 290 295 300  
 Trp Val Asp Val Ser Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala Leu  
 305 310 315 320  
 Arg Leu Leu Asp Glu Ala Gly Val Ala Val Ala Pro Gly Val Asp Phe  
 325 330 335  
 Asp Pro Glu Glu Gly His Lys Trp Ile Arg Leu Ser Leu Cys Ala Ser

340	345	350	
Lys Glu Asp Thr Ile Glu Gly Val Arg Lys Ile Gly Glu Phe Ile Lys			
355	360	365	
Lys			
<210> 487			
<211> 657			
<212> DNA			
<213> Corynebacterium glutamicum			
<220>			
<221> CDS			
<222> (101)..(634)			
<223> FRXA00618			
<400> 487			
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caatgatgct gttcttatct ctgatgagga ctaccacggc atg agc ttt ggt cgt 115			
			Met Ser Phe Gly Arg 5
			1
ccg ctg gca act gcg cat cag ttt tcc aag aac gcc atc gtg gtg ggt 163			
Pro Leu Ala Thr	Ala His Gln Phe Ser Lys Asn Ala Ile Val Val Gly		
10	15	20	
acc ttg tcc aag tac ttc tcc atg acg ggt tgg cgc gtg ggt tgg atc 211			
Thr Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp Arg Val Gly Trp Ile			
25	30	35	
atc gtt cca gat gag ctg gtc aca ccg att gaa aac ctg cag gct tct 259			
Ile Val Pro Asp Glu Leu Val Thr Pro Ile Glu Asn Leu Gln Ala Ser			
40	45	50	
ctt tcc ttg tgt gct cct gcc atc ggg cag gct gcg gga cgc gca gcc 307			
Leu Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala Ala Gly Arg Ala Ala			
55	60	65	
ttc act ttg gag gct ggg gcc gaa ctt gat gcc cac gtt gaa gcg tat 355			
Phe Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala His Val Glu Ala Tyr			
70	75	80	85
cgc gag gcc cgg gag gtg ttc gtc gat aag ctc cct gaa atc ggg ctt 403			
Arg Glu Ala Arg Glu Val Phe Val Asp Lys Leu Pro Glu Ile Gly Leu			
90	95	100	
ggc act ttc gcc gac ccg gat ggc ggc ctg tat ttg tgg gtc gat gtt 451			
Gly Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr Leu Trp Val Asp Val			
105	110	115	
tct gca tac acc gat gat tca gag gaa tgg gca ttg cgt ttg ctc gat 499			
Ser Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala Leu Arg Leu Leu Asp			
120	125	130	
gaa gcg ggc gtg gcc gtc gcg ccg ggt gtt gat ttt gat cct gag gaa 547			
Glu Ala Gly Val Ala Val Ala Pro Gly Val Asp Phe Asp Pro Glu Glu			
135	140	145	

ggc cac aag tgg att cgt ttg agc ctg tgc gcg tca aag gaa gac acc 595  
 Gly His Lys Trp Ile Arg Leu Ser Leu Cys Ala Ser Lys Glu Asp Thr  
 150 155 160 165

att gaa ggt gtg cgc aaa atc gga gaa ttc atc aaa aaa tagcagcgac 644  
 Ile Glu Gly Val Arg Lys Ile Gly Glu Phe Ile Lys Lys  
 170 175

taggttagtt tcg 657

<210> 488

<211> 178

<212> PRT

<213> Corynebacterium glutamicum

<400> 488

Met Ser Phe Gly Arg Pro Leu Ala Thr Ala His Gln Phe Ser Lys Asn  
 1 5 10 15

Ala Ile Val Val Gly Thr Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp  
 20 25 30

Arg Val Gly Trp Ile Ile Val Pro Asp Glu Leu Val Thr Pro Ile Glu  
 35 40 45

Asn Leu Gln Ala Ser Leu Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala  
 50 55 60

Ala Gly Arg Ala Ala Phe Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala  
 65 70 75 80

His Val Glu Ala Tyr Arg Glu Ala Arg Glu Val Phe Val Asp Lys Leu  
 85 90 95

Pro Glu Ile Gly Leu Gly Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr  
 100 105 110

Leu Trp Val Asp Val Ser Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala  
 115 120 125

Leu Arg Leu Leu Asp Glu Ala Gly Val Ala Val Ala Pro Gly Val Asp  
 130 135 140

Phe Asp Pro Glu Glu Gly His Lys Trp Ile Arg Leu Ser Leu Cys Ala  
 145 150 155 160

Ser Lys Glu Asp Thr Ile Glu Gly Val Arg Lys Ile Gly Glu Phe Ile  
 165 170 175

Lys Lys

<210> 489

<211> 385

<212> DNA

<213> Corynebacterium glutamicum

<220>

&lt;221&gt; CDS

&lt;222&gt; (101)..(385)

&lt;223&gt; FRXA00627

&lt;400&gt; 489

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gaagccaagc actagaagca atgttcagcc gtttcgcgctc atg cag atg ttg gac 115  
 Met Gln Met Leu Asp  
 1 5

cga gtc cac cgt cgc agg cgc gaa ggc aaa gac acc tta atg ttc tgc 163  
 Arg Val His Arg Arg Arg Arg Glu Gly Lys Asp Thr Leu Met Phe Cys  
 10 15 20

gct ggc cag ccg tca act ggt gcg cca gaa gca gtc atc gaa gaa gca 211  
 Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala Val Ile Glu Glu Ala  
 25 30 35

gag atc gct ctt cgc tcg ggt cct ttg gga tac acc gag gtg att ggt 259  
 Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr Thr Glu Val Ile Gly  
 40 45 50

gat cgt gag ttc cgt gaa cgc atc gcc gat tgg cac tct gct act tat 307  
 Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp His Ser Ala Thr Tyr  
 55 60 65

gac gta gac acc aac cct gac aat gtt att gtc acc acc ggt tct tca 355  
 Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val Thr Thr Gly Ser Ser  
 70 75 80 85

ggt gga ttc gtg gca tcg ttt atc gcc acc 385  
 Gly Gly Phe Val Ala Ser Phe Ile Ala Thr  
 90 95

&lt;210&gt; 490

&lt;211&gt; 95

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 490

Met Gln Met Leu Asp Arg Val His Arg Arg Arg Arg Glu Gly Lys Asp  
 1 5 10 15

Thr Leu Met Phe Cys Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala  
 20 25 30

Val Ile Glu Glu Ala Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr  
 35 40 45

Thr Glu Val Ile Gly Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp  
 50 55 60

His Ser Ala Thr Tyr Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val  
 65 70 75 80

Thr Thr Gly Ser Ser Gly Gly Phe Val Ala Ser Phe Ile Ala Thr  
 85 90 95



gat gtt gag cgc atc atc aac gtt gcc cca ggc atc gtg atc gtg gat	691
Asp Val Glu Arg Ile Ile Asn Val Ala Pro Gly Ile Val Ile Val Asp	
185 190 195	
gaa gct tat gcg gaa ttc tcc cca tca cct tca gca acc act ctt ctg	739
Glu Ala Tyr Ala Glu Phe Ser Pro Ser Pro Ser Ala Thr Thr Leu Leu	
200 205 210	
gag aag tac cca acc aag ctg gtg gtg tcc cgc acc atg agt aag gct	787
Glu Lys Tyr Pro Thr Lys Leu Val Val Ser Arg Thr Met Ser Lys Ala	
215 220 225	
ttt gat ttc gca ggt gga cgc ctc ggc tac ttc gtg gcc aac cca gcg	835
Phe Asp Phe Ala Gly Gly Arg Leu Gly Tyr Phe Val Ala Asn Pro Ala	
230 235 240 245	
ttt atc gac gcc gtg atg cta gtc cgc ctt ccg tat cat ctt tca gcg	883
Phe Ile Asp Ala Val Met Leu Val Arg Leu Pro Tyr His Leu Ser Ala	
250 255 260	
ctg agc caa gca gcc gca atc gta gcg ctg cgt cac tcc gct gac acg	931
Leu Ser Gln Ala Ala Ala Ile Val Ala Leu Arg His Ser Ala Asp Thr	
265 270 275	
ctg gga acc gtc gaa aag ctc tct gta gag cgt gtt cgc gtg gca gca	979
Leu Gly Thr Val Glu Lys Leu Ser Val Glu Arg Val Arg Val Ala Ala	
280 285 290	
cgc ttg gag gaa ctg ggc tac gct gtg gtt cca agt gag tcc aac ttt	
1027 Arg Leu Glu Glu Leu Gly Tyr Ala Val Val Pro Ser Glu Ser Asn Phe	
295 300 305	
gtg ttc ttt gga gat ttc tcc gat cag cac gcg gca tgg cag gca ttt	
1075 Val Phe Phe Gly Asp Phe Ser Asp Gln His Ala Ala Trp Gln Ala Phe	
310 315 320 325	
ttg gat agg gga gtg ctc atc cgc gat gtg gga atc gct ggg cac ttg	
1123 Leu Asp Arg Gly Val Leu Ile Arg Asp Val Gly Ile Ala Gly His Leu	
330 335 340	
cgc act acc att ggt gtg cct gag gaa aat gat gcg ttt ttg gac gca	
1171 Arg Thr Thr Ile Gly Val Pro Glu Glu Asn Asp Ala Phe Leu Asp Ala	
345 350 355	
gct gca gag atc atc aag ctg aac ctg taagagagaa gaatttttca	
1218 Ala Ala Glu Ile Ile Lys Leu Asn Leu	
360 365	
tga	
1221	

<210> 492  
 <211> 366  
 <212> PRT  
 <213> Corynebacterium glutamicum

&lt;400&gt; 492

Met	Thr	Lys	Ile	Thr	Leu	Ser	Asp	Leu	Pro	Leu	Arg	Glu	Glu	Leu	Arg
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Gly	Glu	His	Ala	Tyr	Gly	Ala	Pro	Gln	Leu	Asn	Val	Asp	Ile	Arg	Leu
			20					25					30		
Asn	Thr	Asn	Glu	Asn	Pro	Tyr	Pro	Pro	Ser	Glu	Ala	Leu	Val	Ala	Asp
		35					40					45			
Leu	Val	Ala	Thr	Val	Asp	Lys	Ile	Ala	Thr	Glu	Leu	Asn	Arg	Tyr	Pro
	50					55					60				
Glu	Arg	Asp	Ala	Val	Glu	Leu	Arg	Asp	Glu	Leu	Ala	Ala	Tyr	Ile	Thr
65					70					75					80
Lys	Gln	Thr	Gly	Val	Ala	Val	Thr	Arg	Asp	Asn	Leu	Trp	Ala	Ala	Asn
				85					90					95	
Gly	Ser	Asn	Glu	Ile	Leu	Gln	Gln	Leu	Leu	Gln	Ala	Phe	Gly	Gly	Pro
			100					105					110		
Gly	Arg	Thr	Ala	Leu	Gly	Phe	Gln	Pro	Ser	Tyr	Ser	Met	His	Pro	Ile
		115					120					125			
Leu	Ala	Lys	Gly	Thr	His	Thr	Glu	Phe	Ile	Ala	Val	Ser	Arg	Gly	Ala
	130					135					140				
Asp	Phe	Arg	Ile	Asp	Met	Asp	Val	Ala	Leu	Glu	Glu	Ile	Arg	Ala	Lys
145					150					155					160
Gln	Pro	Asp	Ile	Val	Phe	Val	Thr	Thr	Pro	Asn	Asn	Pro	Thr	Gly	Asp
				165					170					175	
Val	Thr	Ser	Leu	Asp	Asp	Val	Glu	Arg	Ile	Ile	Asn	Val	Ala	Pro	Gly
			180					185					190		
Ile	Val	Ile	Val	Asp	Glu	Ala	Tyr	Ala	Glu	Phe	Ser	Pro	Ser	Pro	Ser
		195					200					205			
Ala	Thr	Thr	Leu	Leu	Glu	Lys	Tyr	Pro	Thr	Lys	Leu	Val	Val	Ser	Arg
	210					215					220				
Thr	Met	Ser	Lys	Ala	Phe	Asp	Phe	Ala	Gly	Gly	Arg	Leu	Gly	Tyr	Phe
225					230					235					240
Val	Ala	Asn	Pro	Ala	Phe	Ile	Asp	Ala	Val	Met	Leu	Val	Arg	Leu	Pro
				245					250					255	
Tyr	His	Leu	Ser	Ala	Leu	Ser	Gln	Ala	Ala	Ala	Ile	Val	Ala	Leu	Arg
			260					265					270		
His	Ser	Ala	Asp	Thr	Leu	Gly	Thr	Val	Glu	Lys	Leu	Ser	Val	Glu	Arg
		275					280					285			
Val	Arg	Val	Ala	Ala	Arg	Leu	Glu	Glu	Leu	Gly	Tyr	Ala	Val	Val	Pro
	290					295					300				
Ser	Glu	Ser	Asn	Phe	Val	Phe	Phe	Gly	Asp	Phe	Ser	Asp	Gln	His	Ala
305					310					315					320





Thr	Glu	Leu	Asp	Gln	Val	Ala	Gln	Ile	Ala	Glu	Ser	Leu	Ala	Gln	Gly	
135						140					145					
gct	tcc	cag	att	ccg	cgt	cat	ttc	aat	ctt	gca	ctt	gat	gtt	cct	ttg	595
Ala	Ser	Gln	Ile	Pro	Arg	His	Phe	Asn	Leu	Ala	Leu	Asp	Val	Pro	Leu	
150					155					160					165	
ggt	gct	cct	gaa	ctg	cca	gag	ctt	cat	ggc	gag	gca	gtt	gga	gca	tca	643
Val	Ala	Pro	Glu	Leu	Pro	Glu	Leu	His	Gly	Glu	Ala	Val	Gly	Ala	Ser	
				170					175					180		
tgg	acg	cat	cgc	tgg	atc	aac	cac	ggc	gag	gtg	acc	gtg	gac	ctg	ggg	691
Trp	Thr	His	Arg	Trp	Ile	Asn	His	Gly	Glu	Val	Thr	Val	Asp	Leu	Gly	
			185					190					195			
gag	cac	acc	ctc	gtg	att	gcc	ggc	gat	gaa	gca	tgg	gaa	gtg	gaa	ggg	739
Glu	His	Thr	Leu	Val	Ile	Ala	Gly	Asp	Glu	Ala	Trp	Glu	Val	Glu	Gly	
		200					205					210				
ctg	gaa	gat	gtg	ccc	acc	atc	gct	gaa	cct	act	gca	cca	aag	cct	tat	787
Leu	Glu	Asp	Val	Pro	Thr	Ile	Ala	Glu	Pro	Thr	Ala	Pro	Lys	Pro	Tyr	
	215					220					225					
aat	ccg	gtg	cac	cca	ctg	gct	gct	gaa	atc	ttg	ctg	aag	gag	cag	gtc	835
Asn	Pro	Val	His	Pro	Leu	Ala	Ala	Glu	Ile	Leu	Leu	Lys	Glu	Gln	Val	
230					235					240					245	
tcc	gcg	gaa	ggc	tat	gtg	gta	aac	acc	agg	cct	gat	cat	gtg	atc	gtg	883
Ser	Ala	Glu	Gly	Tyr	Val	Val	Asn	Thr	Arg	Pro	Asp	His	Val	Ile	Val	
				250					255					260		
gtg	gga	cac	ccc	acg	ctg	cac	cgc	gga	gtg	ttg	aag	ttg	atg	tca	gat	931
Val	Gly	His	Pro	Thr	Leu	His	Arg	Gly	Val	Leu	Lys	Leu	Met	Ser	Asp	
			265					270					275			
cct	ggc	att	aaa	tta	act	gtg	ctt	tca	cgc	acc	gat	atc	atc	act	gat	979
Pro	Gly	Ile	Lys	Leu	Thr	Val	Leu	Ser	Arg	Thr	Asp	Ile	Ile	Thr	Asp	
		280					285					290				
ccc	ggc	cgc	cat	gcc	gat	cag	gtg	ggc	agc	aca	gtg	aaa	gtc	acc	ggc	
1027																
Pro	Gly	Arg	His	Ala	Asp	Gln	Val	Gly	Ser	Thr	Val	Lys	Val	Thr	Gly	
	295					300					305					
acc	cag	gaa	aag	cag	tgg	cta	aag	atc	tgt	tcg	gca	gca	tca	gaa	ctt	
1075																
Thr	Gln	Glu	Lys	Gln	Trp	Leu	Lys	Ile	Cys	Ser	Ala	Ala	Ser	Glu	Leu	
310					315					320					325	
gcg	gcc	gat	ggc	gtg	cgt	gac	gtc	ctg	gac	aac	caa	gaa	ttc	ggc	ttc	
1123																
Ala	Ala	Asp	Gly	Val	Arg	Asp	Val	Leu	Asp	Asn	Gln	Glu	Phe	Gly	Phe	
				330					335					340		
acc	ggc	ctc	cat	gtt	gcc	gca	gcc	gtg	gcg	gat	acc	tta	ggc	acc	ggc	
1171																
Thr	Gly	Leu	His	Val	Ala	Ala	Ala	Val	Ala	Asp	Thr	Leu	Gly	Thr	Gly	
			345					350					355			
gat	act	ctc	ttt	gct	gca	gca	tcc	aac	tca	atc	cgt	gac	ctc	tcc	ctg	
1219																

Asp Thr Leu Phe Ala Ala Ala Ser Asn Ser Ile Arg Asp Leu Ser Leu  
 360 365 370  
 gtg ggt atg cct ttt gat ggc gtg gat acc ttc tcc cca cga ggt gtc  
 1267  
 Val Gly Met Pro Phe Asp Gly Val Asp Thr Phe Ser Pro Arg Gly Val  
 375 380 385  
 gca ggc att gat ggt tct gtt gct caa gca atc ggc act tca ctt gct  
 1315  
 Ala Gly Ile Asp Gly Ser Val Ala Gln Ala Ile Gly Thr Ser Leu Ala  
 390 395 400 405  
 gtg cag tcc cgc cac ccc gat gaa atc cgc gcg cca cgc act gtg gcc  
 1363  
 Val Gln Ser Arg His Pro Asp Glu Ile Arg Ala Pro Arg Thr Val Ala  
 410 415 420  
 ctt ctg ggc gat ctg tcg ttc ctt cac gat att ggc gga ctg ctc atc  
 1411  
 Leu Leu Gly Asp Leu Ser Phe Leu His Asp Ile Gly Gly Leu Leu Ile  
 425 430 435  
 ggc cct gat gaa cca cgc cca gaa aac ctc acc atc gtg gtc tcc aac  
 1459  
 Gly Pro Asp Glu Pro Arg Pro Glu Asn Leu Thr Ile Val Val Ser Asn  
 440 445 450  
 gac aac ggt ggc gga atc ttc gaa ctc cta gaa acc ggc gca gat ggt  
 1507  
 Asp Asn Gly Gly Gly Ile Phe Glu Leu Leu Glu Thr Gly Ala Asp Gly  
 455 460 465  
 ctc cgc ccc aac ttc gag cgt gct ttc ggt acc cca cac gac gcg tcc  
 1555  
 Leu Arg Pro Asn Phe Glu Arg Ala Phe Gly Thr Pro His Asp Ala Ser  
 470 475 480 485  
 atc gcg gat ctc tgc gca ggc tac ggc att gaa cac caa gtg gta gac  
 1603  
 Ile Ala Asp Leu Cys Ala Gly Tyr Gly Ile Glu His Gln Val Val Asp  
 490 495 500  
 aac ctc caa gac ctc atc atc gcg cta gtt gat acc acc gaa gta tcc  
 1651  
 Asn Leu Gln Asp Leu Ile Ile Ala Leu Val Asp Thr Thr Glu Val Ser  
 505 510 515  
 gga ttc acc att att gaa gct tcg acc gtc cga gat acc cgc cgt gca  
 1699  
 Gly Phe Thr Ile Ile Glu Ala Ser Thr Val Arg Asp Thr Arg Arg Ala  
 520 525 530  
 caa cag caa gct ctc atg gac acg gtg cac taaatggagt ggtaccaagt  
 1749  
 Gln Gln Gln Ala Leu Met Asp Thr Val His  
 535 540  
 gcg  
 1752

<210> 494  
 <211> 543  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 494

Met	Ser	Ser	Thr	Pro	Ala	Gln	Asp	Leu	Ala	Arg	Ala	Val	Ile	Asp	Ser	1	5	10	15
Leu	Ala	Pro	His	Val	Thr	Asp	Val	Val	Leu	Cys	Pro	Gly	Ser	Arg	Asn	20	25	30	
Ser	Pro	Leu	Ser	Leu	Glu	Leu	Leu	Ala	Arg	Gln	Asp	Leu	Arg	Val	His	35	40	45	
Val	Arg	Ile	Asp	Glu	Arg	Ser	Ala	Ser	Phe	Leu	Ala	Leu	Ser	Leu	Ala	50	55	60	
Arg	Thr	Gln	Ala	Arg	Pro	Val	Ala	Val	Val	Met	Thr	Ser	Gly	Thr	Ala	65	70	75	80
Val	Ala	Asn	Cys	Leu	Pro	Ala	Val	Ala	Glu	Ala	Ala	His	Ala	His	Ile	85	90	95	
Pro	Leu	Ile	Val	Leu	Ser	Ala	Asp	Arg	Pro	Ala	His	Leu	Val	Gly	Thr	100	105	110	
Gly	Ala	Ser	Gln	Thr	Ile	Asn	Gln	Thr	Gly	Ile	Phe	Gly	Asp	Leu	Ala	115	120	125	
Pro	Thr	Val	Gly	Ile	Thr	Glu	Leu	Asp	Gln	Val	Ala	Gln	Ile	Ala	Glu	130	135	140	
Ser	Leu	Ala	Gln	Gly	Ala	Ser	Gln	Ile	Pro	Arg	His	Phe	Asn	Leu	Ala	145	150	155	160
Leu	Asp	Val	Pro	Leu	Val	Ala	Pro	Glu	Leu	Pro	Glu	Leu	His	Gly	Glu	165	170	175	
Ala	Val	Gly	Ala	Ser	Trp	Thr	His	Arg	Trp	Ile	Asn	His	Gly	Glu	Val	180	185	190	
Thr	Val	Asp	Leu	Gly	Glu	His	Thr	Leu	Val	Ile	Ala	Gly	Asp	Glu	Ala	195	200	205	
Trp	Glu	Val	Glu	Gly	Leu	Glu	Asp	Val	Pro	Thr	Ile	Ala	Glu	Pro	Thr	210	215	220	
Ala	Pro	Lys	Pro	Tyr	Asn	Pro	Val	His	Pro	Leu	Ala	Ala	Glu	Ile	Leu	225	230	235	240
Leu	Lys	Glu	Gln	Val	Ser	Ala	Glu	Gly	Tyr	Val	Val	Asn	Thr	Arg	Pro	245	250	255	
Asp	His	Val	Ile	Val	Val	Gly	His	Pro	Thr	Leu	His	Arg	Gly	Val	Leu	260	265	270	
Lys	Leu	Met	Ser	Asp	Pro	Gly	Ile	Lys	Leu	Thr	Val	Leu	Ser	Arg	Thr	275	280	285	

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Asp Ile Ile Thr Asp Pro Gly Arg His Ala Asp Gln Val Gly Ser Thr
290                               295                   300

Val Lys Val Thr Gly Thr Gln Glu Lys Gln Trp Leu Lys Ile Cys Ser
305                               310                   315                   320

Ala Ala Ser Glu Leu Ala Ala Asp Gly Val Arg Asp Val Leu Asp Asn
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Gln Glu Phe Gly Phe Thr Gly Leu His Val Ala Ala Ala Val Ala Asp
                               340                   345                   350

Thr Leu Gly Thr Gly Asp Thr Leu Phe Ala Ala Ala Ser Asn Ser Ile
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Arg Asp Leu Ser Leu Val Gly Met Pro Phe Asp Gly Val Asp Thr Phe
                               370                   375                   380

Ser Pro Arg Gly Val Ala Gly Ile Asp Gly Ser Val Ala Gln Ala Ile
385                               390                   395                   400

Gly Thr Ser Leu Ala Val Gln Ser Arg His Pro Asp Glu Ile Arg Ala
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Pro Arg Thr Val Ala Leu Leu Gly Asp Leu Ser Phe Leu His Asp Ile
                               420                   425                   430

Gly Gly Leu Leu Ile Gly Pro Asp Glu Pro Arg Pro Glu Asn Leu Thr
                               435                   440                   445

Ile Val Val Ser Asn Asp Asn Gly Gly Gly Ile Phe Glu Leu Leu Glu
450                               455                   460

Thr Gly Ala Asp Gly Leu Arg Pro Asn Phe Glu Arg Ala Phe Gly Thr
465                               470                   475                   480

Pro His Asp Ala Ser Ile Ala Asp Leu Cys Ala Gly Tyr Gly Ile Glu
                               485                   490                   495

His Gln Val Val Asp Asn Leu Gln Asp Leu Ile Ile Ala Leu Val Asp
                               500                   505                   510

Thr Thr Glu Val Ser Gly Phe Thr Ile Ile Glu Ala Ser Thr Val Arg
515                               520                   525

Asp Thr Arg Arg Ala Gln Gln Gln Ala Leu Met Asp Thr Val His
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&lt;210&gt; 495

&lt;211&gt; 1434

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101) .. (1411)

&lt;223&gt; RXS02550

&lt;400&gt; 495

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				Val	Thr	Thr	Asp	Lys	
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cgc	aaa	acc	tct	aag	acc	acc	gac	acc	163
Arg	Lys	Thr	Ser	Lys	Thr	Thr	Asp	Thr	
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								20	
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Asp	Gln	Ala	Ala	Arg	Pro	Thr	Arg	Arg	
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Gln	Ser	Glu	Lys	Met	Lys	Asp	Val	Leu	
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gcc	gcg	gag	gcg	gaa	cgc	atg	gag	ctt	307
Ala	Ala	Glu	Ala	Glu	Arg	Met	Glu	Leu	
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ctc	aac	acg	gga	aat	cca	gcc	gtg	ttc	355
Leu	Asn	Thr	Gly	Asn	Pro	Ala	Val	Phe	
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								85	
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Ile	Met	Arg	Asp	Met	Ile	Ala	Asn	Leu	
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								100	
acc	tcc	aaa	ggc	att	att	ccg	gcc	cgg	451
Thr	Ser	Lys	Gly	Ile	Ile	Pro	Ala	Arg	
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								115	
gaa	gtt	gtg	ccc	gga	ttc	ccc	cac	ttc	499
Glu	Val	Val	Pro	Gly	Phe	Pro	His	Phe	
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								130	
ggc	aac	ggt	gtc	tca	gaa	cta	atc	acc	547
Gly	Asn	Gly	Val	Ser	Glu	Leu	Ile	Thr	
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								145	
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Asn	Asp	Gly	Asp	Glu	Val	Leu	Ile	Pro	
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								165	
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Thr	Ala	Ala	Thr	Ser	Leu	Ala	Gly	Gly	
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								180	
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Asp	Glu	Glu	Asp	Asp	Trp	Asn	Pro	Ser	
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								195	
atc	tca	gag	aaa	acc	aaa	gct	att	gtg	739
Ile	Ser	Glu	Lys	Thr	Lys	Ala	Ile	Val	
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								210	
acg	gga	gct	gtc	tac	ccg	cgc	cgg	gtg	787
Thr	Gly	Ala	Val	Tyr	Pro	Arg	Arg	Val	
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								225	

gca cgc gag cat gac ctg ctg att ttg gcc gat gaa atc tac gac cgc	835
Ala Arg Glu His Asp Leu Leu Ile Leu Ala Asp Glu Ile Tyr Asp Arg	
230 235 240 245	
att ctc tac gat gat gcc gag cac atc agc ctg gca acc ctt gca cca	883
Ile Leu Tyr Asp Asp Ala Glu His Ile Ser Leu Ala Thr Leu Ala Pro	
250 255 260	
gat ctc ctt tgc atc aca tac aac ggt cta tcc aag gca tac cgc gtc	931
Asp Leu Leu Cys Ile Thr Tyr Asn Gly Leu Ser Lys Ala Tyr Arg Val	
265 270 275	
gca gga tac cga gct ggc tgg atg gta ttg act gga cca aag caa tac	979
Ala Gly Tyr Arg Ala Gly Trp Met Val Leu Thr Gly Pro Lys Gln Tyr	
280 285 290	
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Cys Pro Asn Val Pro Ala Gln His Ala Ile Gln Val Ala Leu Gly Gly	
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Arg Gln Ser Ile Tyr Asp Leu Thr Gly Glu His Gly Arg Leu Leu Glu	
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Gln Arg Asn Met Ala Trp Thr Lys Leu Asn Glu Ile Pro Gly Val Ser	
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1219	
Cys Val Lys Pro Met Gly Ala Leu Tyr Ala Phe Pro Lys Leu Asp Pro	
360 365 370	
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1267	
Asn Val Tyr Glu Ile His Asp Asp Thr Gln Leu Met Leu Asp Leu Leu	
375 380 385	
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1315	
Arg Ala Glu Lys Ile Leu Met Val Gln Gly Thr Gly Phe Asn Trp Pro	
390 395 400 405	
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1363	
His His Asp His Phe Arg Val Val Thr Leu Pro Trp Ala Ser Gln Leu	
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<210> 496

<211> 437

<212> PRT

<213> Corynebacterium glutamicum

<400> 496

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Arg	Arg	Ile	Phe	Asp	Gln	Ser	Glu	Lys	Met	Lys	Asp	Val	Leu	Tyr	Glu
		35					40					45			
Ile	Arg	Gly	Pro	Val	Ala	Ala	Glu	Ala	Glu	Arg	Met	Glu	Leu	Asp	Gly
	50					55					60				
His	Asn	Ile	Leu	Lys	Leu	Asn	Thr	Gly	Asn	Pro	Ala	Val	Phe	Gly	Phe
65					70					75					80
Asp	Ala	Pro	Asp	Val	Ile	Met	Arg	Asp	Met	Ile	Ala	Asn	Leu	Pro	Thr
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Ser	Gln	Gly	Tyr	Ser	Thr	Ser	Lys	Gly	Ile	Ile	Pro	Ala	Arg	Arg	Ala
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Val	Val	Thr	Arg	Tyr	Glu	Val	Val	Pro	Gly	Phe	Pro	His	Phe	Asp	Val
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Asp	Asp	Val	Phe	Leu	Gly	Asn	Gly	Val	Ser	Glu	Leu	Ile	Thr	Met	Thr
	130					135					140				
Thr	Gln	Ala	Leu	Leu	Asn	Asp	Gly	Asp	Glu	Val	Leu	Ile	Pro	Ala	Pro
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Asp	Tyr	Pro	Leu	Trp	Thr	Ala	Ala	Thr	Ser	Leu	Ala	Gly	Gly	Lys	Pro
				165					170					175	
Val	His	Tyr	Leu	Cys	Asp	Glu	Glu	Asp	Asp	Trp	Asn	Pro	Ser	Ile	Glu
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Asp	Ile	Lys	Ser	Lys	Ile	Ser	Glu	Lys	Thr	Lys	Ala	Ile	Val	Val	Ile
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Gln	Ile	Val	Glu	Ile	Ala	Arg	Glu	His	Asp	Leu	Leu	Ile	Leu	Ala	Asp
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Glu	Ile	Tyr	Asp	Arg	Ile	Leu	Tyr	Asp	Asp	Ala	Glu	His	Ile	Ser	Leu
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Ala	Thr	Leu	Ala	Pro	Asp	Leu	Leu	Cys	Ile	Thr	Tyr	Asn	Gly	Leu	Ser
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Lys Ala Tyr Arg Val Ala Gly Tyr Arg Ala Gly Trp Met Val Leu Thr  
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 Gly Pro Lys Gln Tyr Ala Arg Gly Phe Ile Glu Gly Leu Glu Leu Leu  
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 Ala Gly Thr Arg Leu Cys Pro Asn Val Pro Ala Gln His Ala Ile Gln  
 305 310 315 320  
 Val Ala Leu Gly Gly Arg Gln Ser Ile Tyr Asp Leu Thr Gly Glu His  
 325 330 335  
 Gly Arg Leu Leu Glu Gln Arg Asn Met Ala Trp Thr Lys Leu Asn Glu  
 340 345 350  
 Ile Pro Gly Val Ser Cys Val Lys Pro Met Gly Ala Leu Tyr Ala Phe  
 355 360 365  
 Pro Lys Leu Asp Pro Asn Val Tyr Glu Ile His Asp Asp Thr Gln Leu  
 370 375 380  
 Met Leu Asp Leu Leu Arg Ala Glu Lys Ile Leu Met Val Gln Gly Thr  
 385 390 395 400  
 Gly Phe Asn Trp Pro His His Asp His Phe Arg Val Val Thr Leu Pro  
 405 410 415  
 Trp Ala Ser Gln Leu Glu Asn Ala Ile Glu Arg Leu Gly Asn Phe Leu  
 420 425 430  
 Ser Thr Tyr Lys Gln  
 435

&lt;210&gt; 497

&lt;211&gt; 1080

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1057)

&lt;223&gt; RXS02319

&lt;400&gt; 497

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 Met Ser Asn Tyr Ser  
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acc gac aac cct ttt gat ccc acc caa tgg gcc acc gtt cca ggt ttt 163  
 Thr Asp Asn Pro Phe Asp Pro Thr Gln Trp Ala Thr Val Pro Gly Phe  
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gaa gaa ttc acc gac atc acc tac cac cgc cac gtg ggc acc acc cgc 211  
 Glu Glu Phe Thr Asp Ile Thr Tyr His Arg His Val Gly Thr Thr Arg  
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 Ala Asp Gly Ile Val Arg Ile Ala Phe Asp Arg Pro Glu Val Arg Asn



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Ala	Phe	Arg	Pro	His	Thr	Val	Asp	Glu	Leu	Tyr	Gln	Ala	Leu	Asp	His			
	55						60				65							
gcg	cgc	cgg	acc	cca	gat	gtt	gga	acc	atc	ctg	ctc	acc	ggc	aac	ggc			355
Ala	Arg	Arg	Thr	Pro	Asp	Val	Gly	Thr	Ile	Leu	Leu	Thr	Gly	Asn	Gly			
	70				75					80					85			
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Pro	Ser	Glu	Lys	Asp	Gly	Gly	Trp	Ala	Phe	Cys	Ser	Gly	Gly	Asp	Gln			
				90					95					100				
cgc	atc	cgc	ggg	cgc	tcc	ggc	tac	caa	tac	gcc	acc	gaa	cac	gcg	cgc			451
Arg	Ile	Arg	Gly	Arg	Ser	Gly	Tyr	Gln	Tyr	Ala	Thr	Glu	His	Ala	Arg			
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gac	gat	gcc	acc	gct	gat	gtc	ttc	acg	gta	gat	att	gcc	cgc	acc	aaa			499
Asp	Asp	Ala	Thr	Ala	Asp	Val	Phe	Thr	Val	Asp	Ile	Ala	Arg	Thr	Lys			
		120					125					130						
gtt	gaa	ggc	gga	cgc	ctc	cac	att	ttg	gaa	gtc	caa	cgc	ctc	atc	cgc			547
Val	Glu	Gly	Gly	Arg	Leu	His	Ile	Leu	Glu	Val	Gln	Arg	Leu	Ile	Arg			
	135					140					145							
acc	atg	cct	aaa	gtt	gtc	atc	gca	gta	gtc	aac	ggc	tgg	gca	gcc	ggc			595
Thr	Met	Pro	Lys	Val	Val	Ile	Ala	Val	Val	Asn	Gly	Trp	Ala	Ala	Gly			
	150				155					160					165			
ggc	ggg	cac	tcc	ctc	cat	gtc	gtt	tgc	gac	ctc	acc	atc	gct	tcc	cgc			643
Gly	Gly	His	Ser	Leu	His	Val	Val	Cys	Asp	Leu	Thr	Ile	Ala	Ser	Arg			
				170					175					180				
caa	gaa	gca	cgc	ttc	aag	caa	acc	gac	gct	gac	gtg	gga	tcc	ttc	gac			691
Gln	Glu	Ala	Arg	Phe	Lys	Gln	Thr	Asp	Ala	Asp	Val	Gly	Ser	Phe	Asp			
			185					190					195					
gct	ggc	tac	ggc	tcc	gcc	tac	cta	gcg	aaa	atg	gtc	gga	cag	aaa	aac			739
Ala	Gly	Tyr	Gly	Ser	Ala	Tyr	Leu	Ala	Lys	Met	Val	Gly	Gln	Lys	Asn			
		200					205					210						
gcc	cgc	gaa	atc	ttc	ttc	ctc	gga	cgc	acc	tac	gac	gcc	gaa	cgc	atg			787
Ala	Arg	Glu	Ile	Phe	Phe	Leu	Gly	Arg	Thr	Tyr	Asp	Ala	Glu	Arg	Met			
	215					220					225							
caa	caa	atg	ggc	gca	gtc	aac	atc	gtg	gcc	gac	cac	ggc	gac	cta	gaa			835
Gln	Gln	Met	Gly	Ala	Val	Asn	Ile	Val	Ala	Asp	His	Gly	Asp	Leu	Glu			
	230				235					240					245			
aaa	gaa	gcc	atc	caa	gca	gcc	cgc	gaa	atc	aac	acc	aaa	tcc	ccc	acc			883
Lys	Glu	Ala	Ile	Gln	Ala	Ala	Arg	Glu	Ile	Asn	Thr	Lys	Ser	Pro	Thr			
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Gly	Gln	Arg	Met	Leu	Lys	Phe	Ala	Phe	Asn	Leu	Thr	Asp	Asp	Gly	Leu			
			265				270						275					
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Met	Gly	Gln	Gln	Val	Phe	Ala	Gly	Glu	Ala	Thr	Arg	Leu	Ala	Tyr	Met			
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 Thr Asp Glu Ala Val Glu Gly Lys Glu Ala Phe Leu Glu Lys Arg Glu  
 295 300 305

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 Pro Asn Trp Asn Glu Phe Pro Tyr Tyr Tyr  
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 1080

<210> 498  
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 <213> Corynebacterium glutamicum

<400> 498

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Pro Glu Val Arg Asn Ala Phe Arg Pro His Thr Val Asp Glu Leu Tyr  
 50 55 60

Gln Ala Leu Asp His Ala Arg Arg Thr Pro Asp Val Gly Thr Ile Leu  
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Leu Thr Gly Asn Gly Pro Ser Glu Lys Asp Gly Gly Trp Ala Phe Cys  
 85 90 95

Ser Gly Gly Asp Gln Arg Ile Arg Gly Arg Ser Gly Tyr Gln Tyr Ala  
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Thr Glu His Ala Arg Asp Asp Ala Thr Ala Asp Val Phe Thr Val Asp  
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Ile Ala Arg Thr Lys Val Glu Gly Gly Arg Leu His Ile Leu Glu Val  
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Gln Arg Leu Ile Arg Thr Met Pro Lys Val Val Ile Ala Val Val Asn  
 145 150 155 160

Gly Trp Ala Ala Gly Gly Gly His Ser Leu His Val Val Cys Asp Leu  
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Thr Ile Ala Ser Arg Gln Glu Ala Arg Phe Lys Gln Thr Asp Ala Asp  
 180 185 190

Val Gly Ser Phe Asp Ala Gly Tyr Gly Ser Ala Tyr Leu Ala Lys Met  
 195 200 205

Val Gly Gln Lys Asn Ala Arg Glu Ile Phe Phe Leu Gly Arg Thr Tyr

210	215	220
Asp Ala Glu Arg Met Gln Gln Met Gly Ala Val Asn Ile Val Ala Asp 225 230 235 240		
His Gly Asp Leu Glu Lys Glu Ala Ile Gln Ala Ala Arg Glu Ile Asn 245 250 255		
Thr Lys Ser Pro Thr Gly Gln Arg Met Leu Lys Phe Ala Phe Asn Leu 260 265 270		
Thr Asp Asp Gly Leu Met Gly Gln Gln Val Phe Ala Gly Glu Ala Thr 275 280 285		
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 <213> Corynebacterium glutamicum

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 <223> RXS02908

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 Leu Lys Leu His Pro  
 1 5  
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 Glu Val Leu Glu Arg Ala Ile Ala Asp Ile Lys Gly Val Thr Ala Ala  
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 Cys Val Val Gly Ile Pro Asp Pro Arg Leu Gly Gln Ala Ile Val Ala  
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 Ala Tyr Ser Gly Ser Ile Ser Pro Ser Glu Val Ile Glu Gly Leu Asp  
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 Asp Leu Pro Arg Trp Gln Leu Pro Lys Arg Leu Lys His Leu Glu Ser  
 55 60 65  
 ttg ccc agc att ggt cct gga aaa gct gat cga cgt gct atc gcg aag 355  
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 Leu Phe

<210> 500  
 <211> 87  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 500

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Gln	Ala	Ile	Val	Ala	Ala	Tyr	Ser	Gly	Ser	Ile	Ser	Pro	Ser	Glu	Val
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Ile	Glu	Gly	Leu	Asp	Asp	Leu	Pro	Arg	Trp	Gln	Leu	Pro	Lys	Arg	Leu
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Lys	His	Leu	Glu	Ser	Leu	Pro	Ser	Ile	Gly	Pro	Gly	Lys	Ala	Asp	Arg
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Arg	Ala	Ile	Ala	Lys	Leu	Phe									
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				Met Thr Ser Arg Thr		
				1 5		
ccg ctt gtt tct gtt ctt cct gat ttt ccg tgg gat tcg ctc gct tcc	163					
Pro Leu Val Ser Val Leu Pro Asp Phe Pro Trp Asp Ser Leu Ala Ser						
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Ala Lys Ala Lys Ala Ala Ser His Pro Asp Gly Ile Val Asn Leu Ser						
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Ala	Ile	Ala	Leu	Leu	Pro	Phe	Ala	Leu	Gly	Ile	Ser	Gly	Thr	Val	Val	
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Ile	Pro	Ser	Met	Met	Phe	Ile	Asn	Ser	Pro	Ser	Asn	Pro	Thr	Gly	Lys	
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Asp	Asp	Glu	Asn	Pro	Pro	Ile	Ser	Ile	Leu	Asp	Pro	Arg	Val	Cys	Asp	
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Gly	Asp	His	Thr	Asn	Leu	Ile	Ala	Ile	His	Ser	Leu					
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&lt;211&gt; 225

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 502

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His Gln Gly Glu Leu Ile Asp Ala Leu His Asn Ala Arg Gly Thr His  
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&lt;212&gt; PRT

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Ile Val Asn Gly Ala Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr  
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Tyr	Val	Ala	Ile	Ser	Gln	Phe	Gly	Tyr	Ile	Ile	Thr	Thr	Arg	Ile	Ala	195	200	205	
Ser	Ile	Ala	Asp	Asp	Ala	Ala	Pro	Phe	Ile	Tyr	Gln	Gln	His	Trp	Met	210	215	220	
Leu	Leu	Gln	Val	Pro	Tyr	Gly	Ile	Ile	Gly	Val	Thr	Leu	Leu	Thr	Ala	225	230	235	240
Ile	Met	Pro	Arg	Leu	Ser	Arg	Asn	Ala	Ala	Asp	Gly	Asp	Asp	Arg	Ala	245	250	255	
Val	Val	Ser	Asp	Leu	Gln	Leu	Gly	Ser	Lys	Leu	Thr	Phe	Ile	Ala	Leu	260	265	270	
Ile	Pro	Ile	Val	Val	Phe	Phe	Thr	Ala	Phe	Gly	Val	Pro	Ile	Ala	Asn	275	280	285	
Gly	Leu	Phe	Ala	Tyr	Gly	Gln	Phe	Asp	Ala	Asn	Ala	Ala	Asn	Ile	Leu	290	295	300	
Gly	Trp	Thr	Leu	Ser	Phe	Ser	Ala	Phe	Thr	Leu	Ile	Pro	Tyr	Ala	Leu	305	310	315	320
Val	Leu	Leu	His	Leu	Arg	Val	Phe	Tyr	Ala	Arg	Glu	Glu	Val	Trp	Thr	325	330	335	
Pro	Thr	Phe	Ile	Ile	Ala	Gly	Ile	Thr	Ala	Thr	Lys	Val	Val	Leu	Ser	340	345	350	
Leu	Leu	Ala	Pro	Leu	Leu	Ser	Ser	Ser	Pro	Glu	Arg	Val	Val	Val	Leu	355	360	365	
Leu	Gly	Ala	Ala	Asn	Gly	Phe	Ser	Phe	Ile	Thr	Gly	Ala	Val	Ile	Gly	370	375	380	
Ala	Tyr	Leu	Leu	Arg	Asn	Lys	Leu	Gly	Leu	Leu	Gly	Met	Arg	Ser	Leu	385	390	395	400
Ala	Lys	Thr	Ser	Leu	Trp	Ala	Leu	Gly	Ser	Ala	Ala	Val	Gly	Ala	Ala	405	410	415	
Ala	Ala	Trp	Ala	Leu	Gly	Trp	Leu	Ile	Gln	Ala	Val	Val	Gly	Asp	Phe	420	425	430	
Leu	Leu	Gly	Thr	Leu	Ser	Ser	Val	Gly	Tyr	Leu	Leu	Asn	Leu	Ala	Val	435	440	445	
Leu	Gly	Val	Phe	Phe	Ile	Phe	Val	Thr	Gly	Ile	Val	Leu	Ser	Arg	Ser	450	455	460	
Gly	Leu	Pro	Glu	Val	Gln	Asn	Leu	Gly	Gln	Ala	Leu	Thr	Arg	Ile	Pro	465	470	475	480

Gly	Leu	Ser	Arg	Phe	Ile	Arg	Pro	Asn	Thr	Lys	Ile	Ser	Leu	Asp	Val	485	490	495
Gly	Glu	Val	Ser	Glu	Gln	Asp	Phe	Ser	Thr	Gln	Leu	Val	Ala	Pro	Ser	500	505	510
Glu	Phe	Ala	Ala	Thr	Pro	Val	Pro	Pro	Pro	Met	Ser	Ala	Gly	Ile	Val	515	520	525
Arg	Gly	Pro	Arg	Leu	Val	Pro	Gly	Ala	Pro	Val	Gly	Asp	Gly	Arg	Phe	530	535	540
Arg	Leu	Leu	Ala	Asp	His	Gly	Gly	Val	Gln	Gly	Ala	Arg	Phe	Trp	Gln	545	550	555
Ala	Arg	Glu	Ile	Ala	Thr	Gly	Lys	Glu	Val	Ala	Leu	Ile	Phe	Val	Asp	565	570	575
Thr	Ser	Gly	Asn	Ala	Pro	Phe	Ala	Pro	Leu	Ser	Ser	Ala	Ala	Ala	Ala	580	585	590
Gly	Ile	Ala	Tyr	Glu	Val	Gln	Arg	Arg	Thr	Lys	Lys	Leu	Ala	Ser	Leu	595	600	605
Gly	Ser	Leu	Ala	Val	Ala	Pro	Asn	Ile	His	Ser	Glu	Ala	Tyr	Arg	Asn	610	615	620
Gly	Cys	Leu	Ile	Val	Ala	Asp	Trp	Val	Pro	Gly	Ser	Ser	Leu	Ser	Ala	625	630	635
Val	Ala	Glu	Ser	Gly	Ala	Asp	Pro	Arg	Ala	Ala	Ala	Phe	Ala	Leu	Ala	645	650	655
Glu	Leu	Thr	Glu	Thr	Ile	Gly	Glu	Ala	His	Glu	Met	Gly	Ile	Pro	Ala	660	665	670
Gly	Leu	Asp	Asn	Lys	Cys	Arg	Ile	Arg	Ile	Asn	Thr	Asp	Gly	His	Ala	675	680	685
Val	Leu	Ala	Leu	Pro	Ala	Ile	Leu	Pro	Asp	Ala	Ser	Glu	Leu	Arg	Asp	690	695	700
Ala	Lys	Ser	Leu	Ala	Ser	Ala	Ala	Glu	Met	Leu	Ile	Asp	Ala	Thr	Leu	705	710	715
Ala	Pro	Ser	Asp	Val	Lys	Ala	Met	Val	Thr	Glu	Ala	Gln	Gly	Leu	Ala	725	730	735
Thr	Glu	Asp	Asn	Pro	Asp	Tyr	Ala	Ser	Leu	Ala	Met	Ala	Met	Arg	Thr	740	745	750
Cys	Gly	Leu	Phe	Thr	Glu	Glu	Pro	Thr	His	Leu	Val	Val	Lys	Lys	Glu	755	760	765
Lys	Thr	Pro	Lys	Pro	Ala	Thr	Arg	Asp	Gly	Phe	Gly	Ala	Ser	Asp	Tyr	770	775	780
Thr	Val	Lys	Gly	Met	Ala	Ala	Ile	Ala	Ala	Val	Val	Ile	Ile	Leu	Val	785	790	795
Ser	Leu	Val	Ala	Ala	Gly	Thr	Ala	Phe	Leu	Thr	Ser	Phe	Phe	Gly	Ser			



805								810				815			
Ser	Thr	Asn	Glu	Gln	Ser	Pro	Leu	Ala	Ser	Val	Glu	Ala	Thr	Thr	Ser
			820												830
Ala	Thr	Pro	Glu	Pro	Val	Gly	Pro	Pro	Val	Tyr	Leu	Asp	Leu	Asp	Gln
			835												845
Ala	Arg	Thr	Trp	Asp	Asp	Gly	Ala	Gly	Thr	Asp	Val	Thr	Asp	Val	Thr
			850												860
Asp	Gly	Asn	Thr	Ser	Thr	Ala	Trp	Thr	Ser	Thr	Gly	Gly	Asp	Gly	Leu
															880
Leu	Val	Asp	Leu	Ser	Thr	Pro	Ala	Arg	Leu	Asp	Arg	Val	Ile	Leu	Thr
															895
Thr	Gly	Thr	Gly	Ser	Asp	Ser	Asn	Val	Thr	Ser	Thr	Val	Lys	Ile	Tyr
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Ala	Phe	Asn	Asp	Ala	Ser	Pro	His	Ser	Leu	Ser	Glu	Gly	Ile	Glu	Ile
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Gly	Thr	Val	Asp	Tyr	Ser	Gly	Arg	Ser	Leu	Ser	His	Ser	Ile	Arg	Asp
															940
Ser	Ser	Lys	Leu	Pro	Gly	Gln	Val	Glu	Ser	Val	Val	Ile	Leu	Val	Asp
															960
Glu	Val	Arg	Ser	Ser	Gln	Thr	Ser	Asp	Thr	Asn	Pro	Gln	Met	Gln	Ile
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Ala	Glu	Val	Gln	Leu	Val	Gly	Trp								
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 Met Ser Ile Glu Trp  
 1 5  
 tta caa att gtt gaa tta gga gcg atc ttt ggt gca ggt ttc ctc gca 163  
 Leu Gln Ile Val Glu Leu Gly Ala Ile Phe Gly Ala Gly Phe Leu Ala  
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 Gly Ser Ile Asn Val Ile Val Gly Ala Gly Thr Leu Val Ser Phe Pro  
 25 30 35

att ctc gtg ttc ctg ggc ctt cca ccg ttg act gcc acc atc gcc aac	259
Ile Leu Val Phe Leu Gly Leu Pro Pro Leu Thr Ala Thr Ile Ala Asn	
40 45 50	
acc atc ggc atc gtt cct gga agt att tcg ggt gtg gtt gct tat aga	307
Thr Ile Gly Ile Val Pro Gly Ser Ile Ser Gly Val Val Ala Tyr Arg	
55 60 65	
cgt gaa cta cac gcc cat gta aaa acc atc aga ttt ctg ctg cca gca	355
Arg Glu Leu His Ala His Val Lys Thr Ile Arg Phe Leu Leu Pro Ala	
70 75 80 85	
tca atc ctc gga ggg atc acc ggc gcc tcg ctc ttg ctg cat ttc tcc	403
Ser Ile Leu Gly Gly Ile Thr Gly Ala Ser Leu Leu Leu His Phe Ser	
90 95 100	
gca gat gtt ttt aca gca gta att ccc tgg ctg att gga ttc ggc acg	451
Ala Asp Val Phe Thr Ala Val Ile Pro Trp Leu Ile Gly Phe Gly Thr	
105 110 115	
ctg ttg gtt atc gca ggt cca tca att aag aag cat gtt ggc gct cat	499
Leu Leu Val Ile Ala Gly Pro Ser Ile Lys Lys His Val Gly Ala His	
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act tca ggt ggc atc tct gct ggg ttt agg caa ttg cct ttc ccg agc	547
Thr Ser Gly Gly Ile Ser Ala Gly Phe Arg Gln Leu Pro Phe Pro Ser	
135 140 145	
cga acc acc ttc atc gtc tca gta tgt ggt gcc ctg ttg ctg ggc atg	595
Arg Thr Thr Phe Ile Val Ser Val Cys Gly Ala Leu Leu Leu Gly Met	
150 155 160 165	
tat gga ggg tac ttc agc gca gct caa ggc att ctt ctc atc gca ttg	643
Tyr Gly Gly Tyr Phe Ser Ala Ala Gln Gly Ile Leu Leu Ile Ala Leu	
170 175 180	
ctt ggc atc aca tca acg ctg cag atg cag gaa ctc aac gcc atc aaa	691
Leu Gly Ile Thr Ser Thr Leu Gln Met Gln Glu Leu Asn Ala Ile Lys	
185 190 195	
aac ctc aca gtg gcg gca gtt aat ctc atc gca gcc agt gtt ttt ata	739
Asn Leu Thr Val Ala Ala Val Asn Leu Ile Ala Ala Ser Val Phe Ile	
200 205 210	
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Ile Ile Ser Pro Glu Leu Ile Ser Trp Pro Thr Val Ala Leu Ile Ala	
215 220 225	
ctt ggc tca gct tta ggt gga tac atc ggc gga cgg tac gcc cgc cga	835
Leu Gly Ser Ala Leu Gly Gly Tyr Ile Gly Gly Arg Tyr Ala Arg Arg	
230 235 240 245	
ctt cgc ccc agt gtt ttt aga gca ttt gtg gtc atc gtc gga atc acc	883
Leu Arg Pro Ser Val Phe Arg Ala Phe Val Val Ile Val Gly Ile Thr	
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Thr Val Ile Val Met Thr Ile Gly	
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 <213> Corynebacterium glutamicum

<400> 510

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Leu	Val	Ser	Phe	Pro	Ile	Leu	Val	Phe	Leu	Gly	Leu	Pro	Pro	Leu	Thr
		35					40					45			
Ala	Thr	Ile	Ala	Asn	Thr	Ile	Gly	Ile	Val	Pro	Gly	Ser	Ile	Ser	Gly
	50					55					60				
Val	Val	Ala	Tyr	Arg	Arg	Glu	Leu	His	Ala	His	Val	Lys	Thr	Ile	Arg
	65				70					75					80
Phe	Leu	Leu	Pro	Ala	Ser	Ile	Leu	Gly	Gly	Ile	Thr	Gly	Ala	Ser	Leu
				85					90					95	
Leu	Leu	His	Phe	Ser	Ala	Asp	Val	Phe	Thr	Ala	Val	Ile	Pro	Trp	Leu
			100					105					110		
Ile	Gly	Phe	Gly	Thr	Leu	Leu	Val	Ile	Ala	Gly	Pro	Ser	Ile	Lys	Lys
		115					120					125			
His	Val	Gly	Ala	His	Thr	Ser	Gly	Gly	Ile	Ser	Ala	Gly	Phe	Arg	Gln
	130					135					140				
Leu	Pro	Phe	Pro	Ser	Arg	Thr	Thr	Phe	Ile	Val	Ser	Val	Cys	Gly	Ala
	145				150					155					160
Leu	Leu	Leu	Gly	Met	Tyr	Gly	Gly	Tyr	Phe	Ser	Ala	Ala	Gln	Gly	Ile
				165				170						175	
Leu	Leu	Ile	Ala	Leu	Leu	Gly	Ile	Thr	Ser	Thr	Leu	Gln	Met	Gln	Glu
			180					185					190		
Leu	Asn	Ala	Ile	Lys	Asn	Leu	Thr	Val	Ala	Ala	Val	Asn	Leu	Ile	Ala
		195					200					205			
Ala	Ser	Val	Phe	Ile	Ile	Ile	Ser	Pro	Glu	Leu	Ile	Ser	Trp	Pro	Thr
	210					215					220				
Val	Ala	Leu	Ile	Ala	Leu	Gly	Ser	Ala	Leu	Gly	Gly	Tyr	Ile	Gly	Gly
	225				230					235					240
Arg	Tyr	Ala	Arg	Arg	Leu	Arg	Pro	Ser	Val	Phe	Arg	Ala	Phe	Val	Val
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&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(646)

&lt;223&gt; RXC02789

&lt;400&gt; 511

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				Met	Lys	Val	Ser	Ala		
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gat	aca	ccc	ggt	cac	gat	gat	cca	ggc	cca	ggc	cgg	cgc	ctt	ggc	tta		163
Asp	Thr	Pro	Gly	His	Asp	Asp	Pro	Gly	Pro	Gly	Arg	Arg	Leu	Gly	Leu		
				10				15						20			

gat	gtc	ggc	acc	gtg	cgc	atc	gga	gtg	gca	gcc	tct	gac	cgc	gat	gcc		211
Asp	Val	Gly	Thr	Val	Arg	Ile	Gly	Val	Ala	Ala	Ser	Asp	Arg	Asp	Ala		
			25				30						35				

aag	ctt	gcc	atg	cct	gtg	gaa	acc	gtt	ccg	cgg	gaa	act	gga	ttc	aaa		259
Lys	Leu	Ala	Met	Pro	Val	Glu	Thr	Val	Pro	Arg	Glu	Thr	Gly	Phe	Lys		
		40				45					50						

ggg	cca	gac	ctg	gcc	gat	att	gat	cgg	ttg	gtc	gcc	atc	gtt	gag	gaa		307
Gly	Pro	Asp	Leu	Ala	Asp	Ile	Asp	Arg	Leu	Val	Ala	Ile	Val	Glu	Glu		
	55					60					65						

tac	aac	gcc	gtg	gaa	gtc	att	gtt	ggt	cta	ccc	aca	gat	ctg	cag	gga		355
Tyr	Asn	Ala	Val	Glu	Val	Ile	Val	Gly	Leu	Pro	Thr	Asp	Leu	Gln	Gly		
70				75					80					85			

aat	ggc	tcc	gcc	agt	gtg	aag	cat	gca	aag	gaa	att	gct	ttc	cgc	gtc		403
Asn	Gly	Ser	Ala	Ser	Val	Lys	His	Ala	Lys	Glu	Ile	Ala	Phe	Arg	Val		
				90				95					100				

cgt	cgg	cgc	ctc	acc	aat	gct	gga	aag	aac	att	ccg	gta	cgg	ctt	ggc		451
Arg	Arg	Arg	Leu	Thr	Asn	Ala	Gly	Lys	Asn	Ile	Pro	Val	Arg	Leu	Gly		
			105				110						115				

gac	gaa	cgc	ctc	acc	acc	gtc	gtg	gcc	acc	caa	gcc	ttg	cgg	gcc	tca		499
Asp	Glu	Arg	Leu	Thr	Thr	Val	Val	Ala	Thr	Gln	Ala	Leu	Arg	Ala	Ser		
		120				125					130						

gga	gtc	agc	gaa	aaa	gcg	gga	cgt	aaa	gtt	att	gat	caa	gct	gcc	gca		547
Gly	Val	Ser	Glu	Lys	Ala	Gly	Arg	Lys	Val	Ile	Asp	Gln	Ala	Ala	Ala		
	135					140				145							

gta	gaa	atc	ctt	caa	acc	tgg	ttg	gat	gct	cgc	acc	cga	gcc	ctt	gaa		595
Val	Glu	Ile	Leu	Gln	Thr	Trp	Leu	Asp	Ala	Arg	Thr	Arg	Ala	Leu	Glu		
150				155					160					165			

cca	caa	tcc	aca	gac	acc	caa	gat	ttc	gac	gag	aag	gga	aat	ttc	cca		643
Pro	Gln	Ser	Thr	Asp	Thr	Gln	Asp	Phe	Asp	Glu	Lys	Gly	Asn	Phe	Pro		
				170				175					180				

gga	tgaaccaa	aat	ccgaaaccgc	cgg													669
Gly																	



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Ala Ala Ser Gly Trp Gly Ile Leu Ile Ala Gly Ala Ala Val Ala Gly	
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Trp Ile Asp Ala Val Ile Gly Gly Gly Leu Val Leu Ile Pro Leu	
25 30 35	
atc ctc gcg gtc atg ccg caa ctc gca cct gtg aca gcg ctg gcc tcc	259
Ile Leu Ala Val Met Pro Gln Leu Ala Pro Val Thr Ala Leu Ala Ser	
40 45 50	
aac aaa ctg gca gcc gtc acc ggc acg gca tcg gcg gca ttc acc ctg	307
Asn Lys Leu Ala Ala Val Thr Gly Thr Ala Ser Ala Ala Phe Thr Leu	
55 60 65	
gtc agg cgc gtc aaa ccc gac aaa aaa ctg ctt gcg ctc tac gtt ctg	355
Val Arg Arg Val Lys Pro Asp Lys Lys Leu Leu Ala Leu Tyr Val Leu	
70 75 80 85	
gtg gca gct gtg tgc tcc ggt gca ggc gcc ctg gct gcg agt ctc att	403
Val Ala Ala Val Cys Ser Gly Ala Gly Ala Leu Ala Ala Ser Leu Ile	
90 95 100	
gac aaa caa atc atg cga ccg ctg atc atc gtg ttg atg ctg gtc gtt	451
Asp Lys Gln Ile Met Arg Pro Leu Ile Ile Val Leu Met Leu Val Val	
105 110 115	
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Gly Leu Ile Val Val Phe Lys Pro Asn Phe Gly Thr Gly Glu Ser Lys	
120 125 130	
gcc ctg ccc acc gga tgg aaa cgc tgg gcc gcc atc gtt gca gtc gga	547
Ala Leu Pro Thr Gly Trp Lys Arg Trp Ala Ala Ile Val Ala Val Gly	
135 140 145	
ctc atc gca gcc tac gac ggc atc ttc gga ccc gga acc ggc atg ttc	595
Leu Ile Ala Ala Tyr Asp Gly Ile Phe Gly Pro Gly Thr Gly Met Phe	
150 155 160 165	
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Leu Ile Met Ala Phe Thr Ala Leu Leu Ser Gln Asn Phe Leu Ser Ser	
170 175 180	
gca gcc atg gcg aag gtc gta aac acc gca aca aac ctg ggt gcg cta	691
Ala Ala Met Ala Lys Val Val Asn Thr Ala Thr Asn Leu Gly Ala Leu	
185 190 195	
att gta ttc atc atc ggc ggc cac atg tgg tgg acc cta gga ctc gtg	739
Ile Val Phe Ile Ile Gly Gly His Met Trp Trp Thr Leu Gly Leu Val	
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Leu Ala Val Ala Asn Val Ala Gly Ala Gln Leu Gly Ala Arg Thr Val	
215 220 225	
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Leu Gly Gly Gly Thr Arg Leu Ile Arg Tyr Ala Leu Leu Thr Leu Val	
230 235 240 245	

gtc gtc atg agc gtc tac ctc acc tgg caa caa atc caa gga atg 880  
 Val Val Met Ser Val Tyr Leu Thr Trp Gln Gln Ile Gln Gly Met  
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Val Leu Ile Pro Leu Ile Leu Ala Val Met Pro Gln Leu Ala Pro Val  
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Thr Ala Leu Ala Ser Asn Lys Leu Ala Ala Val Thr Gly Thr Ala Ser  
                   50                  55                  60

Ala Ala Phe Thr Leu Val Arg Arg Val Lys Pro Asp Lys Lys Leu Leu  
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Ala Leu Tyr Val Leu Val Ala Ala Val Cys Ser Gly Ala Gly Ala Leu  
                   85                  90                  95

Ala Ala Ser Leu Ile Asp Lys Gln Ile Met Arg Pro Leu Ile Ile Val  
                   100                  105                  110

Leu Met Leu Val Val Gly Leu Ile Val Val Phe Lys Pro Asn Phe Gly  
                   115                  120                  125

Thr Gly Glu Ser Lys Ala Leu Pro Thr Gly Trp Lys Arg Trp Ala Ala  
                   130                  135                  140

Ile Val Ala Val Gly Leu Ile Ala Ala Tyr Asp Gly Ile Phe Gly Pro  
   145                  150                  155                  160

Gly Thr Gly Met Phe Leu Ile Met Ala Phe Thr Ala Leu Leu Ser Gln  
                   165                  170                  175

Asn Phe Leu Ser Ser Ala Ala Met Ala Lys Val Val Asn Thr Ala Thr  
                   180                  185                  190

Asn Leu Gly Ala Leu Ile Val Phe Ile Ile Gly Gly His Met Trp Trp  
                   195                  200                  205

Thr Leu Gly Leu Val Leu Ala Val Ala Asn Val Ala Gly Ala Gln Leu  
                   210                  215                  220

Gly Ala Arg Thr Val Leu Gly Gly Gly Thr Arg Leu Ile Arg Tyr Ala  
   225                  230                  235                  240

Leu Leu Thr Leu Val Val Val Met Ser Val Tyr Leu Thr Trp Gln Gln  
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Ile Gln Gly Met  
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<223> RXN03063

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Val Glu Asp Leu Ser  
1 5

tac cgc atc ccg cag tcg cgc acc gtg gcc gag cag gtg cca ggg ccg 163  
Tyr Arg Ile Pro Gln Ser Arg Thr Val Ala Glu Gln Val Pro Gly Pro  
10 15 20

aag tcg aaa gcg ctg gat gag cgt cga caa gca gca gta gca cga gca 211  
Lys Ser Lys Ala Leu Asp Glu Arg Arg Gln Ala Ala Val Ala Arg Ala  
25 30 35

ctt gca ccg ggt ctg cct gga tac gtg gtg gac gca gac ggt ggc atc 259  
Leu Ala Pro Gly Leu Pro Gly Tyr Val Val Asp Ala Asp Gly Gly Ile  
40 45 50

ttg gct gac gcg gac ggc aac cgt ttc atc gac ctg gcc tcc ggc atc 307  
Leu Ala Asp Ala Asp Gly Asn Arg Phe Ile Asp Leu Ala Ser Gly Ile  
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gcc gtg acc acg gtc ggc gga tcc aac gcg gcc gtc gcg aaa gcc gtc 355  
Ala Val Thr Thr Val Gly Gly Ser Asn Ala Ala Val Ala Lys Ala Val  
70 75 80 85

ggc gcc gca gct gcc cgc ttc acc cac acc tgc ttc atg gtc tca cct 403  
Gly Ala Ala Ala Ala Arg Phe Thr His Thr Cys Phe Met Val Ser Pro  
90 95 100

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Tyr Glu Thr Tyr Val Ala Met Ala Glu Arg Leu Asn Ala Leu Thr Pro  
105 110 115

ggc gat cac gac aag aag agc gcg ctg ttt aac tct ggc gcc gaa gcc 499  
Gly Asp His Asp Lys Lys Ser Ala Leu Phe Asn Ser Gly Ala Glu Ala  
120 125 130

gtg gaa aac gcc gtc aag gtg gca cgc gcc tac acc ggc aag ggc gcg 547  
Val Glu Asn Ala Val Lys Val Ala Arg Ala Tyr Thr Gly Lys Gly Ala  
135 140 145

gtc gtg gtg ttc gac aac gcg tac cac gga cgg acc aac ctc acc atg 595  
Val Val Val Phe Asp Asn Ala Tyr His Gly Arg Thr Asn Leu Thr Met  
150 155 160 165



gcg atg acc gcg aag aac cgc cca tac aag tcc gga ttc gga cca cta 643  
 Ala Met Thr Ala Lys Asn Arg Pro Tyr Lys Ser Gly Phe Gly Pro Leu  
 170 175 180

gcc gca gac gtc tac cgt gca cca atg tct tac cca ctg cgc gac gga 691  
 Ala Ala Asp Val Tyr Arg Ala Pro Met Ser Tyr Pro Leu Arg Asp Gly  
 185 190 195

ctg tcc ggc ccg gaa gcc gca gag cgc gcg atc tcc gtg atc gaa tcc 739  
 Leu Ser Gly Pro Glu Ala Ala Glu Arg Ala Ile Ser Val Ile Glu Ser  
 200 205 210

cag gtc gga gcc gaa aac ctc gcc tgc gtg gtc att gaa ccg atc cag 787  
 Gln Val Gly Ala Glu Asn Leu Ala Cys Val Val Ile Glu Pro Ile Gln  
 215 220 225

ggc gaa ggc gga ttc atc gtc ccc gca cca gga ttc ctc gca gcc att 835  
 Gly Glu Gly Gly Phe Ile Val Pro Ala Pro Gly Phe Leu Ala Ala Ile  
 230 235 240 245

tcc acc tgg tgc cgc gag aac gac gtg gtg ttc atc gcc gat gaa atc 883  
 Ser Thr Trp Cys Arg Glu Asn Asp Val Val Phe Ile Ala Asp Glu Ile  
 250 255 260

caa tct ggc ttc ctg cgc acc ggc gac tgg ttc gcc agc gac gca gaa 931  
 Gln Ser Gly Phe Leu Arg Thr Gly Asp Trp Phe Ala Ser Asp Ala Glu  
 265 270 275

ggt gtg atc ccc gac gtc atc acc acc gca aaa ggc atc gcc ggc ggc 979  
 Gly Val Ile Pro Asp Val Ile Thr Thr Ala Lys Gly Ile Ala Gly Gly  
 280 285 290

atg cca cta tcc gca gtg acc ggc cgc gca gaa atc atg gac gca ccc  
 1027  
 Met Pro Leu Ser Ala Val Thr Gly Arg Ala Glu Ile Met Asp Ala Pro  
 295 300 305

ggc ccc ggc gcg ctc ggc gga acc tac ggc gga aac ccc gtt gct tgc  
 1075  
 Gly Pro Gly Ala Leu Gly Gly Thr Tyr Gly Gly Asn Pro Val Ala Cys  
 310 315 320 325

gcc gcg gca ctt gca gcc att gaa gtg atg gaa caa gcc gac ctt aag  
 1123  
 Ala Ala Ala Leu Ala Ala Ile Glu Val Met Glu Gln Ala Asp Leu Lys  
 330 335 340

acc cgc gcg  
 1132  
 Thr Arg Ala

&lt;210&gt; 516

&lt;211&gt; 344

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 516

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Gln	Val	Pro	Gly	Pro	Lys	Ser	Lys	Ala	Leu	Asp	Glu	Arg	Arg	Gln	Ala		
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Ala	Val	Ala	Arg	Ala	Leu	Ala	Pro	Gly	Leu	Pro	Gly	Tyr	Val	Val	Asp		
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Ala	Asp	Gly	Gly	Ile	Leu	Ala	Asp	Ala	Asp	Gly	Asn	Arg	Phe	Ile	Asp		
	50					55					60						
Leu	Ala	Ser	Gly	Ile	Ala	Val	Thr	Thr	Val	Gly	Gly	Ser	Asn	Ala	Ala		
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Val	Ala	Lys	Ala	Val	Gly	Ala	Ala	Ala	Ala	Arg	Phe	Thr	His	Thr	Cys		
				85					90					95			
Phe	Met	Val	Ser	Pro	Tyr	Glu	Thr	Tyr	Val	Ala	Met	Ala	Glu	Arg	Leu		
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Asn	Ala	Leu	Thr	Pro	Gly	Asp	His	Asp	Lys	Lys	Ser	Ala	Leu	Phe	Asn		
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Ser	Gly	Ala	Glu	Ala	Val	Glu	Asn	Ala	Val	Lys	Val	Ala	Arg	Ala	Tyr		
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Thr	Gly	Lys	Gly	Ala	Val	Val	Val	Phe	Asp	Asn	Ala	Tyr	His	Gly	Arg		
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Thr	Asn	Leu	Thr	Met	Ala	Met	Thr	Ala	Lys	Asn	Arg	Pro	Tyr	Lys	Ser		
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Gly	Phe	Gly	Pro	Leu	Ala	Ala	Asp	Val	Tyr	Arg	Ala	Pro	Met	Ser	Tyr		
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Pro	Leu	Arg	Asp	Gly	Leu	Ser	Gly	Pro	Glu	Ala	Ala	Glu	Arg	Ala	Ile		
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Ser	Val	Ile	Glu	Ser	Gln	Val	Gly	Ala	Glu	Asn	Leu	Ala	Cys	Val	Val		
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Ile	Glu	Pro	Ile	Gln	Gly	Glu	Gly	Gly	Phe	Ile	Val	Pro	Ala	Pro	Gly		
225					230					235					240		
Phe	Leu	Ala	Ala	Ile	Ser	Thr	Trp	Cys	Arg	Glu	Asn	Asp	Val	Val	Phe		
				245					250					255			
Ile	Ala	Asp	Glu	Ile	Gln	Ser	Gly	Phe	Leu	Arg	Thr	Gly	Asp	Trp	Phe		
			260					265					270				
Ala	Ser	Asp	Ala	Glu	Gly	Val	Ile	Pro	Asp	Val	Ile	Thr	Thr	Ala	Lys		
		275					280					285					
Gly	Ile	Ala	Gly	Gly	Met	Pro	Leu	Ser	Ala	Val	Thr	Gly	Arg	Ala	Glu		
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Ile	Met	Asp	Ala	Pro	Gly	Pro	Gly	Ala	Leu	Gly	Gly	Thr	Tyr	Gly	Gly		
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Asn	Pro	Val	Ala	Cys	Ala	Ala	Ala	Leu	Ala	Ala	Ile	Glu	Val	Met	Glu		
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Gln Ala Asp Leu Lys Thr Arg Ala  
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<213> Corynebacterium glutamicum

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<223> RXN02970

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Leu Ala Leu Lys Gly  
1 5  
tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca 163  
Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala  
10 15 20  
aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc 211  
Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe  
25 30 35  
cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct 259  
His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala  
40 45 50  
gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac 307  
Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp  
55 60 65  
atg ggt tcc caa ctt gtc tcg gca aac tta ggc cac aac aac cct cga 355  
Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg  
70 75 80 85  
tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac 403  
Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn  
90 95 100  
ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg 451  
Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val  
105 110 115  
tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc 499  
Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly  
120 125 130  
gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga 547  
Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly  
135 140 145  
cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga 595  
Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly  
150 155 160 165

tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc	643
Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr	
170 175 180	
acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc	691
Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser	
185 190 195	
tca ttc ttt gcc acc acc caa gaa gaa gaa tgc gaa cgc gca ctc aag	739
Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys	
200 205 210	
cac ttg gaa gat gtc atc gcg ttt gaa ggt gct ggc atg atc gca gcg	787
His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala	
215 220 225	
atc gtc ctg gag cca gtg gtg gga tca tca gga atc atc ctg cca cca	835
Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro	
230 235 240 245	
gca ggt tac tta aat ggc gtg cgc gaa ctt tgc aac aag cac ggc atc	883
Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile	
250 255 260	
ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa	931
Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys	
265 270 275	
ctg ttt gct tac gag cat gct ggc gac gat ttc cag cca gac atg atc	979
Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile	
280 285 290	
acc ttc gcc aag ggt gtt aac gca ggt tac gcc cca ctc ggt ggc atc	
1027 Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile	
295 300 305	
gtg atg acc caa tca atc cgc gat acc ttc gga tca gag gca tac tcc	
1075 Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly Ser Glu Ala Tyr Ser	
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1123 Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys	
330 335 340	
gca gcg ctg gag att tac gcg gaa gga gag atc att cca cgc gta gct	
1171 Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala	
345 350 355	
cga ctt ggc gct gaa ctg atc gaa cct cgc ctt cgt gaa cta gcg gaa	
1219 Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu	
360 365 370	
gaa aac gta gcg atc gct gac gtg cgg ggc atc gga ttc ttc tgg gca	
1267 Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile Gly Phe Phe Trp Ala	
375 380 385	

gtg gag ttc aat gca gac gcc act gcc atg gct gcc ggt gct gca gaa  
 1315  
 Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu  
 390 395 400 405

ttc aag gaa cgc ggc gtg tgg ccg atg atc tcc ggc aac cga ttc cac  
 1363  
 Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser Gly Asn Arg Phe His  
 410 415 420

atc gcg ccg ccg ctg acc acc act gat gac gaa ttg gta gca ctg ctg  
 1411  
 Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu Leu Val Ala Leu Leu  
 425 430 435

gac gcg gtg gaa gct gca gcc caa gct gtc gag ctg acc ttc gct ggg  
 1459  
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 1491  
 Ala Leu Phe  
 455

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 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 518  
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 Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro  
 35 40 45  
 Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly  
 50 55 60  
 Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly  
 65 70 75 80  
 His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg  
 85 90 95  
 Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val  
 100 105 110  
 Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe  
 115 120 125  
 Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala  
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 Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr

145				150						155				160		
His	Gly	Ala	Thr	Gly	Ser	Ala	Met	Met	Leu	Thr	Gly	Glu	His	Arg	Arg	
				165					170					175		
Leu	Gly	Asn	Pro	Thr	Thr	Asp	Pro	Asp	Ile	Tyr	His	Phe	Trp	Ala	Pro	
			180					185					190			
Phe	Leu	His	His	Ser	Ser	Phe	Phe	Ala	Thr	Thr	Gln	Glu	Glu	Glu	Cys	
		195					200					205				
Glu	Arg	Ala	Leu	Lys	His	Leu	Glu	Asp	Val	Ile	Ala	Phe	Glu	Gly	Ala	
	210					215					220					
Gly	Met	Ile	Ala	Ala	Ile	Val	Leu	Glu	Pro	Val	Val	Gly	Ser	Ser	Gly	
225					230					235					240	
Ile	Ile	Leu	Pro	Pro	Ala	Gly	Tyr	Leu	Asn	Gly	Val	Arg	Glu	Leu	Cys	
				245					250					255		
Asn	Lys	His	Gly	Ile	Leu	Phe	Ile	Ala	Asp	Glu	Val	Met	Val	Gly	Phe	
			260					265					270			
Gly	Arg	Thr	Gly	Lys	Leu	Phe	Ala	Tyr	Glu	His	Ala	Gly	Asp	Asp	Phe	
		275					280					285				
Gln	Pro	Asp	Met	Ile	Thr	Phe	Ala	Lys	Gly	Val	Asn	Ala	Gly	Tyr	Ala	
	290					295					300					
Pro	Leu	Gly	Gly	Ile	Val	Met	Thr	Gln	Ser	Ile	Arg	Asp	Thr	Phe	Gly	
305					310					315					320	
Ser	Glu	Ala	Tyr	Ser	Gly	Gly	Leu	Thr	Tyr	Ser	Gly	His	Pro	Leu	Ala	
				325					330					335		
Val	Ala	Pro	Ala	Lys	Ala	Ala	Leu	Glu	Ile	Tyr	Ala	Glu	Gly	Glu	Ile	
			340					345					350			
Ile	Pro	Arg	Val	Ala	Arg	Leu	Gly	Ala	Glu	Leu	Ile	Glu	Pro	Arg	Leu	
		355					360					365				
Arg	Glu	Leu	Ala	Glu	Glu	Asn	Val	Ala	Ile	Ala	Asp	Val	Arg	Gly	Ile	
	370					375					380					
Gly	Phe	Phe	Trp	Ala	Val	Glu	Phe	Asn	Ala	Asp	Ala	Thr	Ala	Met	Ala	
385					390				395						400	
Ala	Gly	Ala	Ala	Glu	Phe	Lys	Glu	Arg	Gly	Val	Trp	Pro	Met	Ile	Ser	
				405					410					415		
Gly	Asn	Arg	Phe	His	Ile	Ala	Pro	Pro	Leu	Thr	Thr	Thr	Asp	Asp	Glu	
			420					425					430			
Leu	Val	Ala	Leu	Leu	Asp	Ala	Val	Glu	Ala	Ala	Ala	Gln	Ala	Val	Glu	
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&lt;210&gt; 519

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 <213> Corynebacterium glutamicum

<220>  
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 Leu Ala Leu Lys Gly  
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tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca 163  
 Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala  
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aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc 211  
 Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe  
 25 30 35

cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct 259  
 His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala  
 40 45 50

gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac 307  
 Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp  
 55 60 65

atg ggt tcc caa ctt gtc tcg gca aac tta ggc cac aac aac cct cga 355  
 Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg  
 70 75 80 85

tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac 403  
 Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn  
 90 95 100

ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg 451  
 Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val  
 105 110 115

tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc 499  
 Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly  
 120 125 130

gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga 547  
 Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly  
 135 140 145

cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga 595  
 Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly  
 150 155 160 165

tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc 643  
 Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr  
 170 175 180

acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc 691

Thr	Asp	Pro	Asp	Ile	Tyr	His	Phe	Trp	Ala	Pro	Phe	Leu	His	His	Ser		
			185					190					195				
tca	ttc	ttt	gcc	acc	acc	caa	gaa	gaa	gaa	tgc	gaa	cgc	gca	ctc	aag	739	
Ser	Phe	Phe	Ala	Thr	Thr	Gln	Glu	Glu	Glu	Cys	Glu	Arg	Ala	Leu	Lys		
		200					205					210					
cac	ttg	gaa	gat	gtc	atc	gcg	ttt	gaa	ggc	gct	ggc	atg	atc	gca	gcg	787	
His	Leu	Glu	Asp	Val	Ile	Ala	Phe	Glu	Gly	Ala	Gly	Met	Ile	Ala	Ala		
	215					220					225						
atc	gtc	ctg	gag	cca	gtg	gtg	gga	tca	tca	gga	atc	atc	ctg	cca	cca	835	
Ile	Val	Leu	Glu	Pro	Val	Val	Gly	Ser	Ser	Gly	Ile	Ile	Leu	Pro	Pro		
230					235					240					245		
gca	ggc	tac	tta	aat	ggc	gtg	cgc	gaa	ctt	tgc	aac	aag	cac	ggc	atc	883	
Ala	Gly	Tyr	Leu	Asn	Gly	Val	Arg	Glu	Leu	Cys	Asn	Lys	His	Gly	Ile		
				250					255					260			
ctc	ttc	atc	gcc	gac	gaa	gtc	atg	gtc	gga	ttc	gga	cgc	acc	gga	aaa	931	
Leu	Phe	Ile	Ala	Asp	Glu	Val	Met	Val	Gly	Phe	Gly	Arg	Thr	Gly	Lys		
			265					270					275				
ctg	ttt	gct	tac	gag	cat	gct	ggc	gac	gat	ttc	cag	cca	gac	atg	atc	979	
Leu	Phe	Ala	Tyr	Glu	His	Ala	Gly	Asp	Asp	Phe	Gln	Pro	Asp	Met	Ile		
		280					285					290					
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1027																	
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1075																	
Val	Met	Thr	Gln	Ser	Ile	Arg	Asp	Thr	Phe	Gly	Ser	Glu	Ala	Tyr	Ser		
310					315					320					325		
ggc	gga	ctc	acc	tac	tcc	gga	cac	cca	ctt	gca	gta	gca	ccc	gcc	aag		
1123																	
Gly	Gly	Leu	Thr	Tyr	Ser	Gly	His	Pro	Leu	Ala	Val	Ala	Pro	Ala	Lys		
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gca	gcg	ctg	gag	att	tac	gcg	gaa	gga	gag	atc	att	cca	cgc	gta	gct		
1171																	
Ala	Ala	Leu	Glu	Ile	Tyr	Ala	Glu	Gly	Glu	Ile	Ile	Pro	Arg	Val	Ala		
			345					350					355				
cga	ctt	ggc	gct	gaa	ctg	atc	gaa	cct	cgc	ctt	cgt	gaa	cta	gcg	gaa		
1219																	
Arg	Leu	Gly	Ala	Glu	Leu	Ile	Glu	Pro	Arg	Leu	Arg	Glu	Leu	Ala	Glu		
		360					365					370					
gaa	aac	gta	gcg	atc	gct	gac	gtg	cgg	ggc	atc	gga	ttc	ttc	tgg	gca		
1267																	
Glu	Asn	Val	Ala	Ile	Ala	Asp	Val	Arg	Gly	Ile	Gly	Phe	Phe	Trp	Ala		
	375					380					385						
gtg	gag	ttc	aat	gca	gac	gcc	act	gcc	atg	gct	gcc	ggc	gct	gca	gaa		
1315																	
Val	Glu	Phe	Asn	Ala	Asp	Ala	Thr	Ala	Met	Ala	Ala	Gly	Ala	Ala	Glu		
390					395					400					405		



ttc aag gaa cgc ggc  
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 Phe Lys Glu Arg Gly  
 410

<210> 520  
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 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 520  
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 Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro  
 35 40 45  
 Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly  
 50 55 60  
 Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly  
 65 70 75 80  
 His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg  
 85 90 95  
 Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val  
 100 105 110  
 Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe  
 115 120 125  
 Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala  
 130 135 140  
 Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr  
 145 150 155 160  
 His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg  
 165 170 175  
 Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro  
 180 185 190  
 Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys  
 195 200 205  
 Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala  
 210 215 220  
 Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly  
 225 230 235 240  
 Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys  
 245 250 255

Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe  
 260 265 270  
 Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe  
 275 280 285  
 Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala  
 290 295 300  
 Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly  
 305 310 315 320  
 Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala  
 325 330 335  
 Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile  
 340 345 350  
 Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu  
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 Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile  
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 Leu Lys Ala Val Pro  
 1 5  
 acg ggc gcc cga gca cgg gct gag atc gcg ctg att gct gcg cga gca 163  
 Thr Gly Ala Arg Ala Arg Ala Glu Ile Ala Leu Ile Ala Ala Arg Ala  
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 ccg ttt gaa cct gtc cgg tta gca ccg gcg aag gaa gag agg aat ggt 211  
 Pro Phe Glu Pro Val Arg Leu Ala Pro Ala Lys Glu Glu Arg Asn Gly  
 25 30 35  
 gca atg acg cct acc caa aat gag atc cac ccg aaa cat agc tac tcc 259  
 Ala Met Thr Pro Thr Gln Asn Glu Ile His Pro Lys His Ser Tyr Ser  
 40 45 50  
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Pro	Ile	Arg	Lys	Asp	Gly	Leu	Glu	Val	Pro	Glu	Thr	Glu	Ile	Arg	Leu		
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gat	gac	tcg	cca	agc	ggc	ccc	aac	gaa	ccc	ttc	cgc	atc	tac	cgc	acc	355	
Asp	Asp	Ser	Pro	Ser	Gly	Pro	Asn	Glu	Pro	Phe	Arg	Ile	Tyr	Arg	Thr		
	70				75					80					85		
cgt	ggc	cca	gaa	acc	aac	ccc	aag	cag	gga	ctt	ccg	cgg	ctg	cgc	gag	403	
Arg	Gly	Pro	Glu	Thr	Asn	Pro	Lys	Gln	Gly	Leu	Pro	Arg	Leu	Arg	Glu		
				90					95					100			
tca	tgg	atc	acc	gcc	cgc	ggc	gac	gtt	gcc	acc	tat	cag	ggg	cgc	gag	451	
Ser	Trp	Ile	Thr	Ala	Arg	Gly	Asp	Val	Ala	Thr	Tyr	Gln	Gly	Arg	Glu		
			105					110					115				
cgt	ttg	ctt	atc	gac	gac	ggc	cgc	tcg	gca	atg	cgt	cga	ggt	caa	gct	499	
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tcg	gct	gag	tgg	aaa	ggc	caa	aaa	cca	gct	cct	ttg	aag	gcg	cta	cct	547	
Ser	Ala	Glu	Trp	Lys	Gly	Gln	Lys	Pro	Ala	Pro	Leu	Lys	Ala	Leu	Pro		
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ggc	aaa	aga	gtc	acc	caa	atg	gcc	tat	gca	cgt	gct	ggc	gtg	att	act	595	
Gly	Lys	Arg	Val	Thr	Gln	Met	Ala	Tyr	Ala	Arg	Ala	Gly	Val	Ile	Thr		
	150				155					160					165		
cgt	gaa	atg	gag	ttt	gta	gcg	ctg	cgc	gaa	cac	gtt	gat	gcg	gag	ttt	643	
Arg	Glu	Met	Glu	Phe	Val	Ala	Leu	Arg	Glu	His	Val	Asp	Ala	Glu	Phe		
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gtg	cgc	tct	gag	gtg	gcg	cgc	ggc	cgg	gcc	att	att	ccc	aac	aac	gtc	691	
Val	Arg	Ser	Glu	Val	Ala	Arg	Gly	Arg	Ala	Ile	Ile	Pro	Asn	Asn	Val		
			185					190					195				
aac	cac	ccc	gaa	tct	gaa	ccg	atg	att	att	ggc	cgc	aaa	ttt	ttg	acc	739	
Asn	His	Pro	Glu	Ser	Glu	Pro	Met	Ile	Ile	Gly	Arg	Lys	Phe	Leu	Thr		
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aaa	atc	aac	gcc	aat	att	ggc	aat	tct	gcg	gtc	acc	tct	tca	atc	gag	787	
Lys	Ile	Asn	Ala	Asn	Ile	Gly	Asn	Ser	Ala	Val	Thr	Ser	Ser	Ile	Glu		
	215					220					225						
gaa	gag	gtg	tcc	aag	ctg	cag	tgg	gcc	acg	cgc	tgg	ggt	gcc	gat	acc	835	
Glu	Glu	Val	Ser	Lys	Leu	Gln	Trp	Ala	Thr	Arg	Trp	Gly	Ala	Asp	Thr		
	230				235					240				245			
gtg	atg	gat	cta	tcc	acc	ggc	gat	gat	att	cac	acc	acc	cgc	gaa	tgg	883	
Val	Met	Asp	Leu	Ser	Thr	Gly	Asp	Asp	Ile	His	Thr	Thr	Arg	Glu	Trp		
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att	atc	cgc	aac	tcc	ccc	gtt	cct	atc	ggc	acc	gtc	ccg	atc	tac	caa	931	
Ile	Ile	Arg	Asn	Ser	Pro	Val	Pro	Ile	Gly	Thr	Val	Pro	Ile	Tyr	Gln		
			265				270						275				
gcg	ctg	gaa	aaa	gta	aat	ggc	gtg	gcc	gca	gac	ctt	aac	tgg	gaa	gta	979	
Ala	Leu	Glu	Lys	Val	Asn	Gly	Val	Ala	Ala	Asp	Leu	Asn	Trp	Glu	Val		
		280					285					290					
ttc	cgc	gat	acc	atc	att	gag	cag	tgt	gaa	caa	ggc	gtg	gac	tat	atg		
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Phe	Arg	Asp	Thr	Ile	Ile	Glu	Gln	Cys	Glu	Gln	Gly	Val	Asp	Tyr	Met
295						300					305				
acc	atc	cac	gcc	ggc	gtc	ctg	ctg	gct	tat	atc	cca	ctg	act	acc	cgt
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Thr	Ile	His	Ala	Gly	Val	Leu	Leu	Ala	Tyr	Ile	Pro	Leu	Thr	Thr	Arg
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cgt	gtc	acc	ggc	att	gtc	tcc	cgc	ggc	gga	tcc	att	atg	gcc	ggc	tgg
1123															
Arg	Val	Thr	Gly	Ile	Val	Ser	Arg	Gly	Gly	Ser	Ile	Met	Ala	Gly	Trp
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tgt	ctg	gcg	cat	cac	cgc	gaa	tca	ttc	ctc	tac	gag	cat	ttc	gac	gag
1171															
Cys	Leu	Ala	His	His	Arg	Glu	Ser	Phe	Leu	Tyr	Glu	His	Phe	Asp	Glu
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ctg	tgc	gaa	atc	ttt	gca	caa	tat	gac	gtc	gca	ttc	tcc	ctc	ggc	gat
1219															
Leu	Cys	Glu	Ile	Phe	Ala	Gln	Tyr	Asp	Val	Ala	Phe	Ser	Leu	Gly	Asp
		360					365					370			
ggc	cta	cgc	ccc	gga	tcg	ctt	gcc	gat	gcc	aac	gac	gcc	gcg	caa	ttc
1267															
Gly	Leu	Arg	Pro	Gly	Ser	Leu	Ala	Asp	Ala	Asn	Asp	Ala	Ala	Gln	Phe
	375					380					385				
gcc	gag	ctg	aaa	acc	att	ggc	gag	ctc	acc	caa	cgc	gcc	tgg	gaa	tac
1315															
Ala	Glu	Leu	Lys	Thr	Ile	Gly	Glu	Leu	Thr	Gln	Arg	Ala	Trp	Glu	Tyr
390					395					400					405
gat	gta	caa	gta	atg	gtc	gaa	gga	cct	gga	cac	gtg	cca	cta	aac	atg
1363															
Asp	Val	Gln	Val	Met	Val	Glu	Gly	Pro	Gly	His	Val	Pro	Leu	Asn	Met
				410					415					420	
atc	cag	gaa	aac	aac	gag	ctg	gaa	caa	aag	tgg	gca	gcg	gac	gca	cct
1411															
Ile	Gln	Glu	Asn	Asn	Glu	Leu	Glu	Gln	Lys	Trp	Ala	Ala	Asp	Ala	Pro
			425					430					435		
ttt	tac	act	ctt	gga	cca	cta	gtt	acc	gac	atc	gct	cca	ggc	tat	gac
1459															
Phe	Tyr	Thr	Leu	Gly	Pro	Leu	Val	Thr	Asp	Ile	Ala	Pro	Gly	Tyr	Asp
		440					445					450			
cac	atc	act	tct	gcc	att	ggc	gca	gct	cac	atc	gcc	atg	ggc	ggc	acc
1507															
His	Ile	Thr	Ser	Ala	Ile	Gly	Ala	Ala	His	Ile	Ala	Met	Gly	Gly	Thr
	455					460					465				
gcc	atg	ctg	tgt	tat	gtc	acc	ccg	aaa	gaa	cac	ctt	ggc	ctg	ccc	aac
1555															
Ala	Met	Leu	Cys	Tyr	Val	Thr	Pro	Lys	Glu	His	Leu	Gly	Leu	Pro	Asn
470					475					480					485
cgt	gac	gac	gtc	aaa	acc	ggc	gta	atc	acc	tac	aag	ctc	gct	gcc	cac
1603															
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490								495				500			
gca gca gat gtg gcc aag ggt cat ccc ggc gcg cgt gcc tgg gac gac															
1651															
Ala	Ala	Asp	Val	Ala	Lys	Gly	His	Pro	Gly	Ala	Arg	Ala	Trp	Asp	Asp
505				510				515							
gcc atg agt aaa gcg cgt ttt gaa ttc cgt tgg aat gat cag ttt gcg															
1699															
Ala	Met	Ser	Lys	Ala	Arg	Phe	Glu	Phe	Arg	Trp	Asn	Asp	Gln	Phe	Ala
520				525				530							
ctc tcc ctc gac ccc gac act gca atc gct tat cac gac gaa acc ctg															
1747															
Leu	Ser	Leu	Asp	Pro	Asp	Thr	Ala	Ile	Ala	Tyr	His	Asp	Glu	Thr	Leu
535				540				545							
ccg gca gag cct gcg aaa acc gca cac ttc tgt tca atg tgt ggc ccg															
1795															
Pro	Ala	Glu	Pro	Ala	Lys	Thr	Ala	His	Phe	Cys	Ser	Met	Cys	Gly	Pro
550				555				560				565			
aag ttc tgc tcc atg cga att agc cag gac att cgc gat atg ttt ggc															
1843															
Lys	Phe	Cys	Ser	Met	Arg	Ile	Ser	Gln	Asp	Ile	Arg	Asp	Met	Phe	Gly
570				575				580							
gat caa atc gcg gaa ttg ggg atg cct ggg gtt ggg gat tct tct agt															
1891															
Asp	Gln	Ile	Ala	Glu	Leu	Gly	Met	Pro	Gly	Val	Gly	Asp	Ser	Ser	Ser
585				590				595							
gct gtt gct tct agt ggg gca cgg gag ggg atg gct gag aaa tcc cgg															
1939															
Ala	Val	Ala	Ser	Ser	Gly	Ala	Arg	Glu	Gly	Met	Ala	Glu	Lys	Ser	Arg
600				605				610							
gaa ttt att gct ggt ggt gcg gag gtt tat cgg cgt tagacagagc															
1985															
Glu	Phe	Ile	Ala	Gly	Gly	Ala	Glu	Val	Tyr	Arg	Arg				
615				620				625							
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1998															

&lt;210&gt; 522

&lt;211&gt; 625

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 522

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Ile	Ala	Ala	Arg	Ala	Pro	Phe	Glu	Pro	Val	Arg	Leu	Ala	Pro	Ala	Lys
			20					25					30		

Glu	Glu	Arg	Asn	Gly	Ala	Met	Thr	Pro	Thr	Gln	Asn	Glu	Ile	His	Pro
		35					40					45			

Lys	His	Ser	Tyr	Ser	Pro	Ile	Arg	Lys	Asp	Gly	Leu	Glu	Val	Pro	Glu	50	55	60
Thr	Glu	Ile	Arg	Leu	Asp	Asp	Ser	Pro	Ser	Gly	Pro	Asn	Glu	Pro	Phe	65	70	75
Arg	Ile	Tyr	Arg	Thr	Arg	Gly	Pro	Glu	Thr	Asn	Pro	Lys	Gln	Gly	Leu	85	90	95
Pro	Arg	Leu	Arg	Glu	Ser	Trp	Ile	Thr	Ala	Arg	Gly	Asp	Val	Ala	Thr	100	105	110
Tyr	Gln	Gly	Arg	Glu	Arg	Leu	Leu	Ile	Asp	Asp	Gly	Arg	Ser	Ala	Met	115	120	125
Arg	Arg	Gly	Gln	Ala	Ser	Ala	Glu	Trp	Lys	Gly	Gln	Lys	Pro	Ala	Pro	130	135	140
Leu	Lys	Ala	Leu	Pro	Gly	Lys	Arg	Val	Thr	Gln	Met	Ala	Tyr	Ala	Arg	145	150	155
Ala	Gly	Val	Ile	Thr	Arg	Glu	Met	Glu	Phe	Val	Ala	Leu	Arg	Glu	His	165	170	175
Val	Asp	Ala	Glu	Phe	Val	Arg	Ser	Glu	Val	Ala	Arg	Gly	Arg	Ala	Ile	180	185	190
Ile	Pro	Asn	Asn	Val	Asn	His	Pro	Glu	Ser	Glu	Pro	Met	Ile	Ile	Gly	195	200	205
Arg	Lys	Phe	Leu	Thr	Lys	Ile	Asn	Ala	Asn	Ile	Gly	Asn	Ser	Ala	Val	210	215	220
Thr	Ser	Ser	Ile	Glu	Glu	Glu	Val	Ser	Lys	Leu	Gln	Trp	Ala	Thr	Arg	225	230	235
Trp	Gly	Ala	Asp	Thr	Val	Met	Asp	Leu	Ser	Thr	Gly	Asp	Asp	Ile	His	245	250	255
Thr	Thr	Arg	Glu	Trp	Ile	Ile	Arg	Asn	Ser	Pro	Val	Pro	Ile	Gly	Thr	260	265	270
Val	Pro	Ile	Tyr	Gln	Ala	Leu	Glu	Lys	Val	Asn	Gly	Val	Ala	Ala	Asp	275	280	285
Leu	Asn	Trp	Glu	Val	Phe	Arg	Asp	Thr	Ile	Ile	Glu	Gln	Cys	Glu	Gln	290	295	300
Gly	Val	Asp	Tyr	Met	Thr	Ile	His	Ala	Gly	Val	Leu	Leu	Ala	Tyr	Ile	305	310	315
Pro	Leu	Thr	Thr	Arg	Arg	Val	Thr	Gly	Ile	Val	Ser	Arg	Gly	Gly	Ser	325	330	335
Ile	Met	Ala	Gly	Trp	Cys	Leu	Ala	His	His	Arg	Glu	Ser	Phe	Leu	Tyr	340	345	350
Glu	His	Phe	Asp	Glu	Leu	Cys	Glu	Ile	Phe	Ala	Gln	Tyr	Asp	Val	Ala	355	360	365
Phe	Ser	Leu	Gly	Asp	Gly	Leu	Arg	Pro	Gly	Ser	Leu	Ala	Asp	Ala	Asn			

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Asp	Ala	Ala	Gln	Phe	Ala	Glu	Leu	Lys	Thr	Ile	Gly	Glu	Leu	Thr	Gln
385					390					395					400
Arg	Ala	Trp	Glu	Tyr	Asp	Val	Gln	Val	Met	Val	Glu	Gly	Pro	Gly	His
				405					410					415	
Val	Pro	Leu	Asn	Met	Ile	Gln	Glu	Asn	Asn	Glu	Leu	Glu	Gln	Lys	Trp
			420					425					430		
Ala	Ala	Asp	Ala	Pro	Phe	Tyr	Thr	Leu	Gly	Pro	Leu	Val	Thr	Asp	Ile
		435					440					445			
Ala	Pro	Gly	Tyr	Asp	His	Ile	Thr	Ser	Ala	Ile	Gly	Ala	Ala	His	Ile
	450					455					460				
Ala	Met	Gly	Gly	Thr	Ala	Met	Leu	Cys	Tyr	Val	Thr	Pro	Lys	Glu	His
465					470					475					480
Leu	Gly	Leu	Pro	Asn	Arg	Asp	Asp	Val	Lys	Thr	Gly	Val	Ile	Thr	Tyr
				485					490					495	
Lys	Leu	Ala	Ala	His	Ala	Ala	Asp	Val	Ala	Lys	Gly	His	Pro	Gly	Ala
			500					505					510		
Arg	Ala	Trp	Asp	Asp	Ala	Met	Ser	Lys	Ala	Arg	Phe	Glu	Phe	Arg	Trp
		515					520					525			
Asn	Asp	Gln	Phe	Ala	Leu	Ser	Leu	Asp	Pro	Asp	Thr	Ala	Ile	Ala	Tyr
	530					535					540				
His	Asp	Glu	Thr	Leu	Pro	Ala	Glu	Pro	Ala	Lys	Thr	Ala	His	Phe	Cys
545					550					555					560
Ser	Met	Cys	Gly	Pro	Lys	Phe	Cys	Ser	Met	Arg	Ile	Ser	Gln	Asp	Ile
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Arg	Asp	Met	Phe	Gly	Asp	Gln	Ile	Ala	Glu	Leu	Gly	Met	Pro	Gly	Val
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Gly	Asp	Ser	Ser	Ser	Ala	Val	Ala	Ser	Ser	Gly	Ala	Arg	Glu	Gly	Met
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Thr	Leu	Ala	His	Ser	Leu	Ser	Phe	Pro	Asp	Ser	Leu	Arg	Asp	Gly	Pro	
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acc	gtt	gga	gac	ctc	ggg	gaa	ttt	gaa	gtg	att	cgg	gta	atc	acg	gag	96
Thr	Val	Gly	Asp	Leu	Gly	Glu	Phe	Glu	Val	Ile	Arg	Val	Ile	Thr	Glu	
			20					25					30			
caa	gct	gga	tca	tct	ctc	aac	ggc	gat	gac	gca	gct	gtg	ctt	cgg	cat	144
Gln	Ala	Gly	Ser	Ser	Leu	Asn	Gly	Asp	Asp	Ala	Ala	Val	Leu	Arg	His	
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gca	tca	ccc	aat	tcc	agg	gct	gtt	gtc	acc	acc	gac	atg	ttg	gtt	gcg	192
Ala	Ser	Pro	Asn	Ser	Arg	Ala	Val	Val	Thr	Thr	Asp	Met	Leu	Val	Ala	
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Gly	Arg	His	Phe	Gln	Leu	Asp	Trp	Ser	Thr	Pro	Glu	Gln	Ile	Gly	Gln	
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aag	gcg	att	gtg	cag	aac	ttt	gct	gat	att	gag	gcg	atg	ggc	gca	cgt	288
Lys	Ala	Ile	Val	Gln	Asn	Phe	Ala	Asp	Ile	Glu	Ala	Met	Gly	Ala	Arg	
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cca	gta	gcc	gca	ttg	ttg	gcg	att	tcc	gcc	ccc	aca	cac	acc	ccc	gtg	336
Pro	Val	Ala	Ala	Leu	Leu	Ala	Ile	Ser	Ala	Pro	Thr	His	Thr	Pro	Val	
			100					105					110			
gag	ttt	gtc	cga	ggc	tta	gcc	cgt	ggc	atg	aat	caa	cgc	ttg	gag	gag	384
Glu	Phe	Val	Arg	Gly	Leu	Ala	Arg	Gly	Met	Asn	Gln	Arg	Leu	Glu	Glu	
	115						120					125				
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Tyr	Ser	Ala	Glu	Leu	Val	Gly	Gly	Asp	Ile	Thr	Ser	Gly	Asp	Ser	Leu	
	130					135					140					
gtt	att	gct	gta	act	gca	att	ggc	caa	ctg	ggc	gga	tcc	ttg	cca	gag	480
Val	Ile	Ala	Val	Thr	Ala	Ile	Gly	Gln	Leu	Gly	Gly	Ser	Leu	Pro	Glu	
145					150					155				160		
ctg	acg	ttg	gga	cgt	gcc	cga	cca	gga	cag	acc	ctg	gtg	gcc	cac	gga	528
Leu	Thr	Leu	Gly	Arg	Ala	Arg	Pro	Gly	Gln	Thr	Leu	Val	Ala	His	Gly	
				165					170					175		
aag	atc	ggc	tac	tcc	gca	gca	ggc	ctt	gct	cta	ctg	cag	cac	ttt	ggc	576
Lys	Ile	Gly	Tyr	Ser	Ala	Ala	Gly	Leu	Ala	Leu	Leu	Gln	His	Phe	Gly	
			180					185					190			
cca	gac	aac	gtt	cca	gag	cac	ctt	cgc	ccc	ttg	gtg	gat	gca	cac	tgc	624
Pro	Asp	Asn	Val	Pro	Glu	His	Leu	Arg	Pro	Leu	Val	Asp	Ala	His	Cys	
		195					200					205				
gca	cca	gtt	ctc	acc	cca	ggc	cga	ggc	atg	gtg	gca	cgc	gct	gct	gga	672
Ala	Pro	Val	Leu	Thr	Pro	Gly	Arg	Gly	Met	Val	Ala	Arg	Ala	Ala	Gly	
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gcg	acc	gcc	atg	act	gat	aac	tcg	gac	gga	ctg	att	gtg	gat	ctt	aac	720
Ala	Thr	Ala	Met	Thr	Asp	Asn	Ser	Asp	Gly	Leu	Ile	Val	Asp	Leu	Asn	
225					230					235				240		



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 Gln Met Ala Met Lys Ser Gly Val Arg Ile Asp Val Asp Ser Cys Ser  
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atc agc ccc gat gaa ctc ctt agc gaa gcc gct tcc gta ctc gga aca 816  
 Ile Ser Pro Asp Glu Leu Leu Ser Glu Ala Ala Ser Val Leu Gly Thr  
                   260                  265                  270

gac gcc tgg cga tgg atc tta agc ggc ggg gaa gac cac acc ctg ctc 864  
 Asp Ala Trp Arg Trp Ile Leu Ser Gly Gly Glu Asp His Thr Leu Leu  
                   275                  280                  285

tct acg acg ttt ggc gat gcc ccc tct gga ttc cgc acc atc ggc caa 912  
 Ser Thr Thr Phe Gly Asp Ala Pro Ser Gly Phe Arg Thr Ile Gly Gln  
                   290                  295                  300

gtc acc aaa aca cgc cac gaa gac ctc gtc acc gta gat aag aaa acc 960  
 Val Thr Lys Thr Arg His Glu Asp Leu Val Thr Val Asp Lys Lys Thr  
                   305                  310                  315                  320

ccc gca ttt tcc gat gga tgg aga agc ttc taatgaccaa caccctatgg  
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 Pro Ala Phe Ser Asp Gly Trp Arg Ser Phe  
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 1013

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   1                  5                  10                  15  
 Thr Val Gly Asp Leu Gly Glu Phe Glu Val Ile Arg Val Ile Thr Glu  
                   20                  25                  30  
 Gln Ala Gly Ser Ser Leu Asn Gly Asp Asp Ala Ala Val Leu Arg His  
                   35                  40                  45  
 Ala Ser Pro Asn Ser Arg Ala Val Val Thr Thr Asp Met Leu Val Ala  
                   50                  55                  60  
 Gly Arg His Phe Gln Leu Asp Trp Ser Thr Pro Glu Gln Ile Gly Gln  
   65                  70                  75                  80  
 Lys Ala Ile Val Gln Asn Phe Ala Asp Ile Glu Ala Met Gly Ala Arg  
                   85                  90                  95  
 Pro Val Ala Ala Leu Leu Ala Ile Ser Ala Pro Thr His Thr Pro Val  
                   100                  105                  110  
 Glu Phe Val Arg Gly Leu Ala Arg Gly Met Asn Gln Arg Leu Glu Glu  
                   115                  120                  125  
 Tyr Ser Ala Glu Leu Val Gly Gly Asp Ile Thr Ser Gly Asp Ser Leu  
   130                  135                  140

Val Ile Ala Val Thr Ala Ile Gly Gln Leu Gly Gly Ser Leu Pro Glu  
 145 150 155 160  
 Leu Thr Leu Gly Arg Ala Arg Pro Gly Gln Thr Leu Val Ala His Gly  
 165 170 175  
 Lys Ile Gly Tyr Ser Ala Ala Gly Leu Ala Leu Leu Gln His Phe Gly  
 180 185 190  
 Pro Asp Asn Val Pro Glu His Leu Arg Pro Leu Val Asp Ala His Cys  
 195 200 205  
 Ala Pro Val Leu Thr Pro Gly Arg Gly Met Val Ala Arg Ala Ala Gly  
 210 215 220  
 Ala Thr Ala Met Thr Asp Asn Ser Asp Gly Leu Ile Val Asp Leu Asn  
 225 230 235 240  
 Gln Met Ala Met Lys Ser Gly Val Arg Ile Asp Val Asp Ser Cys Ser  
 245 250 255  
 Ile Ser Pro Asp Glu Leu Leu Ser Glu Ala Ala Ser Val Leu Gly Thr  
 260 265 270  
 Asp Ala Trp Arg Trp Ile Leu Ser Gly Gly Glu Asp His Thr Leu Leu  
 275 280 285  
 Ser Thr Thr Phe Gly Asp Ala Pro Ser Gly Phe Arg Thr Ile Gly Gln  
 290 295 300  
 Val Thr Lys Thr Arg His Glu Asp Leu Val Thr Val Asp Lys Lys Thr  
 305 310 315 320  
 Pro Ala Phe Ser Asp Gly Trp Arg Ser Phe  
 325 330

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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <223> RXA01352

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ctgggtaaca ccagcgaagg aagcgaggat tgattgtccc gtg ttt gaa aat cgt 115  
 Val Phe Glu Asn Arg  
 1 5

ttt gac ctg cgt tgt tat gtt gtg act ggt gcg ggc tcg gtg gat gag 163  
 Phe Asp Leu Arg Cys Tyr Val Val Thr Gly Ala Gly Ser Val Asp Glu  
 10 15 20

gtt gtg cac act gcg tct gct gcg gct cgt ggt ggc gcg ggt gtg gtg 211  
 Val Val His Thr Ala Ser Ala Ala Ala Arg Gly Gly Ala Gly Val Val

25					30					35						
cag	gtg	cgt	tca	aag	cct	att	tcg	cca	gaa	gcg	atg	agg	gag	ttg	gca	259
Gln	Val	Arg	Ser	Lys	Pro	Ile	Ser	Pro	Glu	Ala	Met	Arg	Glu	Leu	Ala	
		40					45					50				
tca	aag	gtt	gcg	ctt	gag	gtt	gcg	cgg	tgc	agc	cca	aca	acg	agg	gtg	307
Ser	Lys	Val	Ala	Leu	Glu	Val	Ala	Arg	Cys	Ser	Pro	Thr	Thr	Arg	Val	
	55					60					65					
ctt	atc	gac	gac	cac	ctc	cac	gtt	gct	tct	tcc	tta	atg	cgc	gaa	gga	355
Leu	Ile	Asp	Asp	His	Leu	His	Val	Ala	Ser	Ser	Leu	Met	Arg	Glu	Gly	
	70				75					80					85	
ctc	ccg	att	cac	ggt	gtg	cat	ctt	ggg	cag	gat	gat	atg	tcg	gtg	ctt	403
Leu	Pro	Ile	His	Gly	Val	His	Leu	Gly	Gln	Asp	Asp	Met	Ser	Val	Leu	
				90					95					100		
gag	gct	cgt	gag	ttg	ttg	ggg	cct	gag	gcg	atc	att	ggg	ttg	act	act	451
Glu	Ala	Arg	Glu	Leu	Leu	Gly	Pro	Glu	Ala	Ile	Ile	Gly	Leu	Thr	Thr	
			105					110					115			
gga	acc	cta	gaa	ctt	gtg	gcg	gcg	gcg	aat	gag	ctg	tcc	gat	gtg	ttg	499
Gly	Thr	Leu	Glu	Leu	Val	Ala	Ala	Ala	Asn	Glu	Leu	Ser	Asp	Val	Leu	
		120					125					130				
gat	tac	atc	ggt	gct	ggg	ccg	ttt	cgg	aag	act	ccc	acc	aag	gat	tca	547
Asp	Tyr	Ile	Gly	Ala	Gly	Pro	Phe	Arg	Lys	Thr	Pro	Thr	Lys	Asp	Ser	
	135					140					145					
ggt	cgg	cca	ccg	att	ggc	ctt	gcg	ggt	tat	ccc	cct	ttg	gtg	gaa	ttg	595
Gly	Arg	Pro	Pro	Ile	Gly	Leu	Ala	Gly	Tyr	Pro	Pro	Leu	Val	Glu	Leu	
	150				155					160					165	
tcc	aag	gtg	ccg	atc	gtt	gcg	att	ggt	gat	gtc	acc	cct	gcc	gat	gtg	643
Ser	Lys	Val	Pro	Ile	Val	Ala	Ile	Gly	Asp	Val	Thr	Pro	Ala	Asp	Val	
				170					175					180		
cgc	gct	ctc	agc	gca	acc	ggt	gtg	gct	ggc	gtt	gcc	atg	gtg	cgg	gct	691
Arg	Ala	Leu	Ser	Ala	Thr	Gly	Val	Ala	Gly	Val	Ala	Met	Val	Arg	Ala	
			185					190					195			
ttt	tct	gaa	tct	gat												706
Phe	Ser	Glu	Ser	Asp												
		200														

&lt;210&gt; 526

&lt;211&gt; 202

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 526

Val	Phe	Glu	Asn	Arg	Phe	Asp	Leu	Arg	Cys	Tyr	Val	Val	Thr	Gly	Ala
1				5					10					15	

Gly	Ser	Val	Asp	Glu	Val	Val	His	Thr	Ala	Ser	Ala	Ala	Ala	Arg	Gly
			20					25					30		

Gly	Ala	Gly	Val	Val	Gln	Val	Arg	Ser	Lys	Pro	Ile	Ser	Pro	Glu	Ala
		35					40					45			

Met Arg Glu Leu Ala Ser Lys Val Ala Leu Glu Val Ala Arg Cys Ser  
 50 55 60

Pro Thr Thr Arg Val Leu Ile Asp Asp His Leu His Val Ala Ser Ser  
 65 70 75 80

Leu Met Arg Glu Gly Leu Pro Ile His Gly Val His Leu Gly Gln Asp  
 85 90 95

Asp Met Ser Val Leu Glu Ala Arg Glu Leu Leu Gly Pro Glu Ala Ile  
 100 105 110

Ile Gly Leu Thr Thr Gly Thr Leu Glu Leu Val Ala Ala Ala Asn Glu  
 115 120 125

Leu Ser Asp Val Leu Asp Tyr Ile Gly Ala Gly Pro Phe Arg Lys Thr  
 130 135 140

Pro Thr Lys Asp Ser Gly Arg Pro Pro Ile Gly Leu Ala Gly Tyr Pro  
 145 150 155 160

Pro Leu Val Glu Leu Ser Lys Val Pro Ile Val Ala Ile Gly Asp Val  
 165 170 175

Thr Pro Ala Asp Val Arg Ala Leu Ser Ala Thr Gly Val Ala Gly Val  
 180 185 190

Ala Met Val Arg Ala Phe Ser Glu Ser Asp  
 195 200

&lt;210&gt; 527

&lt;211&gt; 944

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(921)

&lt;223&gt; RXA01381

&lt;400&gt; 527

tcc gca ggc gtt gga acc atc acg gtc atc gat gac gac acc gtc gac	48
Ser Ala Gly Val Gly Thr Ile Thr Val Ile Asp Asp Asp Thr Val Asp	
1 5 10 15	
att tcc aac att cac cgc caa atc ctc ttc ggc gca agc gat gtc ggt	96
Ile Ser Asn Ile His Arg Gln Ile Leu Phe Gly Ala Ser Asp Val Gly	
20 25 30	
cga ccc aag gtc gag gtt gcc gcc gag cgc ctc aaa gaa ctc caa cca	144
Arg Pro Lys Val Glu Val Ala Ala Glu Arg Leu Lys Glu Leu Gln Pro	
35 40 45	
gac atc acc gtc aac gcg ttg cac gaa cgg atc act cca gaa aac gcc	192
Asp Ile Thr Val Asn Ala Leu His Glu Arg Ile Thr Pro Glu Asn Ala	
50 55 60	
tgc gag ctg ctc aat tcc gtg gac ctc gtc tta gac ggc tcc gat tct	240
Cys Glu Leu Leu Asn Ser Val Asp Leu Val Leu Asp Gly Ser Asp Ser	

65				70				75				80					
ttc	tcc	aca	aaa	tac	tta	gtg	tct	gat	gcc	gcc	gaa	atc	acc	gga	act	288	
Phe	Ser	Thr	Lys	Tyr	Leu	Val	Ser	Asp	Ala	Ala	Glu	Ile	Thr	Gly	Thr		
				85					90					95			
ccc	ctc	atc	tgg	gca	acg	gta	ctg	cgc	ttt	cac	ggc	gaa	ctg	gca	ctc	336	
Pro	Leu	Ile	Trp	Ala	Thr	Val	Leu	Arg	Phe	His	Gly	Glu	Leu	Ala	Leu		
				100					105					110			
ttc	aac	tct	ggc	ccc	gac	cac	cgc	gga	gtc	ggc	ctg	cgc	gac	gtc	ttc	384	
Phe	Asn	Ser	Gly	Pro	Asp	His	Arg	Gly	Val	Gly	Leu	Arg	Asp	Val	Phe		
				115					120					125			
ccc	gaa	caa	ccc	tcc	gcc	gat	ttc	gtc	cct	gac	tgc	gcc	acc	gct	ggt	432	
Pro	Glu	Gln	Pro	Ser	Ala	Asp	Phe	Val	Pro	Asp	Cys	Ala	Thr	Ala	Gly		
				130					135					140			
gtt	ctt	ggc	gcc	acc	aca	gcc	acc	atc	ggc	gca	ctc	atg	gcc	act	cac	480	
Val	Leu	Gly	Ala	Thr	Thr	Ala	Thr	Ile	Gly	Ala	Leu	Met	Ala	Thr	His		
				145					150					155			
gcc	atc	gga	ttt	ctc	aca	gaa	atc	ggc	gac	gtc	caa	cca	ggc	aca	atc	528	
Ala	Ile	Gly	Phe	Leu	Thr	Glu	Ile	Gly	Asp	Val	Gln	Pro	Gly	Thr	Ile		
				165					170					175			
ctc	tcc	tac	gac	gca	ttc	ccc	gcc	gcc	acg	cgc	agc	ttc	cgc	gtc	tcc	576	
Leu	Ser	Tyr	Asp	Ala	Phe	Pro	Ala	Ala	Thr	Arg	Ser	Phe	Arg	Val	Ser		
				180					185					190			
gcc	gac	ccg	gcg	cgc	cca	ctg	gtc	acc	cgc	ctc	cgc	gcc	tcc	tac	gag	624	
Ala	Asp	Pro	Ala	Arg	Pro	Leu	Val	Thr	Arg	Leu	Arg	Ala	Ser	Tyr	Glu		
				195					200					205			
gca	gcg	cgc	acc	gat	aca	act	tcg	ctt	atc	gac	gcc	acc	ctc	aac	ggc	672	
Ala	Ala	Arg	Thr	Asp	Thr	Thr	Ser	Leu	Ile	Asp	Ala	Thr	Leu	Asn	Gly		
				210					215					220			
tcc	ctc	acc	gcc	ctc	gat	atc	cga	gag	cca	cat	gaa	gtt	ctg	ctc	aaa	720	
Ser	Leu	Thr	Ala	Leu	Asp	Ile	Arg	Glu	Pro	His	Glu	Val	Leu	Leu	Lys		
				225					230					235			
gac	ctc	ccc	gag	ggc	gca	acg	tca	ctg	aag	ctc	ccc	tta	agc	cag	atc	768	
Asp	Leu	Pro	Glu	Gly	Ala	Thr	Ser	Leu	Lys	Leu	Pro	Leu	Ser	Gln	Ile		
				245					250					255			
acc	tcg	gac	agc	gac	att	tta	gag	gca	ctg	tct	gga	atc	gac	ggc	gac	816	
Thr	Ser	Asp	Ser	Asp	Ile	Leu	Glu	Ala	Leu	Ser	Gly	Ile	Asp	Gly	Asp		
				260					265					270			
att	ttg	gtc	tac	tgc	gct	tcg	gga	atc	cgc	agt	tcc	gac	ttc	atc	gac	864	
Ile	Leu	Val	Tyr	Cys	Ala	Ser	Gly	Ile	Arg	Ser	Ser	Asp	Phe	Ile	Asp		
				275					280					285			
aac	tac	tcc	cac	ctc	ggc	cac	aaa	ttt	gtg	aat	ctt	ccc	ggt	ggg	gtc	912	
Asn	Tyr	Ser	His	Leu	Gly	His	Lys	Phe	Val	Asn	Leu	Pro	Gly	Gly	Val		
				290					295					300			
aac	gcg	ctg	tagctgtcaa	tttaagaggc				cag								944	
Asn	Ala	Leu															
				305													

&lt;210&gt; 528

&lt;211&gt; 307

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 528

Ser Ala Gly Val Gly Thr Ile Thr Val Ile Asp Asp Asp Thr Val Asp  
1 5 10 15

Ile Ser Asn Ile His Arg Gln Ile Leu Phe Gly Ala Ser Asp Val Gly  
20 25 30

Arg Pro Lys Val Glu Val Ala Ala Glu Arg Leu Lys Glu Leu Gln Pro  
35 40 45

Asp Ile Thr Val Asn Ala Leu His Glu Arg Ile Thr Pro Glu Asn Ala  
50 55 60

Cys Glu Leu Leu Asn Ser Val Asp Leu Val Leu Asp Gly Ser Asp Ser  
65 70 75 80

Phe Ser Thr Lys Tyr Leu Val Ser Asp Ala Ala Glu Ile Thr Gly Thr  
85 90 95

Pro Leu Ile Trp Ala Thr Val Leu Arg Phe His Gly Glu Leu Ala Leu  
100 105 110

Phe Asn Ser Gly Pro Asp His Arg Gly Val Gly Leu Arg Asp Val Phe  
115 120 125

Pro Glu Gln Pro Ser Ala Asp Phe Val Pro Asp Cys Ala Thr Ala Gly  
130 135 140

Val Leu Gly Ala Thr Thr Ala Thr Ile Gly Ala Leu Met Ala Thr His  
145 150 155 160

Ala Ile Gly Phe Leu Thr Glu Ile Gly Asp Val Gln Pro Gly Thr Ile  
165 170 175

Leu Ser Tyr Asp Ala Phe Pro Ala Ala Thr Arg Ser Phe Arg Val Ser  
180 185 190

Ala Asp Pro Ala Arg Pro Leu Val Thr Arg Leu Arg Ala Ser Tyr Glu  
195 200 205

Ala Ala Arg Thr Asp Thr Thr Ser Leu Ile Asp Ala Thr Leu Asn Gly  
210 215 220

Ser Leu Thr Ala Leu Asp Ile Arg Glu Pro His Glu Val Leu Leu Lys  
225 230 235 240

Asp Leu Pro Glu Gly Ala Thr Ser Leu Lys Leu Pro Leu Ser Gln Ile  
245 250 255

Thr Ser Asp Ser Asp Ile Leu Glu Ala Leu Ser Gly Ile Asp Gly Asp  
260 265 270

Ile Leu Val Tyr Cys Ala Ser Gly Ile Arg Ser Ser Asp Phe Ile Asp  
275 280 285

Asn Tyr Ser His Leu Gly His Lys Phe Val Asn Leu Pro Gly Gly Val  
 290 295 300

Asn Ala Leu  
 305

<210> 529  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(259)  
 <223> RXA01360

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gattccgtag aagttctcac cgcaattcag ggaggttaaa atg ctg cat att gct 115  
 Met Leu His Ile Ala  
 1 5

gat aaa act ttc gat tcc cac ctc atc atg ggc acc ggc gga gcc acc 163  
 Asp Lys Thr Phe Asp Ser His Leu Ile Met Gly Thr Gly Gly Ala Thr  
 10 15 20

tct cag gcg ttg ctg gag gaa tcc ctt gtc gcc agt gga act caa ttg 211  
 Ser Gln Ala Leu Leu Glu Glu Ser Leu Val Ala Ser Gly Thr Gln Leu  
 25 30 35

acc acc gtg gcg atg cgt cga cac caa gca acc acc tct agc gga gaa 259  
 Thr Thr Val Ala Met Arg Arg His Gln Ala Thr Thr Ser Ser Gly Glu  
 40 45 50

<210> 530  
 <211> 53  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 530  
 Met Leu His Ile Ala Asp Lys Thr Phe Asp Ser His Leu Ile Met Gly  
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Thr Gly Gly Ala Thr Ser Gln Ala Leu Leu Glu Glu Ser Leu Val Ala  
 20 25 30

Ser Gly Thr Gln Leu Thr Thr Val Ala Met Arg Arg His Gln Ala Thr  
 35 40 45

Thr Ser Ser Gly Glu  
 50

<210> 531  
 <211> 629  
 <212> DNA  
 <213> Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(606)

&lt;223&gt; RXA01361

&lt;400&gt; 531

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Ala Asp Ala Val Ile Ser Ile Asp Gly His Asp Pro Cys Leu Thr Val	
1 5 10 15	
acg atg aat tcg ggg gtg agg gtt gcg tcg aaa agc gtt gtt gtt ttg	96
Thr Met Asn Ser Gly Val Arg Val Ala Ser Lys Ser Val Val Val Leu	
20 25 30	
gcg gcg ggc ctg ggc gcc gca agc att ccc ggc tgg ttt gag ggc gcg	144
Ala Ala Gly Leu Gly Ala Ala Ser Ile Pro Gly Trp Phe Glu Gly Ala	
35 40 45	
aac cca ttg cag ttg agg ccg gtg tac ggc gat att gtg cgc gtg cgc	192
Asn Pro Leu Gln Leu Arg Pro Val Tyr Gly Asp Ile Val Arg Val Arg	
50 55 60	
gtg ccg gag cga ctg cag ccg atg gtc acc aag gtg gtg cgc ggg ttt	240
Val Pro Glu Arg Leu Gln Pro Met Val Thr Lys Val Val Arg Gly Phe	
65 70 75 80	
gtg gaa gat cgt cag att tat atc att ccg cgt acc gat ggc acc ctc	288
Val Glu Asp Arg Gln Ile Tyr Ile Ile Pro Arg Thr Asp Gly Thr Leu	
85 90 95	
gcg atc ggc gcg aca agc cgt gag gat cac ccg caa cct cga acg ggc	336
Ala Ile Gly Ala Thr Ser Arg Glu Asp His Pro Gln Pro Arg Thr Gly	
100 105 110	
gca gtg cat gat ttg cta cgc gat gct atc cgt ttg att ccg ggc att	384
Ala Val His Asp Leu Leu Arg Asp Ala Ile Arg Leu Ile Pro Gly Ile	
115 120 125	
gaa gaa acc gaa ttt atc gaa gtc acc tgc ggc gcc cgc ccc ggc acc	432
Glu Glu Thr Glu Phe Ile Glu Val Thr Cys Gly Ala Arg Pro Gly Thr	
130 135 140	
ccg gat gac ctg ccg tac ctg gga tgg gtt gga tcc aat gtg att gcg	480
Pro Asp Asp Leu Pro Tyr Leu Gly Trp Val Gly Ser Asn Val Ile Ala	
145 150 155 160	
tcc aca gga tat ttc cgc cat gga att ttg ctg tca gcc ctt ggt gca	528
Ser Thr Gly Tyr Phe Arg His Gly Ile Leu Leu Ser Ala Leu Gly Ala	
165 170 175	
cgc gct gcc gtt gat atg gca acc aac cag cca ctg ttc ccc act ctt	576
Arg Ala Ala Val Asp Met Ala Thr Asn Gln Pro Leu Phe Pro Thr Leu	
180 185 190	
gat gtg tgc gat ccg ttt cgc cac caa att taaggatttt tcacaagtga	626
Asp Val Cys Asp Pro Phe Arg His Gln Ile	
195 200	
tta	629



<210> 532  
 <211> 202  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 532  
 Ala Asp Ala Val Ile Ser Ile Asp Gly His Asp Pro Cys Leu Thr Val  
   1                  5                  10                  15  
 Thr Met Asn Ser Gly Val Arg Val Ala Ser Lys Ser Val Val Val Leu  
           20                  25                  30  
 Ala Ala Gly Leu Gly Ala Ala Ser Ile Pro Gly Trp Phe Glu Gly Ala  
           35                  40                  45  
 Asn Pro Leu Gln Leu Arg Pro Val Tyr Gly Asp Ile Val Arg Val Arg  
       50                  55                  60  
 Val Pro Glu Arg Leu Gln Pro Met Val Thr Lys Val Val Arg Gly Phe  
   65                  70                  75                  80  
 Val Glu Asp Arg Gln Ile Tyr Ile Ile Pro Arg Thr Asp Gly Thr Leu  
           85                  90                  95  
 Ala Ile Gly Ala Thr Ser Arg Glu Asp His Pro Gln Pro Arg Thr Gly  
          100                 105                 110  
 Ala Val His Asp Leu Leu Arg Asp Ala Ile Arg Leu Ile Pro Gly Ile  
      115                 120                 125  
 Glu Glu Thr Glu Phe Ile Glu Val Thr Cys Gly Ala Arg Pro Gly Thr  
   130                 135                 140  
 Pro Asp Asp Leu Pro Tyr Leu Gly Trp Val Gly Ser Asn Val Ile Ala  
  145                 150                 155                 160  
 Ser Thr Gly Tyr Phe Arg His Gly Ile Leu Leu Ser Ala Leu Gly Ala  
          165                 170                 175  
 Arg Ala Ala Val Asp Met Ala Thr Asn Gln Pro Leu Phe Pro Thr Leu  
          180                 185                 190  
 Asp Val Cys Asp Pro Phe Arg His Gln Ile  
      195                 200

<210> 533  
 <211> 927  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(904)  
 <223> RXA01208

<400> 533  
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 aacctgctct agctcgctact agcgaaggga tggccttaac gtg gct aac tcg ttt 115

																Val 1	Ala	Asn	Ser	Phe 5	
ttg	gat	tct	tta	act	ctt	gtt	cga	caa	aac	act	ccc	ctt	gtt	cag	tgt	163					
Leu	Asp	Ser	Leu	Thr 10	Leu	Val	Arg	Gln	Asn 15	Thr	Pro	Leu	Val	Gln 20	Cys						
ttg	acc	aac	tct	gtg	gtc	atg	caa	ttc	acg	gcc	aat	gtg	ttg	ctt	gcc	211					
Leu	Thr	Asn	Ser 25	Val	Val	Met	Gln	Phe 30	Thr	Ala	Asn	Val	Leu 35	Leu	Ala						
gcg	ggt	gcg	acc	cct	gcg	atg	gtg	gat	act	cca	gct	gaa	tcg	gca	gaa	259					
Ala	Gly	Ala 40	Thr	Pro	Ala	Met	Val 45	Asp	Thr	Pro	Ala	Glu 50	Ser	Ala	Glu						
ttc	gcc	gct	gtg	gcc	aat	gga	gtg	ctc	atc	aat	gcg	gga	act	cct	tct	307					
Phe	Ala 55	Ala	Val	Ala	Asn	Gly 60	Val	Leu	Ile	Asn	Ala 65	Gly	Thr	Pro	Ser						
gcg	gag	caa	tac	caa	ggc	atg	acc	aag	gcc	att	gag	ggt	gca	cga	aaa	355					
Ala 70	Glu	Gln	Tyr	Gln	Gly 75	Met	Thr	Lys	Ala	Ile 80	Glu	Gly	Ala	Arg	Lys 85						
gct	ggc	aca	cca	tgg	gtg	tta	gac	cca	gtt	gct	gtg	ggt	ggg	ttg	tcg	403					
Ala	Gly	Thr	Pro	Trp 90	Val	Leu	Asp	Pro	Val 95	Ala	Val	Gly	Gly	Leu 100	Ser						
gag	agg	acc	aag	tat	gcg	gag	gga	atc	gtc	gat	aag	cag	cct	gcc	gca	451					
Glu	Arg	Thr	Lys 105	Tyr	Ala	Glu	Gly	Ile 110	Val	Asp	Lys	Gln	Pro 115	Ala	Ala						
att	cgt	gga	aac	gcc	tca	gag	gtc	gtg	gcg	ctt	gcg	ggg	ctc	ggt	gcc	499					
Ile	Arg	Gly 120	Asn	Ala	Ser	Glu	Val 125	Val	Ala	Leu	Ala	Gly 130	Leu	Gly	Ala						
ggt	ggg	cgc	ggc	gta	gac	gcg	acc	gat	tcc	gtg	gaa	gtg	gcg	ttg	gag	547					
Gly	Gly 135	Arg	Gly	Val	Asp	Ala 140	Thr	Asp	Ser	Val	Glu 145	Val	Ala	Leu	Glu						
gcg	gcg	caa	ttg	ttg	gcc	aag	cgc	act	ggt	ggc	gtc	gtg	gct	gtc	tct	595					
Ala 150	Ala	Gln	Leu	Leu	Ala 155	Lys	Arg	Thr	Gly	Gly 160	Val	Val	Ala	Val	Ser 165						
ggt	gcg	gag	gac	ttg	att	gtg	tct	gcg	gat	cgg	gtg	acg	tgg	ttg	cgt	643					
Gly	Ala	Glu	Asp 170	Leu	Ile	Val	Ser	Ala	Asp 175	Arg	Val	Thr	Trp	Leu 180	Arg						
tcg	ggg	gat	ccg	atg	ttg	cag	ctg	gtg	att	ggc	act	gga	tgc	tct	ttg	691					
Ser	Gly	Asp	Pro 185	Met	Leu	Gln	Leu	Val 190	Ile	Gly	Thr	Gly	Cys 195	Ser	Leu						
ggc	gcg	ctg	aca	gct	gca	tat	cta	ggc	gcc	acg	gtt	gac	tca	gat	att	739					
Gly	Ala	Leu 200	Thr	Ala	Ala	Tyr	Leu 205	Gly	Ala	Thr	Val	Asp 210	Ser	Asp	Ile						
tcc	gcg	cac	gat	gct	gtg	ttg	gct	gcg	cat	gcc	cat	gtg	ggt	gct	gct	787					
Ser	Ala 215	His	Asp	Ala	Val	Leu 220	Ala	Ala	His	Ala 225	His	Val	Gly	Ala	Ala						
ggc	cag	att	gca	gca	cag	aag	gca	tcg	gcg	cca	ggc	agc	ttt	gcg	gtg	835					
Gly	Gln	Ile	Ala	Ala	Gln	Lys	Ala	Ser	Ala	Pro	Gly	Ser	Phe	Ala	Val						

230	235	240	245	
gcg ttt att gat	gcg ctt tat gac	gtg gat gcc cag gct	gtg gcc tcg	883
Ala Phe Ile Asp	Ala Leu Tyr Asp	Val Asp Ala Gln	Ala Val Ala Ser	
	250	255	260	
ttg gtt gat gtg	cga gag gcc	tgaaaagtac	gtgactgatt ttt	927
Leu Val Asp Val	Arg Glu Ala			
	265			

&lt;210&gt; 534

&lt;211&gt; 268

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 534

Val	Ala	Asn	Ser	Phe	Leu	Asp	Ser	Leu	Thr	Leu	Val	Arg	Gln	Asn	Thr
1				5					10					15	
Pro	Leu	Val	Gln	Cys	Leu	Thr	Asn	Ser	Val	Val	Met	Gln	Phe	Thr	Ala
			20					25					30		
Asn	Val	Leu	Leu	Ala	Ala	Gly	Ala	Thr	Pro	Ala	Met	Val	Asp	Thr	Pro
		35					40					45			
Ala	Glu	Ser	Ala	Glu	Phe	Ala	Ala	Val	Ala	Asn	Gly	Val	Leu	Ile	Asn
	50					55					60				
Ala	Gly	Thr	Pro	Ser	Ala	Glu	Gln	Tyr	Gln	Gly	Met	Thr	Lys	Ala	Ile
	65				70					75					80
Glu	Gly	Ala	Arg	Lys	Ala	Gly	Thr	Pro	Trp	Val	Leu	Asp	Pro	Val	Ala
				85					90					95	
Val	Gly	Gly	Leu	Ser	Glu	Arg	Thr	Lys	Tyr	Ala	Glu	Gly	Ile	Val	Asp
			100					105					110		
Lys	Gln	Pro	Ala	Ala	Ile	Arg	Gly	Asn	Ala	Ser	Glu	Val	Val	Ala	Leu
		115					120					125			
Ala	Gly	Leu	Gly	Ala	Gly	Gly	Arg	Gly	Val	Asp	Ala	Thr	Asp	Ser	Val
	130					135					140				
Glu	Val	Ala	Leu	Glu	Ala	Ala	Gln	Leu	Leu	Ala	Lys	Arg	Thr	Gly	Gly
	145				150					155					160
Val	Val	Ala	Val	Ser	Gly	Ala	Glu	Asp	Leu	Ile	Val	Ser	Ala	Asp	Arg
				165					170					175	
Val	Thr	Trp	Leu	Arg	Ser	Gly	Asp	Pro	Met	Leu	Gln	Leu	Val	Ile	Gly
			180					185					190		
Thr	Gly	Cys	Ser	Leu	Gly	Ala	Leu	Thr	Ala	Ala	Tyr	Leu	Gly	Ala	Thr
		195					200					205			
Val	Asp	Ser	Asp	Ile	Ser	Ala	His	Asp	Ala	Val	Leu	Ala	Ala	His	Ala
	210					215					220				
His	Val	Gly	Ala	Ala	Gly	Gln	Ile	Ala	Ala	Gln	Lys	Ala	Ser	Ala	Pro
	225				230					235					240



tct ggt gaa ctt tct agg caa ttc gca agc act ctt gaa cag gcc ggt 595  
 Ser Gly Glu Leu Ser Arg Gln Phe Ala Ser Thr Leu Glu Gln Ala Gly  
 150 155 160 165  
  
 att gac gga gtt ctg cat ccc gat att ttg gtg gat gtg tgg gag aaa 643  
 Ile Asp Gly Val Leu His Pro Asp Ile Leu Val Asp Val Trp Glu Lys  
 170 175 180  
  
 gcc atg ttc gta gag gtt ttc ggc ggg ttg ggg gct ttc gtc gaa aag 691  
 Ala Met Phe Val Glu Val Phe Gly Gly Leu Gly Ala Phe Val Glu Lys  
 185 190 195  
  
 caa tta ggt acc ttg cgt acg cat ttt agg gct tcc ctg gaa gcc ttg 739  
 Gln Leu Gly Thr Leu Arg Thr His Phe Arg Ala Ser Leu Glu Ala Leu  
 200 205 210  
  
 atg gaa gag gtg gct gag gtg gct cgc gcg gca ggt gtt gcg ttg ccg 787  
 Met Glu Glu Val Ala Glu Val Ala Arg Ala Ala Gly Val Ala Leu Pro  
 215 220 225  
  
 agc gat gcg gtg gag cgc acc atg aat ttt gcg gat cgg atg cct gag 835  
 Ser Asp Ala Val Glu Arg Thr Met Asn Phe Ala Asp Arg Met Pro Glu  
 230 235 240 245  
  
 aat tcg acg agt tcg atg cag cgt gat ttg gcc gcg gga gtg gct agt 883  
 Asn Ser Thr Ser Ser Met Gln Arg Asp Leu Ala Ala Gly Val Ala Ser  
 250 255 260  
  
 gag ctt gag gct cag aca ggt gca att gtg cgg gca gcg cac aaa gtg 931  
 Glu Leu Glu Ala Gln Thr Gly Ala Ile Val Arg Ala Ala His Lys Val  
 265 270 275  
  
 ggt gtg aaa act ccg ctt cat gac ctt att tat gct ggt ctt aag ctg 979  
 Gly Val Lys Thr Pro Leu His Asp Leu Ile Tyr Ala Gly Leu Lys Leu  
 280 285 290  
  
 aaa gaa gag gaa aat tca ctt tagggataga atcaagatcc atg  
 1023  
 Lys Glu Glu Glu Asn Ser Leu  
 295 300

&lt;210&gt; 536

&lt;211&gt; 300

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 536

Met Lys Ile Ala Ile Val Gly Ala Gly Ala Val Gly Gly Tyr Phe Gly  
 1 5 10 15  
  
 Ala Leu Leu Gln Glu Ser Gly Ala Asp Ile Thr Met Val Ala Arg Gly  
 20 25 30  
  
 Arg Thr Leu Glu Ala Leu Lys Ser Lys Gly Leu His Ile Asn Asp Ala  
 35 40 45  
  
 Arg Gly Glu Arg Tyr Val Pro Ile Pro Ala Val Ala Ser Val Gln Glu  
 50 55 60  
  
 Leu Lys Asp Ala Asp Val Val Met Ile Ala Thr Lys Ala Leu Ser Arg

65	70	75	80
Ser Leu Asp Leu Ala Glu Leu Leu Gly Gly Ile Pro Ala Asn Ser Val	85	90	95
Val Ala Ile Thr Gln Asn Ser Ile Glu Ser Ala Asp Leu Ala Ala Lys	100	105	110
Ser Ile Gly Ala Asp Arg Val Trp Pro Gly Val Val Arg Gly Phe Phe	115	120	125
Val His Glu Gly Pro Ala Ser Val Ser Tyr Lys Gly Gly Pro Leu Ser	130	135	140
Tyr Thr Phe Gly Asp Ser Gly Glu Leu Ser Arg Gln Phe Ala Ser Thr	145	150	155
Leu Glu Gln Ala Gly Ile Asp Gly Val Leu His Pro Asp Ile Leu Val	165	170	175
Asp Val Trp Glu Lys Ala Met Phe Val Glu Val Phe Gly Gly Leu Gly	180	185	190
Ala Phe Val Glu Lys Gln Leu Gly Thr Leu Arg Thr His Phe Arg Ala	195	200	205
Ser Leu Glu Ala Leu Met Glu Glu Val Ala Glu Val Ala Arg Ala Ala	210	215	220
Gly Val Ala Leu Pro Ser Asp Ala Val Glu Arg Thr Met Asn Phe Ala	225	230	235
Asp Arg Met Pro Glu Asn Ser Thr Ser Ser Met Gln Arg Asp Leu Ala	245	250	255
Ala Gly Val Ala Ser Glu Leu Glu Ala Gln Thr Gly Ala Ile Val Arg	260	265	270
Ala Ala His Lys Val Gly Val Lys Thr Pro Leu His Asp Leu Ile Tyr	275	280	285
Ala Gly Leu Lys Leu Lys Glu Glu Glu Asn Ser Leu	290	295	300

&lt;210&gt; 537

&lt;211&gt; 693

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(670)

&lt;223&gt; RXA02400

&lt;400&gt; 537

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tttaagtcgc	cagattaaag	tcgtcaatga	aaggacatac	atg	tct	att	tcc	cgc	115
				Met	Ser	Ile	Ser	Arg	
				1				5	

acc gtc ttc ggc atc gca gcc acc gca gcc ctg tct gca gct ctc gtt	163
Thr Val Phe Gly Ile Ala Ala Thr Ala Ala Leu Ser Ala Ala Leu Val	
10 15 20	
gcg tgt tct cca cct cac cag cag gat tcc cca gtc cag cgc acc aat	211
Ala Cys Ser Pro Pro His Gln Gln Asp Ser Pro Val Gln Arg Thr Asn	
25 30 35	
gag atc ttg act act tct cag aac cca act tct gcg agc agc acc tca	259
Glu Ile Leu Thr Thr Ser Gln Asn Pro Thr Ser Ala Ser Ser Thr Ser	
40 45 50	
acc tct tcc gca acg act act tcc tca gct cct gtg gaa gag gac gta	307
Thr Ser Ser Ala Thr Thr Thr Ser Ser Ala Pro Val Glu Glu Asp Val	
55 60 65	
gag atc gtt gtt tca cca gca gcg ttg gtg gac ggt gag cag gtt acc	355
Glu Ile Val Val Ser Pro Ala Ala Leu Val Asp Gly Glu Gln Val Thr	
70 75 80 85	
ttc gaa atc tct gga ctt gat cca gag ggc ggc tac tac gca gcg atc	403
Phe Glu Ile Ser Gly Leu Asp Pro Glu Gly Gly Tyr Tyr Ala Ala Ile	
90 95 100	
tgc gat tcc gta gcg aac cct ggt aac cca gtt cct tct tgc acc ggc	451
Cys Asp Ser Val Ala Asn Pro Gly Asn Pro Val Pro Ser Cys Thr Gly	
105 110 115	
gaa atg gct gat ttc acg tcc cag gca tgg ttg agc aac tcc cag ccc	499
Glu Met Ala Asp Phe Thr Ser Gln Ala Trp Leu Ser Asn Ser Gln Pro	
120 125 130	
ggc gcg act gta gag atc gca gaa gac ggc acc gca act gtg gag ctt	547
Gly Ala Thr Val Glu Ile Ala Glu Asp Gly Thr Ala Thr Val Glu Leu	
135 140 145	
gaa gct acc gca acc ggc act ggc ttg gac tgc acc act cag gct tgt	595
Glu Ala Thr Ala Thr Gly Thr Gly Leu Asp Cys Thr Thr Gln Ala Cys	
150 155 160 165	
gta gcg aag gtc ttc ggc gat cat acc gaa ggt ttc cgc gat gtt gct	643
Val Ala Lys Val Phe Gly Asp His Thr Glu Gly Phe Arg Asp Val Ala	
170 175 180	
gaa gtc cca gtt act ttc gca gcc gct taagttttct taaaacgcac	690
Glu Val Pro Val Thr Phe Ala Ala Ala	
185 190	
tca	693

&lt;210&gt; 538

&lt;211&gt; 190

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 538

Met Ser Ile Ser Arg Thr Val Phe Gly Ile Ala Ala Thr Ala Ala Leu
1 5 10 15

Ser Ala Ala Leu Val Ala Cys Ser Pro Pro His Gln Gln Asp Ser Pro  
                   20                  25                  30  
 Val Gln Arg Thr Asn Glu Ile Leu Thr Thr Ser Gln Asn Pro Thr Ser  
                   35                  40                  45  
 Ala Ser Ser Thr Ser Thr Ser Ser Ala Thr Thr Thr Ser Ser Ala Pro  
           50                  55                  60  
 Val Glu Glu Asp Val Glu Ile Val Val Ser Pro Ala Ala Leu Val Asp  
   65                  70                  75                  80  
 Gly Glu Gln Val Thr Phe Glu Ile Ser Gly Leu Asp Pro Glu Gly Gly  
                   85                  90                  95  
 Tyr Tyr Ala Ala Ile Cys Asp Ser Val Ala Asn Pro Gly Asn Pro Val  
           100                  105                  110  
 Pro Ser Cys Thr Gly Glu Met Ala Asp Phe Thr Ser Gln Ala Trp Leu  
           115                  120                  125  
 Ser Asn Ser Gln Pro Gly Ala Thr Val Glu Ile Ala Glu Asp Gly Thr  
   130                  135                  140  
 Ala Thr Val Glu Leu Glu Ala Thr Ala Thr Gly Thr Gly Leu Asp Cys  
  145                  150                  155                  160  
 Thr Thr Gln Ala Cys Val Ala Lys Val Phe Gly Asp His Thr Glu Gly  
           165                  170                  175  
 Phe Arg Asp Val Ala Glu Val Pro Val Thr Phe Ala Ala Ala  
           180                  185                  190

&lt;210&gt; 539

&lt;211&gt; 1528

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1528)

&lt;223&gt; RXN01209

&lt;400&gt; 539

cagattgcag cacagaaggc atcggcgcca ggcagctttg cggtggcggt tattgatgcg 60

ctttatgacg tggatgccca ggctgtggcc tcgttggttg atg tgc gag agg cct 115  
   Met Cys Glu Arg Pro  
   1                  5

gaa aag tac gtg act gat ttt tct ttg tat ctg gtc acc gat ccc gtt 163  
 Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu Val Thr Asp Pro Val  
                   10                  15                  20

ttg ggt ggc ggg cca aaa aaa gta gct gga att gtt gac agc gca att 211  
 Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile Val Asp Ser Ala Ile  
           25                  30                  35

tcc ggc gga gtt tct gtg gtg cag ctg cgc gat aag aac tca ggc gtg 259  
 Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp Lys Asn Ser Gly Val



40					45					50						
gaa Glu	gat Asp	gtt Val	cgt Arg	gcg Ala	gca Ala	gca Ala	aag Lys	gag Glu	ctg Leu	aaa Lys	gaa Glu	ctc Leu	tgc Cys	gat Asp	gct Ala	307
	55					60					65					
cgc Arg	ggg Gly	gtg Val	gcg Ala	ctt Leu	gtt Val	gtc Val	aac Asn	gat Asp	tac Tyr	tta Leu	gat Asp	atc Ile	gcc Ala	gtt Val	gag Glu	355
	70				75					80					85	
ctg Leu	ggt Gly	ctt Leu	cac His	ctg Leu	cac His	att Ile	ggt Gly	caa Gln	ggc Gly	gat Asp	aca Thr	cct Pro	tat Tyr	acg Thr	caa Gln	403
				90					95					100		
gca Ala	cgg Arg	gag Glu	ctg Leu	ctt Leu	cca Pro	gct Ala	cat His	ctt Leu	gaa Glu	ttg Leu	ggt Gly	ttg Leu	agc Ser	att Ile	gaa Glu	451
			105					110					115			
aac Asn	ctg Leu	gat Asp	caa Gln	ttg Leu	cat His	gct Ala	gtg Val	atc Ile	gcg Ala	cag Gln	tgc Cys	gcc Ala	gag Glu	act Thr	ggt Gly	499
		120					125					130				
gtg Val	gca Ala	ttg Leu	ccc Pro	gat Asp	gtg Val	att Ile	ggc Gly	att Ile	ggt Gly	ccg Pro	gtg Val	gcc Ala	tct Ser	act Thr	gcg Ala	547
	135					140					145					
acc Thr	aaa Lys	cca Pro	gat Asp	gcg Ala	gca Ala	ccc Pro	gca Ala	ttg Leu	ggt Gly	gtg Val	gag Glu	ggc Gly	atc Ile	gct Ala	gag Glu	595
					155					160					165	
atc Ile	gcc Ala	gct Ala	gta Val	gct Ala	caa Gln	gac Asp	cac His	ggc Gly	atc Ile	gca Ala	tca Ser	gta Val	gct Ala	att Ile	gga Gly	643
				170				175						180		
ggc Gly	gtt Val	ggt Gly	cta Leu	cgc Arg	aac Asn	gcg Ala	gcc Ala	gaa Glu	ctc Leu	gct Ala	gct Ala	acg Thr	ccc Pro	atc Ile	gac Asp	691
			185					190					195			
ggt Gly	ctg Leu	tgc Cys	gtg Val	gtc Val	tct Ser	gaa Glu	atc Ile	atg Met	acc Thr	gcc Ala	gcc Ala	aat Asn	cca Pro	gca Ala	gct Ala	739
		200					205					210				
gcg Ala	gca Ala	act Thr	cgc Arg	ctg Leu	cgg Arg	act Thr	gct Ala	ttt Phe	caa Gln	cct Pro	act Thr	ttc Phe	tcg Ser	cct Pro	gaa Glu	787
	215					220					225					
act Thr	caa Gln	act Thr	gaa Glu	ctc Leu	tct Ser	caa Gln	aca Thr	gaa Glu	ctc Leu	caa Gln	gga Gly	gcc Ala	ttc Phe	gtg Val	aat Asn	835
	230				235					240					245	
tcg Ser	cct Pro	tct Ser	gcc Ala	cca Pro	cgt Arg	gtg Val	ttg Leu	tct Ser	att Ile	gca Ala	ggc Gly	act Thr	gat Asp	ccc Pro	aca Thr	883
				250					255					260		
ggt Gly	ggt Gly	gca Ala	ggt Gly	att Ile	cag Gln	gct Ala	gat Asp	ctg Leu	aag Lys	tcc Ser	att Ile	gca Ala	gca Ala	ggt Gly	ggc Gly	931
			265					270					275			
ggc Gly	tac Tyr	ggc Gly	atg Met	tgc Cys	gtt Val	gtg Val	acc Thr	tcg Ser	ctg Leu	gtc Val	gcg Ala	caa Gln	aac Asn	acc Thr	cac His	979
		280					285					290				

ggc gtc aac acg atc cac acc cca ccc ttg acc ttt ttg gaa gaa cag  
1027

Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr Phe Leu Glu Glu Gln  
295 300 305

ctg gaa gcg gtc ttt tcc gat gtc acc gtc gat gcc atc aag ctc ggc  
1075

Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp Ala Ile Lys Leu Gly  
310 315 320 325

atg ttg ggc tct gcc gac acc gtc gat ctg gtg gct tca tgg ctt ggt  
1123

Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val Ala Ser Trp Leu Gly  
330 335 340

tcc cac gag cac ggt ccc gtg gtg ctt gat ccc gtc atg atc gcc acc  
1171

Ser His Glu His Gly Pro Val Val Leu Asp Pro Val Met Ile Ala Thr  
345 350 355

agc ggt gat cgc cta ctg gat gcg agc gct gaa gaa tcg ctg cgc cgc  
1219

Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu Glu Ser Leu Arg Arg  
360 365 370

ctg gcc gtg cac gtc gat gtg gtc acc ccg aat atc ccc gaa ctt gcc  
1267

Leu Ala Val His Val Asp Val Val Thr Pro Asn Ile Pro Glu Leu Ala  
375 380 385

gtg ttg tgc gac agt gct cct gcc atc acc atg gat gag gcc att gct  
1315

Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met Asp Glu Ala Ile Ala  
390 395 400 405

cag gct cag gga ttt gcg cgg act cat gac acc atc gtc att gtc aag  
1363

Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr Ile Val Ile Val Lys  
410 415 420

ggt gga cat ctg act ggc gcg ctt gct gat aac gct gtc gtg cgc ccc  
1411

Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn Ala Val Val Arg Pro  
425 430 435

gac ggc tcg gtg ttc cag gtg gaa aac ctg cgt gtc aac acc acc aac  
1459

Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg Val Asn Thr Thr Asn  
440 445 450

tcc cat ggc aca ggc tgt tcg ctc tct gcg tca ctt gcc acc aag atc  
1507

Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser Leu Ala Thr Lys Ile  
455 460 465

gcc gcc ggc gaa agc gtg gaa  
1528

Ala Ala Gly Glu Ser Val Glu  
470 475

<210> 540  
 <211> 476  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 540

Met	Cys	Glu	Arg	Pro	Glu	Lys	Tyr	Val	Thr	Asp	Phe	Ser	Leu	Tyr	Leu
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Val	Thr	Asp	Pro	Val	Leu	Gly	Gly	Gly	Pro	Lys	Lys	Val	Ala	Gly	Ile
			20					25					30		
Val	Asp	Ser	Ala	Ile	Ser	Gly	Gly	Val	Ser	Val	Val	Gln	Leu	Arg	Asp
		35					40					45			
Lys	Asn	Ser	Gly	Val	Glu	Asp	Val	Arg	Ala	Ala	Ala	Lys	Glu	Leu	Lys
	50					55					60				
Glu	Leu	Cys	Asp	Ala	Arg	Gly	Val	Ala	Leu	Val	Val	Asn	Asp	Tyr	Leu
65					70					75					80
Asp	Ile	Ala	Val	Glu	Leu	Gly	Leu	His	Leu	His	Ile	Gly	Gln	Gly	Asp
				85					90					95	
Thr	Pro	Tyr	Thr	Gln	Ala	Arg	Glu	Leu	Leu	Pro	Ala	His	Leu	Glu	Leu
			100					105						110	
Gly	Leu	Ser	Ile	Glu	Asn	Leu	Asp	Gln	Leu	His	Ala	Val	Ile	Ala	Gln
		115					120					125			
Cys	Ala	Glu	Thr	Gly	Val	Ala	Leu	Pro	Asp	Val	Ile	Gly	Ile	Gly	Pro
	130					135					140				
Val	Ala	Ser	Thr	Ala	Thr	Lys	Pro	Asp	Ala	Ala	Pro	Ala	Leu	Gly	Val
145					150					155					160
Glu	Gly	Ile	Ala	Glu	Ile	Ala	Ala	Val	Ala	Gln	Asp	His	Gly	Ile	Ala
				165					170					175	
Ser	Val	Ala	Ile	Gly	Gly	Val	Gly	Leu	Arg	Asn	Ala	Ala	Glu	Leu	Ala
			180					185					190		
Ala	Thr	Pro	Ile	Asp	Gly	Leu	Cys	Val	Val	Ser	Glu	Ile	Met	Thr	Ala
		195					200					205			
Ala	Asn	Pro	Ala	Ala	Ala	Ala	Thr	Arg	Leu	Arg	Thr	Ala	Phe	Gln	Pro
	210					215					220				
Thr	Phe	Ser	Pro	Glu	Thr	Gln	Thr	Glu	Leu	Ser	Gln	Thr	Glu	Leu	Gln
225					230					235					240
Gly	Ala	Phe	Val	Asn	Ser	Pro	Ser	Ala	Pro	Arg	Val	Leu	Ser	Ile	Ala
				245					250					255	
Gly	Thr	Asp	Pro	Thr	Gly	Gly	Ala	Gly	Ile	Gln	Ala	Asp	Leu	Lys	Ser
			260					265					270		
Ile	Ala	Ala	Gly	Gly	Gly	Tyr	Gly	Met	Cys	Val	Val	Thr	Ser	Leu	Val
		275					280					285			

Ala Gln Asn Thr His Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr  
 290 295 300

Phe Leu Glu Glu Gln Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp  
 305 310 315 320

Ala Ile Lys Leu Gly Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val  
 325 330 335

Ala Ser Trp Leu Gly Ser His Glu His Gly Pro Val Val Leu Asp Pro  
 340 345 350

Val Met Ile Ala Thr Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu  
 355 360 365

Glu Ser Leu Arg Arg Leu Ala Val His Val Asp Val Val Thr Pro Asn  
 370 375 380

Ile Pro Glu Leu Ala Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met  
 385 390 395 400

Asp Glu Ala Ile Ala Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr  
 405 410 415

Ile Val Ile Val Lys Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn  
 420 425 430

Ala Val Val Arg Pro Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg  
 435 440 445

Val Asn Thr Thr Asn Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser  
 450 455 460

Leu Ala Thr Lys Ile Ala Ala Gly Glu Ser Val Glu  
 465 470 475

<210> 541  
 <211> 1528  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1528)  
 <223> FRXA01209

<400> 541  
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ctttatgacg tggatgccca ggctgtggcc tcgttggttg atg tgc gag agg cct 115  
 Met Cys Glu Arg Pro  
 1 5

gaa aag tac gtg act gat ttt tct ttg tat ctg gtc acc gat ccc gtt 163  
 Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu Val Thr Asp Pro Val  
 10 15 20

ttg ggt ggc ggg cca aaa aaa gta gct gga att gtt gac agc gca att 211  
 Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile Val Asp Ser Ala Ile  
 25 30 35

tcc	ggc	gga	gtt	tct	gtg	gtg	cag	ctg	cgc	gat	aag	aac	tca	ggc	gtg	259
Ser	Gly	Gly	Val	Ser	Val	Val	Gln	Leu	Arg	Asp	Lys	Asn	Ser	Gly	Val	
		40					45					50				
gaa	gat	gtt	cgt	gcg	gca	gca	aag	gag	ctg	aaa	gaa	ctc	tgc	gat	gct	307
Glu	Asp	Val	Arg	Ala	Ala	Ala	Lys	Glu	Leu	Lys	Glu	Leu	Cys	Asp	Ala	
	55					60					65					
cgc	ggg	gtg	gcg	ctt	gtt	gtc	aac	gat	tac	tta	gat	atc	gcc	gtt	gag	355
Arg	Gly	Val	Ala	Leu	Val	Val	Asn	Asp	Tyr	Leu	Asp	Ile	Ala	Val	Glu	
70					75					80					85	
ctg	ggg	ctt	cac	ctg	cac	att	ggg	caa	ggc	gat	aca	cct	tat	acg	caa	403
Leu	Gly	Leu	His	Leu	His	Ile	Gly	Gln	Gly	Asp	Thr	Pro	Tyr	Thr	Gln	
				90					95					100		
gca	cgg	gag	ctg	ctt	cca	gct	cat	ctt	gaa	ttg	ggg	ttg	agc	att	gaa	451
Ala	Arg	Glu	Leu	Leu	Pro	Ala	His	Leu	Glu	Leu	Gly	Leu	Ser	Ile	Glu	
			105					110					115			
aac	ctg	gat	caa	ttg	cat	gct	gtg	atc	gcg	cag	tgc	gcc	gag	act	ggg	499
Asn	Leu	Asp	Gln	Leu	His	Ala	Val	Ile	Ala	Gln	Cys	Ala	Glu	Thr	Gly	
		120					125					130				
gtg	gca	ttg	ccc	gat	gtg	att	ggc	att	ggg	ccg	gtg	gcc	tct	act	gcg	547
Val	Ala	Leu	Pro	Asp	Val	Ile	Gly	Ile	Gly	Pro	Val	Ala	Ser	Thr	Ala	
	135					140					145					
acc	aaa	cca	gat	gcg	gca	ccc	gca	ttg	ggg	gtg	gag	ggc	atc	gct	gag	595
Thr	Lys	Pro	Asp	Ala	Ala	Pro	Ala	Leu	Gly	Val	Glu	Gly	Ile	Ala	Glu	
150					155					160					165	
atc	gcc	gct	gta	gct	caa	gac	cac	ggc	atc	gca	tca	gta	gct	att	gga	643
Ile	Ala	Ala	Val	Ala	Gln	Asp	His	Gly	Ile	Ala	Ser	Val	Ala	Ile	Gly	
				170				175						180		
ggc	gtt	ggg	cta	cgc	aac	gcg	gcc	gaa	ctc	gct	gct	acg	ccc	atc	gac	691
Gly	Val	Gly	Leu	Arg	Asn	Ala	Ala	Glu	Leu	Ala	Ala	Thr	Pro	Ile	Asp	
			185					190					195			
ggg	ctg	tgc	gtg	gtc	tct	gaa	atc	atg	acc	gcc	gcc	aat	cca	gca	gct	739
Gly	Leu	Cys	Val	Val	Ser	Glu	Ile	Met	Thr	Ala	Ala	Asn	Pro	Ala	Ala	
		200					205					210				
gcg	gca	act	cgc	ctg	cgg	act	gct	ttt	caa	cct	act	ttc	tgc	cct	gaa	787
Ala	Ala	Thr	Arg	Leu	Arg	Thr	Ala	Phe	Gln	Pro	Thr	Phe	Ser	Pro	Glu	
	215					220					225					
act	caa	act	gaa	ctc	tct	caa	aca	gaa	ctc	caa	gga	gcc	ttc	gtg	aat	835
Thr	Gln	Thr	Glu	Leu	Ser	Gln	Thr	Glu	Leu	Gln	Gly	Ala	Phe	Val	Asn	
230					235					240					245	
tgc	cct	tct	gcc	cca	cgt	gtg	ttg	tct	att	gca	ggc	act	gat	ccc	aca	883
Ser	Pro	Ser	Ala	Pro	Arg	Val	Leu	Ser	Ile	Ala	Gly	Thr	Asp	Pro	Thr	
				250					255					260		
ggg	ggg	gca	ggg	att	cag	gct	gat	ctg	aag	tcc	att	gca	gca	ggg	ggc	931
Gly	Gly	Ala	Gly	Ile	Gln	Ala	Asp	Leu	Lys	Ser	Ile	Ala	Ala	Gly	Gly	
			265					270					275			

ggc tac ggc atg tgc gtt gtg acc tcg ctg gtc gcg caa aac acc cac 979  
 Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val Ala Gln Asn Thr His  
 280 285 290

ggc gtc aac acg atc cac acc cca ccc ttg acc ttt ttg gaa gaa cag  
 1027  
 Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr Phe Leu Glu Glu Gln  
 295 300 305

ctg gaa gcg gtc ttt tcc gat gtc acc gtc gat gcc atc aag ctc ggc  
 1075  
 Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp Ala Ile Lys Leu Gly  
 310 315 320 325

atg ttg ggc tct gcc gac acc gtc gat ctg gtg gct tca tgg ctt ggt  
 1123  
 Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val Ala Ser Trp Leu Gly  
 330 335 340

tcc cac gag cac ggt ccc gtg gtg ctt gat ccc gtc atg atc gcc acc  
 1171  
 Ser His Glu His Gly Pro Val Val Leu Asp Pro Val Met Ile Ala Thr  
 345 350 355

agc ggt gat cgc cta ctg gat gcg agc gct gaa gaa tcg ctg cgc cgc  
 1219  
 Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu Glu Ser Leu Arg Arg  
 360 365 370

ctg gcc gtg cac gtc gat gtg gtc acc ccg aat atc ccc gaa ctt gcc  
 1267  
 Leu Ala Val His Val Asp Val Val Thr Pro Asn Ile Pro Glu Leu Ala  
 375 380 385

gtg ttg tgc gac agt gct cct gcc atc acc atg gat gag gcc att gct  
 1315  
 Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met Asp Glu Ala Ile Ala  
 390 395 400 405

cag gct cag gga ttt gcg cgg act cat gac acc atc gtc att gtc aag  
 1363  
 Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr Ile Val Ile Val Lys  
 410 415 420

ggt gga cat ctg act ggc gcg ctt gct gat aac gct gtc gtg cgc ccc  
 1411  
 Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn Ala Val Val Arg Pro  
 425 430 435

gac ggc tcg gtg ttc cag gtg gaa aac ctg cgt gtc aac acc acc aac  
 1459  
 Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg Val Asn Thr Thr Asn  
 440 445 450

tcc cat ggc aca ggc tgt tcg ctc tct gcg tca ctt gcc acc aag atc  
 1507  
 Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser Leu Ala Thr Lys Ile  
 455 460 465

gcc gcc ggc gaa agc gtg gaa  
 1528

Ala Ala Gly Glu Ser Val Glu  
470 475

<210> 542

<211> 476

<212> PRT

<213> Corynebacterium glutamicum

<400> 542

Met Cys Glu Arg Pro Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu  
1 5 10 15

Val Thr Asp Pro Val Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile  
20 25 30

Val Asp Ser Ala Ile Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp  
35 40 45

Lys Asn Ser Gly Val Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys  
50 55 60

Glu Leu Cys Asp Ala Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu  
65 70 75 80

Asp Ile Ala Val Glu Leu Gly Leu His Leu His Ile Gly Gln Gly Asp  
85 90 95

Thr Pro Tyr Thr Gln Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu  
100 105 110

Gly Leu Ser Ile Glu Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln  
115 120 125

Cys Ala Glu Thr Gly Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro  
130 135 140

Val Ala Ser Thr Ala Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val  
145 150 155 160

Glu Gly Ile Ala Glu Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala  
165 170 175

Ser Val Ala Ile Gly Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala  
180 185 190

Ala Thr Pro Ile Asp Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala  
195 200 205

Ala Asn Pro Ala Ala Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro  
210 215 220

Thr Phe Ser Pro Glu Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln  
225 230 235 240

Gly Ala Phe Val Asn Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala  
245 250 255

Gly Thr Asp Pro Thr Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser  
260 265 270

Ile Ala Ala Gly Gly Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val  
 275 280 285  
 Ala Gln Asn Thr His Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr  
 290 295 300  
 Phe Leu Glu Glu Gln Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp  
 305 310 315 320  
 Ala Ile Lys Leu Gly Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val  
 325 330 335  
 Ala Ser Trp Leu Gly Ser His Glu His Gly Pro Val Val Leu Asp Pro  
 340 345 350  
 Val Met Ile Ala Thr Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu  
 355 360 365  
 Glu Ser Leu Arg Arg Leu Ala Val His Val Asp Val Val Thr Pro Asn  
 370 375 380  
 Ile Pro Glu Leu Ala Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met  
 385 390 395 400  
 Asp Glu Ala Ile Ala Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr  
 405 410 415  
 Ile Val Ile Val Lys Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn  
 420 425 430  
 Ala Val Val Arg Pro Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg  
 435 440 445  
 Val Asn Thr Thr Asn Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser  
 450 455 460  
 Leu Ala Thr Lys Ile Ala Ala Gly Glu Ser Val Glu  
 465 470 475

&lt;210&gt; 543

&lt;211&gt; 723

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(700)

&lt;223&gt; RXN01413

&lt;400&gt; 543

ttgcccctat tggaagaagt aaattccaca ccttcacttt ccaatacttc ttttggtgag 60

 cgggtttcct cagcgtttaa ccatctgaaa ccatctgaga ttg acc cat ctg ttc 115  
 Leu Thr His Leu Phe  
 1 5

 tta gaa ctc gat gag cgt tta gta ctg ggt gtt cag caa gat ggt tac 163  
 Leu Glu Leu Asp Glu Arg Leu Val Leu Gly Val Gln Gln Asp Gly Tyr  
 10 15 20



[illegible]

**<210> 544**

<211> 200

<212> PRT

<213> Corynebacterium glutamicum

**<400> 544**

Leu Thr His Leu Phe Leu Glu Leu Asp Glu Arg Leu Val Leu Gly Val  
1 5 10 15

Gln Gln Asp Gly Tyr Gln Trp Thr Glu His Leu Phe Arg Leu Pro Leu  
20 25 30

Gln His Leu Arg Asn Ser Pro Asn Asp Leu Gln Gly Leu Lys Ile Arg  
 35 40 45  
 Trp Cys Glu Leu Tyr Ser Thr Thr Gly Lys Asp Gln Gly Val Glu Leu  
 50 55 60  
 Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn Phe Glu Ala Ser Thr  
 65 70 75 80  
 Leu Ser Gly Leu Glu Lys Leu Glu Thr Val Glu Asp Leu Lys Glu Ala  
 85 90 95  
 Ala Arg Leu Ile Tyr Glu Gln Gly Pro Gln Tyr Val Val Val Lys Gly  
 100 105 110  
 Gly Met Asp Phe Pro Gly Glu Asn Ala Val Asp Val Leu Phe Asp Gly  
 115 120 125  
 Ser Ser Tyr His Val Phe Ser Glu Pro Lys Ile Gly Glu Glu Arg Val  
 130 135 140  
 Ser Gly Ala Val Cys Thr Phe Ala Ala Val Ile Thr Ala Glu Leu Ala  
 145 150 155 160  
 Lys Gly Ala Glu Val Val Asp Pro Val Ala Thr Ala Lys Arg Val Val  
 165 170 175  
 Thr Arg Ala Val Gln Asp Ala Val Ala Ser Asn Ala Pro Phe Thr Ser  
 180 185 190  
 Val Trp Leu Ala Glu Asp Asn Lys  
 195 200

&lt;210&gt; 545

&lt;211&gt; 795

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(772)

&lt;223&gt; RXN01617

&lt;400&gt; 545

tcagaagcta ccggcggcgc cggcatccag gttgatttga agaccttcca gcatttaaga 60  
 tgtttatggc attgggtcca tcacatgctt ggggtggcctt ttg atc cta aag aca 115  
 Leu Ile Leu Lys Thr 5  
 act gga atc acc gtt ttg tcc cgg ttt gat gcg cag gtt atc gct aat 163  
 Thr Gly Ile Thr Val Leu Ser Arg Phe Asp Ala Gln Val Ile Ala Asn 20  
 10 15  
 cag att gag gcc gcc acc gca gcg cac gat ctt gat gtg gtg aag atc 211  
 Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu Asp Val Val Lys Ile 35  
 25 30  
 ggt atg ttg ggt act cct gca acg atc gat act gtg gca acc gct ttg 259  
 Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr Val Ala Thr Ala Leu

40					45					50							
gag	gaa	aac	agc	ttc	aag	cac	gtt	gtc	cta	gac	ccg	gta	ctg	atc	tgc	307	
Glu	Glu	Asn	Ser	Phe	Lys	His	Val	Val	Leu	Asp	Pro	Val	Leu	Ile	Cys		
55					60					65							
aag	ggc	cag	gag	ccc	ggc	gcg	gca	ctt	gat	act	gac	act	gcc	ctt	cgc	355	
Lys	Gly	Gln	Glu	Pro	Gly	Ala	Ala	Leu	Asp	Thr	Asp	Thr	Ala	Leu	Arg		
70					75					80					85		
gcg	aag	gtg	ctg	cca	cag	gca	acc	gtg	gtt	act	cca	aac	aac	ttc	gag	403	
Ala	Lys	Val	Leu	Pro	Gln	Ala	Thr	Val	Val	Thr	Pro	Asn	Asn	Phe	Glu		
90					95					100							
gcc	acc	acc	ctg	tct	ggc	cta	gac	aag	ctg	gag	acc	atc	gac	gac	ctg	451	
Ala	Thr	Thr	Leu	Ser	Gly	Leu	Asp	Lys	Leu	Glu	Thr	Ile	Asp	Asp	Leu		
105					110					115							
aag	gaa	gca	gcc	cgc	ctc	att	cat	gag	caa	gga	cct	cag	tac	gtc	gtt	499	
Lys	Glu	Ala	Ala	Arg	Leu	Ile	His	Glu	Gln	Gly	Pro	Gln	Tyr	Val	Val		
120					125					130							
gtt	aag	ggt	ggc	atc	gac	ttc	cca	ggc	gac	aac	gct	gtg	gac	gta	ctt	547	
Val	Lys	Gly	Gly	Ile	Asp	Phe	Pro	Gly	Asp	Asn	Ala	Val	Asp	Val	Leu		
135					140					145							
ttc	gac	ggc	acc	gac	tac	cac	gtg	ttc	tct	gaa	cca	aag	atc	ggc	gac	595	
Phe	Asp	Gly	Thr	Asp	Tyr	His	Val	Phe	Ser	Glu	Pro	Lys	Ile	Gly	Asp		
150					155					160					165		
gag	cgc	gtc	tcc	ggc	gct	ggc	tgt	acc	ttc	gca	gct	gtc	atc	acc	gca	643	
Glu	Arg	Val	Ser	Gly	Ala	Gly	Cys	Thr	Phe	Ala	Ala	Val	Ile	Thr	Ala		
170					175					180							
gag	ctg	gcc	aag	ggc	aac	tct	gcc	gtt	gat	gca	gtg	acc	acc	gct	aag	691	
Glu	Leu	Ala	Lys	Gly	Asn	Ser	Ala	Val	Asp	Ala	Val	Thr	Thr	Ala	Lys		
185					190					195							
cgc	gta	gtc	acc	cgc	gca	gtg	aag	gac	gct	gtc	gca	tcc	aac	gca	ccg	739	
Arg	Val	Val	Thr	Arg	Ala	Val	Lys	Asp	Ala	Val	Ala	Ser	Asn	Ala	Pro		
200					205					210							
ttt	acc	tct	gtg	tgg	ttg	gcg	gaa	gac	aac	aag	tagaaatcctt	aaacaagctc				792	
Phe	Thr	Ser	Val	Trp	Leu	Ala	Glu	Asp	Asn	Lys							
215					220												
cct																795	
<210> 546																	
<211> 224																	
<212> PRT																	
<213> Corynebacterium glutamicum																	
<400> 546																	
Leu	Ile	Leu	Lys	Thr	Thr	Gly	Ile	Thr	Val	Leu	Ser	Arg	Phe	Asp	Ala		
1				5					10					15			
Gln	Val	Ile	Ala	Asn	Gln	Ile	Glu	Ala	Ala	Thr	Ala	Ala	His	Asp	Leu		
20					25					30							

Asp Val Val Lys Ile Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr  
                   35                                  40                                  45  
 Val Ala Thr Ala Leu Glu Glu Asn Ser Phe Lys His Val Val Leu Asp  
                   50                                  55                                  60  
 Pro Val Leu Ile Cys Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr  
                   65                                  70                                  75                                  80  
 Asp Thr Ala Leu Arg Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr  
                                   85                                  90                                  95  
 Pro Asn Asn Phe Glu Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu  
                                   100                                  105                                  110  
 Thr Ile Asp Asp Leu Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly  
                   115                                  120                                  125  
 Pro Gln Tyr Val Val Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn  
                   130                                  135                                  140  
 Ala Val Asp Val Leu Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu  
                   145                                  150                                  155                                  160  
 Pro Lys Ile Gly Asp Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala  
                                   165                                  170                                  175  
 Ala Val Ile Thr Ala Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala  
                                   180                                  185                                  190  
 Val Thr Thr Ala Lys Arg Val Val Thr Arg Ala Val Lys Asp Ala Val  
                   195                                  200                                  205  
 Ala Ser Asn Ala Pro Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys  
                   210                                  215                                  220

&lt;210&gt; 547

&lt;211&gt; 638

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(615)

&lt;223&gt; FRXA01617

&lt;400&gt; 547

gct aat cag att gag gcc gcc acc gca gcg cac gat ctt gat gtg gtg 48  
 Ala Asn Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu Asp Val Val  
           1                                  5                                  10                                  15  
 aag atc ggt atg ttg ggt act cct gca acg atc gat act gtg gca acc 96  
 Lys Ile Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr Val Ala Thr  
                                   20                                  25                                  30  
 gct ttg gag gaa aac agc ttc aag cac gtt gtc cta gac ccg gta ctg 144  
 Ala Leu Glu Glu Asn Ser Phe Lys His Val Val Leu Asp Pro Val Leu

35					40					45						
atc	tgc	aag	ggc	cag	gag	ccc	ggc	gcg	gca	ctt	gat	act	gac	act	gcc	192
Ile	Cys	Lys	Gly	Gln	Glu	Pro	Gly	Ala	Ala	Leu	Asp	Thr	Asp	Thr	Ala	
50						55				60						
ctt	cgc	gcg	aag	gtg	ctg	cca	cag	gca	acc	gtg	gtt	act	cca	aac	aac	240
Leu	Arg	Ala	Lys	Val	Leu	Pro	Gln	Ala	Thr	Val	Val	Thr	Pro	Asn	Asn	
65				70						75				80		
ttc	gag	gcc	acc	acc	ctg	tct	ggc	cta	gac	aag	ctg	gag	acc	atc	gac	288
Phe	Glu	Ala	Thr	Thr	Leu	Ser	Gly	Leu	Asp	Lys	Leu	Glu	Thr	Ile	Asp	
				85				90						95		
gac	ctg	aag	gaa	gca	gcc	cgc	ctc	att	cat	gag	caa	gga	cct	cag	tac	336
Asp	Leu	Lys	Glu	Ala	Ala	Arg	Leu	Ile	His	Glu	Gln	Gly	Pro	Gln	Tyr	
		100						105				110				
gtc	gtt	gtt	aag	ggg	ggc	atc	gac	ttc	cca	ggc	gac	aac	gct	gtg	gac	384
Val	Val	Val	Lys	Gly	Gly	Ile	Asp	Phe	Pro	Gly	Asp	Asn	Ala	Val	Asp	
115						120						125				
gta	ctt	ttc	gac	ggc	acc	gac	tac	cac	gtg	ttc	tct	gaa	cca	aag	atc	432
Val	Leu	Phe	Asp	Gly	Thr	Asp	Tyr	His	Val	Phe	Ser	Glu	Pro	Lys	Ile	
130						135				140						
ggc	gac	gag	cgc	gtc	tcc	ggc	gct	ggc	tgt	acc	ttc	gca	gct	gtc	atc	480
Gly	Asp	Glu	Arg	Val	Ser	Gly	Ala	Gly	Cys	Thr	Phe	Ala	Ala	Val	Ile	
145				150						155				160		
acc	gca	gag	ctg	gcc	aag	ggc	aac	tct	gcc	gtt	gat	gca	gtg	acc	acc	528
Thr	Ala	Glu	Leu	Ala	Lys	Gly	Asn	Ser	Ala	Val	Asp	Ala	Val	Thr	Thr	
				165				170						175		
gct	aag	cgc	gta	gtc	acc	cgc	gca	gtg	aag	gac	gct	gtc	gca	tcc	aac	576
Ala	Lys	Arg	Val	Val	Thr	Arg	Ala	Val	Lys	Asp	Ala	Val	Ala	Ser	Asn	
		180						185				190				
gca	ccg	ttt	acc	tct	gtg	tgg	ttg	gcg	gaa	gac	aac	aag	tag	aa	tctt	625
Ala	Pro	Phe	Thr	Ser	Val	Trp	Leu	Ala	Glu	Asp	Asn	Lys				
195						200						205				
aaacaagctc cct																638

&lt;210&gt; 548

&lt;211&gt; 205

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 548

Ala	Asn	Gln	Ile	Glu	Ala	Ala	Thr	Ala	Ala	His	Asp	Leu	Asp	Val	Val
1				5				10						15	

Lys	Ile	Gly	Met	Leu	Gly	Thr	Pro	Ala	Thr	Ile	Asp	Thr	Val	Ala	Thr
			20					25					30		

Ala	Leu	Glu	Glu	Asn	Ser	Phe	Lys	His	Val	Val	Leu	Asp	Pro	Val	Leu
		35					40					45			

Ile	Cys	Lys	Gly	Gln	Glu	Pro	Gly	Ala	Ala	Leu	Asp	Thr	Asp	Thr	Ala
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50					55					60					
Leu	Arg	Ala	Lys	Val	Leu	Pro	Gln	Ala	Thr	Val	Val	Thr	Pro	Asn	Asn
65					70					75					80
Phe	Glu	Ala	Thr	Thr	Leu	Ser	Gly	Leu	Asp	Lys	Leu	Glu	Thr	Ile	Asp
				85					90					95	
Asp	Leu	Lys	Glu	Ala	Ala	Arg	Leu	Ile	His	Glu	Gln	Gly	Pro	Gln	Tyr
			100					105					110		
Val	Val	Val	Lys	Gly	Gly	Ile	Asp	Phe	Pro	Gly	Asp	Asn	Ala	Val	Asp
			115				120					125			
Val	Leu	Phe	Asp	Gly	Thr	Asp	Tyr	His	Val	Phe	Ser	Glu	Pro	Lys	Ile
	130					135					140				
Gly	Asp	Glu	Arg	Val	Ser	Gly	Ala	Gly	Cys	Thr	Phe	Ala	Ala	Val	Ile
145						150					155				160
Thr	Ala	Glu	Leu	Ala	Lys	Gly	Asn	Ser	Ala	Val	Asp	Ala	Val	Thr	Thr
				165					170					175	
Ala	Lys	Arg	Val	Val	Thr	Arg	Ala	Val	Lys	Asp	Ala	Val	Ala	Ser	Asn
			180					185					190		
Ala	Pro	Phe	Thr	Ser	Val	Trp	Leu	Ala	Glu	Asp	Asn	Lys			
	195						200					205			

&lt;210&gt; 549

&lt;211&gt; 915

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(892)

&lt;223&gt; RXS01807

&lt;400&gt; 549

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gcagtggctg gaactcggcg aggaaatcga gggctagttc atg ccg tcg gca ggc 115  
 Met Pro Ser Ala Gly  
 1 5

gag gag att tta gag cag cgc gca cag ctg gag ttt gat cag cgc cgc 163  
 Glu Glu Ile Leu Glu Gln Arg Ala Gln Leu Glu Phe Asp Gln Arg Arg  
 10 15 20

gcc gat gtg gtg atg atc ggc agc cag gtg gtt tat ggt tcc gtg ggg 211  
 Ala Asp Val Val Met Ile Gly Ser Gln Val Val Tyr Gly Ser Val Gly  
 25 30 35

ctc agt gct gcc att ccg gtg atg cac aac gaa ggc ctc cgc gtg gtc 259  
 Leu Ser Ala Ala Ile Pro Val Met His Asn Glu Gly Leu Arg Val Val  
 40 45 50

gct gtc ccc acc gtg gtg tta agt tcc atg ccg cgt tat gca agt tct 307  
 Ala Val Pro Thr Val Val Leu Ser Ser Met Pro Arg Tyr Ala Ser Ser

55	60	65	
cac cgc cag ccg atg tcg gac caa tgg ctc gcc gac gcg ctg caa gac His Arg Gln Pro Met Ser Asp Gln Trp Leu Ala Asp Ala Leu Gln Asp 70 75 80 85			355
ctg gtg gat ctg ggg att atc gat gag gtt tcc acc att tcc acc ggc Leu Val Asp Leu Gly Ile Ile Asp Glu Val Ser Thr Ile Ser Thr Gly 90 95 100			403
tat ttt acc tcc gct tct cag gtg cgt gtg gtc gct gcg tgg ctg cag Tyr Phe Thr Ser Ala Ser Gln Val Arg Val Val Ala Ala Trp Leu Gln 105 110 115			451
aaa atc cgc gaa acc cat ccg cat gtg cgc atc gtg gtg gat ccc atc Lys Ile Arg Glu Thr His Pro His Val Arg Ile Val Val Asp Pro Ile 120 125 130			499
atg ggg gac agt gac gtg gga att tat gtc gcc gac gag atc gca acc Met Gly Asp Ser Asp Val Gly Ile Tyr Val Ala Asp Glu Ile Ala Thr 135 140 145			547
gcc atc tgc cag gac tta tgc cct ctg gct acc gga atc att ccc aat Ala Ile Cys Gln Asp Leu Cys Pro Leu Ala Thr Gly Ile Ile Pro Asn 150 155 160 165			595
gct ttc gag ctc tcc cac atg gtt ggc tcc ggc gat ccg cgc tcg ctg Ala Phe Glu Leu Ser His Met Val Gly Ser Gly Asp Pro Arg Ser Leu 170 175 180			643
ctc ggc ccg ttt ggc gag tgg atc atc atc acc agc gcc act gaa act Leu Gly Pro Phe Gly Glu Trp Ile Ile Ile Thr Ser Ala Thr Glu Thr 185 190 195			691
gtg ggc acc acc gtc acc cgc atc gtc acc cgt gac agc gtc cag gaa Val Gly Thr Thr Val Thr Arg Ile Val Thr Arg Asp Ser Val Gln Glu 200 205 210			739
atc gcc tcc gcc acc gtc gat acc acg gcc aaa ggg gca ggc gac gtc Ile Ala Ser Ala Thr Val Asp Thr Thr Ala Lys Gly Ala Gly Asp Val 215 220 225			787
tac gcc gca gca tta atc gcc gcc ctg cat aaa gat ttt tcg ctt atc Tyr Ala Ala Ala Leu Ile Ala Ala Leu His Lys Asp Phe Ser Leu Ile 230 235 240 245			835
gac gcc gcc agc cac gca tcc aac acc gtc tgc gcc ggc ctg cag acc Asp Ala Ala Ser His Ala Ser Asn Thr Val Cys Ala Gly Leu Gln Thr 250 255 260			883
aaa gcg ctt taggtttcgt ccgtctctga cag Lys Ala Leu			915

&lt;210&gt; 550

&lt;211&gt; 264

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 550

Met Pro Ser Ala Gly Glu Glu Ile Leu Glu Gln Arg Ala Gln Leu Glu  
 1 5 10 15  
 Phe Asp Gln Arg Arg Ala Asp Val Val Met Ile Gly Ser Gln Val Val  
 20 25 30  
 Tyr Gly Ser Val Gly Leu Ser Ala Ala Ile Pro Val Met His Asn Glu  
 35 40 45  
 Gly Leu Arg Val Val Ala Val Pro Thr Val Val Leu Ser Ser Met Pro  
 50 55 60  
 Arg Tyr Ala Ser Ser His Arg Gln Pro Met Ser Asp Gln Trp Leu Ala  
 65 70 75 80  
 Asp Ala Leu Gln Asp Leu Val Asp Leu Gly Ile Ile Asp Glu Val Ser  
 85 90 95  
 Thr Ile Ser Thr Gly Tyr Phe Thr Ser Ala Ser Gln Val Arg Val Val  
 100 105 110  
 Ala Ala Trp Leu Gln Lys Ile Arg Glu Thr His Pro His Val Arg Ile  
 115 120 125  
 Val Val Asp Pro Ile Met Gly Asp Ser Asp Val Gly Ile Tyr Val Ala  
 130 135 140  
 Asp Glu Ile Ala Thr Ala Ile Cys Gln Asp Leu Cys Pro Leu Ala Thr  
 145 150 155 160  
 Gly Ile Ile Pro Asn Ala Phe Glu Leu Ser His Met Val Gly Ser Gly  
 165 170 175  
 Asp Pro Arg Ser Leu Leu Gly Pro Phe Gly Glu Trp Ile Ile Ile Thr  
 180 185 190  
 Ser Ala Thr Glu Thr Val Gly Thr Thr Val Thr Arg Ile Val Thr Arg  
 195 200 205  
 Asp Ser Val Gln Glu Ile Ala Ser Ala Thr Val Asp Thr Thr Ala Lys  
 210 215 220  
 Gly Ala Gly Asp Val Tyr Ala Ala Ala Leu Ile Ala Ala Leu His Lys  
 225 230 235 240  
 Asp Phe Ser Leu Ile Asp Ala Ala Ser His Ala Ser Asn Thr Val Cys  
 245 250 255  
 Ala Gly Leu Gln Thr Lys Ala Leu  
 260

&lt;210&gt; 551

&lt;211&gt; 622

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(622)

&lt;223&gt; RXC01021



&lt;400&gt; 551

cgagaggctt ttttggctct aagcctttta gtcgtgcgaa cgaaatctta agcagcctcg 60

gtgccaccga gatcgattgg tcgctgtaag gtatctgatt atg tcc agt tcc gaa 115  
 Met Ser Ser Ser Glu  
 1 5

agc tcg cgt tcc gaa ggc tcg cag cca gca ccg tct gta cag cct gaa 163  
 Ser Ser Arg Ser Glu Gly Ser Gln Pro Ala Pro Ser Val Gln Pro Glu  
 10 15 20

cgc cgt gct gat tca acg ggg gct cct gcg gca gct tcc aag gaa gct 211  
 Arg Arg Ala Asp Ser Thr Gly Ala Pro Ala Ala Ala Ser Lys Glu Ala  
 25 30 35

tcc caa caa atg gac gct gcc gga gtt ctt gag tgg gcc agg acc gct 259  
 Ser Gln Gln Met Asp Ala Ala Gly Val Leu Glu Trp Ala Arg Thr Ala  
 40 45 50

gtc gag cag ctt tct gaa cgt cgt gca gag atc aat gca ctg aat gtc 307  
 Val Glu Gln Leu Ser Glu Arg Arg Ala Glu Ile Asn Ala Leu Asn Val  
 55 60 65

ttt cct gtt cca gat gca gac act gga tca aac atg acc tac acc atg 355  
 Phe Pro Val Pro Asp Ala Asp Thr Gly Ser Asn Met Thr Tyr Thr Met  
 70 75 80 85

aca gct gcg ttg gat gaa gcg ctg aaa ctg ggg gag ttg ggt gat gtc 403  
 Thr Ala Ala Leu Asp Glu Ala Leu Lys Leu Gly Glu Leu Gly Asp Val  
 90 95 100

gca agg att act gag gct ttg gct gtt ggt tct gtg cgt gga gcc cga 451  
 Ala Arg Ile Thr Glu Ala Leu Ala Val Gly Ser Val Arg Gly Ala Arg  
 105 110 115

gga aat tct gga gta gtc ctt agt cag gtc ctt cgc gct att gct cag 499  
 Gly Asn Ser Gly Val Val Leu Ser Gln Val Leu Arg Ala Ile Ala Gln  
 120 125 130

gca gct gct gac ggg gtt att gat ggc cac aca atc caa gaa gcg cta 547  
 Ala Ala Ala Asp Gly Val Ile Asp Gly His Thr Ile Gln Glu Ala Leu  
 135 140 145

tcc att gct cgc tcc cta gtt gat cgc gca att aca gat cct gtg gag 595  
 Ser Ile Ala Arg Ser Leu Val Asp Arg Ala Ile Thr Asp Pro Val Glu  
 150 155 160 165

ggc act gtt gtc act gtg ttg cgt tct 622  
 Gly Thr Val Val Thr Val Leu Arg Ser  
 170

&lt;210&gt; 552

&lt;211&gt; 174

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 552

Met Ser Ser Ser Glu Ser Ser Arg Ser Glu Gly Ser Gln Pro Ala Pro  
 1 5 10 15

<400> 553																	
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caacaaggcg					atccaggagt	tgcgagcact	cgcgcagtaa	atg	gat	gtt	gcg	cac					115
								Met	Asp	Val	Ala	His					
								1				5					
gcg	tta	gat	ctg	gcc	cac	cac	gtg	tca	gat	caa	gtc	cga	ggc	acc	acc	163	
Ala	Leu	Asp	Leu	Ala	His	His	Val	Ser	Asp	Gln	Val	Arg	Gly	Thr	Thr		
					10						15						20
agc	cct	aat	ccg	cca	gtc	ggc	gct	gtc	att	ttg	gac	gcc	gac	ggc	gag	211	
Ser	Pro	Asn	Pro	Pro	Val	Gly	Ala	Val	Ile	Leu	Asp	Ala	Asp	Gly	Glu		
					25						30						35
gtc	gtt	ggc	gtt	ggc	gcc	acg	gca	cct	cct	ggc	ggc	ccg	cac	gcc	gaa	259	
Val	Val	Gly	Val	Gly	Ala	Thr	Ala	Pro	Pro	Gly	Gly	Pro	His	Ala	Glu		
					40						45						50

gtg	gtg	gcg	ctt	gca	gct	gcc	gga	gtg	cgt	gcc	aac	ggg	ggc	acg	gcg	307
Val	Val	Ala	Leu	Ala	Ala	Ala	Gly	Val	Arg	Ala	Asn	Gly	Gly	Thr	Ala	
	55					60					65					
gtg	gtc	acc	ctc	gag	ccg	tgc	aac	cat	tac	ggc	cgc	acg	ggg	cca	tgt	355
Val	Val	Thr	Leu	Glu	Pro	Cys	Asn	His	Tyr	Gly	Arg	Thr	Gly	Pro	Cys	
	70				75					80					85	
tcc	aag	gcg	ctt	ctc	gac	gcc	ggg	atc	gca	cac	gtg	ttt	tac	gcc	aat	403
Ser	Lys	Ala	Leu	Leu	Asp	Ala	Gly	Ile	Ala	His	Val	Phe	Tyr	Ala	Asn	
				90					95					100		
gcg	gat	ccc	ttc	ccg	tca	gcc	gct	ggg	ggc	ggg	gcc	ttt	ttg	gcg	gag	451
Ala	Asp	Pro	Phe	Pro	Ser	Ala	Ala	Gly	Gly	Gly	Ala	Phe	Leu	Ala	Glu	
			105					110					115			
gcg	ggc	gtc	gat	acg	cat	ttt	tta	gat	gag	cgg	atc	agg	gca	ctg	gag	499
Ala	Gly	Val	Asp	Thr	His	Phe	Leu	Asp	Glu	Arg	Ile	Arg	Ala	Leu	Glu	
		120					125					130				
ccc	tgg	ctg	gtt	gcg	acg	cgt	ctg	ggc	agg	ccc	cat	gtc	acg	ttg	aag	547
Pro	Trp	Leu	Val	Ala	Thr	Arg	Leu	Gly	Arg	Pro	His	Val	Thr	Leu	Lys	
	135					140					145					
ttt	gcg	tcc	acc	gtg	gac	ggg	ttt	gct	ggg	gcc	acc	gat	ggc	acc	agc	595
Phe	Ala	Ser	Thr	Val	Asp	Gly	Phe	Ala	Gly	Ala	Thr	Asp	Gly	Thr	Ser	
150					155					160					165	
cag	tgg	att	acc	ggg	ccg	gat	gcg	cgg	gcg	ttt	gtg	cac	gaa	gat	cga	643
Gln	Trp	Ile	Thr	Gly	Pro	Asp	Ala	Arg	Ala	Phe	Val	His	Glu	Asp	Arg	
				170				175						180		
agt	aaa	aga	gat	gcg	atc	atc	gtg	ggg	acc	ggg	act	gcg	ttg	act	gat	691
Ser	Lys	Arg	Asp	Ala	Ile	Ile	Val	Gly	Thr	Gly	Thr	Ala	Leu	Thr	Asp	
			185				190						195			
aat	ccc	tcc	ttg	acg	gcg	cgg	acc	gat	acg	ggg	ctt	tat	gaa	aat	caa	739
Asn	Pro	Ser	Leu	Thr	Ala	Arg	Thr	Asp	Thr	Gly	Leu	Tyr	Glu	Asn	Gln	
		200					205					210				
ccc	agg	cgc	gtt	gtt	att	ggc	tcc	cgc	gag	gtt	cca	gca	gat	tcc	aac	787
Pro	Arg	Arg	Val	Val	Ile	Gly	Ser	Arg	Glu	Val	Pro	Ala	Asp	Ser	Asn	
	215					220					225					
ttg	gct	cgc	ttg	gga	tat	gag	cag	tac	gcg	gga	ata	cca	gag	gct	tta	835
Leu	Ala	Arg	Leu	Gly	Tyr	Glu	Gln	Tyr	Ala	Gly	Ile	Pro	Glu	Ala	Leu	
230					235					240					245	
tca	gcg	ctg	tgg	gat	aaa	ggg	tgc	cga	gac	att	tta	atc	gaa	ggg	ggc	883
Ser	Ala	Leu	Trp	Asp	Lys	Gly	Cys	Arg	Asp	Ile	Leu	Ile	Glu	Gly	Gly	
				250					255					260		
cca	acg	tta	gct	ggg	gca	gcg	ctg	cgc	tta	ggc	att	gtt	gat	cag	gtg	931
Pro	Thr	Leu	Ala	Gly	Ala	Ala	Leu	Arg	Leu	Gly	Ile	Val	Asp	Gln	Val	
			265				270						275			
cag	gcc	tat	gtt	gcc	ccc	gct	ttg	ttg	ggc	gct	gga	cga	tca	gtg	att	979
Gln	Ala	Tyr	Val	Ala	Pro	Ala	Leu	Leu	Gly	Ala	Gly	Arg	Ser	Val	Ile	
		280					285					290				

aac tgg cca caa gaa acc acg atg gat cag att atg cgt ttt gac acc  
 1027  
 Asn Trp Pro Gln Glu Thr Thr Met Asp Gln Ile Met Arg Phe Asp Thr  
 295 300 305

acg tcc gtg aga cag ttg ggt tca gat gta ttg ata gaa atg atg aga  
 1075  
 Thr Ser Val Arg Gln Leu Gly Ser Asp Val Leu Ile Glu Met Met Arg  
 310 315 320 325

aag gaa cac taaatgttca caggtattgt cga  
 1107  
 Lys Glu His

<210> 554  
 <211> 328  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 554  
 Met Asp Val Ala His Ala Leu Asp Leu Ala His His Val Ser Asp Gln  
 1 5 10 15  
 Val Arg Gly Thr Thr Ser Pro Asn Pro Pro Val Gly Ala Val Ile Leu  
 20 25 30  
 Asp Ala Asp Gly Glu Val Val Gly Val Gly Ala Thr Ala Pro Pro Gly  
 35 40 45  
 Gly Pro His Ala Glu Val Val Ala Leu Ala Ala Ala Gly Val Arg Ala  
 50 55 60  
 Asn Gly Gly Thr Ala Val Val Thr Leu Glu Pro Cys Asn His Tyr Gly  
 65 70 75 80  
 Arg Thr Gly Pro Cys Ser Lys Ala Leu Leu Asp Ala Gly Ile Ala His  
 85 90 95  
 Val Phe Tyr Ala Asn Ala Asp Pro Phe Pro Ser Ala Ala Gly Gly Gly  
 100 105 110  
 Ala Phe Leu Ala Glu Ala Gly Val Asp Thr His Phe Leu Asp Glu Arg  
 115 120 125  
 Ile Arg Ala Leu Glu Pro Trp Leu Val Ala Thr Arg Leu Gly Arg Pro  
 130 135 140  
 His Val Thr Leu Lys Phe Ala Ser Thr Val Asp Gly Phe Ala Gly Ala  
 145 150 155 160  
 Thr Asp Gly Thr Ser Gln Trp Ile Thr Gly Pro Asp Ala Arg Ala Phe  
 165 170 175  
 Val His Glu Asp Arg Ser Lys Arg Asp Ala Ile Ile Val Gly Thr Gly  
 180 185 190  
 Thr Ala Leu Thr Asp Asn Pro Ser Leu Thr Ala Arg Thr Asp Thr Gly  
 195 200 205

Leu Tyr Glu Asn Gln Pro Arg Arg Val Val Ile Gly Ser Arg Glu Val  
 210 215 220  
 Pro Ala Asp Ser Asn Leu Ala Arg Leu Gly Tyr Glu Gln Tyr Ala Gly  
 225 230 235 240  
 Ile Pro Glu Ala Leu Ser Ala Leu Trp Asp Lys Gly Cys Arg Asp Ile  
 245 250 255  
 Leu Ile Glu Gly Gly Pro Thr Leu Ala Gly Ala Ala Leu Arg Leu Gly  
 260 265 270  
 Ile Val Asp Gln Val Gln Ala Tyr Val Ala Pro Ala Leu Leu Gly Ala  
 275 280 285  
 Gly Arg Ser Val Ile Asn Trp Pro Gln Glu Thr Thr Met Asp Gln Ile  
 290 295 300  
 Met Arg Phe Asp Thr Thr Ser Val Arg Gln Leu Gly Ser Asp Val Leu  
 305 310 315 320  
 Ile Glu Met Met Arg Lys Glu His  
 325

&lt;210&gt; 555

&lt;211&gt; 1107

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1084)

&lt;223&gt; FRXA02246

&lt;400&gt; 555

tgccgacgct ggcgtggatg ccttcgttgc aggttccgct gtgtacggcg ctgaggatcc 60

caacaaggcg atccaggagt tgcgagcact cgcgcagtaa atg gat gtt gcg cac 115  
 Met Asp Val Ala His  
 1 5

gcg tta gat ctg gcc cac cac gtg tca gat caa gtc cga ggc acc acc 163  
 Ala Leu Asp Leu Ala His His Val Ser Asp Gln Val Arg Gly Thr Thr  
 10 15 20

agc cct aat ccg cca gtc ggc gct gtc att ttg gac gcc gac ggc gag 211  
 Ser Pro Asn Pro Pro Val Gly Ala Val Ile Leu Asp Ala Asp Gly Glu  
 25 30 35

gtc gtt ggc gtt ggc gcc acg gca cct cct ggt ggc ccg cac gcc gaa 259  
 Val Val Gly Val Gly Ala Thr Ala Pro Pro Gly Gly Pro His Ala Glu  
 40 45 50

gtg gtg gcg ctt gca gct gcc gga gtg cgt gcc aac ggg ggc acg gcg 307  
 Val Val Ala Leu Ala Ala Ala Gly Val Arg Ala Asn Gly Gly Thr Ala  
 55 60 65

gtg gtc acc ctc gag ccg tgc aac cat tac ggc cgc acg ggt cca tgt 355  
 Val Val Thr Leu Glu Pro Cys Asn His Tyr Gly Arg Thr Gly Pro Cys  
 70 75 80 85

tcc aag gcg ctt ctc gac gcc ggg atc gca cac gtg ttt tac gcc aat	403
Ser Lys Ala Leu Leu Asp Ala Gly Ile Ala His Val Phe Tyr Ala Asn	
90 95 100	
gcg gat ccc ttc ccg tca gcc gct ggg ggc ggt gcc ttt ttg gcg gag	451
Ala Asp Pro Phe Pro Ser Ala Ala Gly Gly Ala Phe Leu Ala Glu	
105 110 115	
gcg ggc gtc gat acg cat ttt tta gat gag cgg atc agg gca ctg gag	499
Ala Gly Val Asp Thr His Phe Leu Asp Glu Arg Ile Arg Ala Leu Glu	
120 125 130	
ccc tgg ctg gtt gcg acg cgt ctg ggc agg ccc cat gtc acg ttg aag	547
Pro Trp Leu Val Ala Thr Arg Leu Gly Arg Pro His Val Thr Leu Lys	
135 140 145	
ttt gcg tcc acc gtg gac ggt ttt gct ggt gcc acc gat ggc acc agc	595
Phe Ala Ser Thr Val Asp Gly Phe Ala Gly Ala Thr Asp Gly Thr Ser	
150 155 160 165	
cag tgg att acc ggg ccg gat gcg cgg gcg ttt gtg cac gaa gat cga	643
Gln Trp Ile Thr Gly Pro Asp Ala Arg Ala Phe Val His Glu Asp Arg	
170 175 180	
agt aaa aga gat gcg atc atc gtg ggt acc ggt act gcg ttg act gat	691
Ser Lys Arg Asp Ala Ile Ile Val Gly Thr Gly Thr Ala Leu Thr Asp	
185 190 195	
aat ccc tcc ttg acg gcg cgg acc gat acg ggt ctt tat gaa aat caa	739
Asn Pro Ser Leu Thr Ala Arg Thr Asp Thr Gly Leu Tyr Glu Asn Gln	
200 205 210	
ccc agg cgc gtt gtt att ggc tcc cgc gag gtt cca gca gat tcc aac	787
Pro Arg Arg Val Val Ile Gly Ser Arg Glu Val Pro Ala Asp Ser Asn	
215 220 225	
ttg gct cgc ttg gga tat gag cag tac gcg gga ata cca gag gct tta	835
Leu Ala Arg Leu Gly Tyr Glu Gln Tyr Ala Gly Ile Pro Glu Ala Leu	
230 235 240 245	
tca gcg ctg tgg gat aaa ggg tgc cga gac att tta atc gaa ggt ggc	883
Ser Ala Leu Trp Asp Lys Gly Cys Arg Asp Ile Leu Ile Glu Gly Gly	
250 255 260	
cca acg tta gct ggg gca gcg ctg cgc tta ggc att gtt gat cag gtg	931
Pro Thr Leu Ala Gly Ala Ala Leu Arg Leu Gly Ile Val Asp Gln Val	
265 270 275	
cag gcc tat gtt gcc ccc gct ttg ttg ggc gct gga cga tca gtg att	979
Gln Ala Tyr Val Ala Pro Ala Leu Leu Gly Ala Gly Arg Ser Val Ile	
280 285 290	
aac tgg cca caa gaa acc acg atg gat cag att atg cgt ttt gac acc	
1027	
Asn Trp Pro Gln Glu Thr Thr Met Asp Gln Ile Met Arg Phe Asp Thr	
295 300 305	
acg tcc gtg aga cag ttg ggt tca gat gta ttg ata gaa atg atg aga	
1075	
Thr Ser Val Arg Gln Leu Gly Ser Asp Val Leu Ile Glu Met Met Arg	

310

315

320

325

aag gaa cac taaatgttca caggtattgt cga

1107

Lys Glu His

&lt;210&gt; 556

&lt;211&gt; 328

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 556

Met	Asp	Val	Ala	His	Ala	Leu	Asp	Leu	Ala	His	His	Val	Ser	Asp	Gln
1				5					10					15	

Val	Arg	Gly	Thr	Thr	Ser	Pro	Asn	Pro	Pro	Val	Gly	Ala	Val	Ile	Leu
			20					25					30		

Asp	Ala	Asp	Gly	Glu	Val	Val	Gly	Val	Gly	Ala	Thr	Ala	Pro	Pro	Gly
		35					40					45			

Gly	Pro	His	Ala	Glu	Val	Val	Ala	Leu	Ala	Ala	Ala	Gly	Val	Arg	Ala
	50					55					60				

Asn	Gly	Gly	Thr	Ala	Val	Val	Thr	Leu	Glu	Pro	Cys	Asn	His	Tyr	Gly
65					70					75					80

Arg	Thr	Gly	Pro	Cys	Ser	Lys	Ala	Leu	Leu	Asp	Ala	Gly	Ile	Ala	His
				85					90					95	

Val	Phe	Tyr	Ala	Asn	Ala	Asp	Pro	Phe	Pro	Ser	Ala	Ala	Gly	Gly	Gly
			100					105					110		

Ala	Phe	Leu	Ala	Glu	Ala	Gly	Val	Asp	Thr	His	Phe	Leu	Asp	Glu	Arg
		115					120					125			

Ile	Arg	Ala	Leu	Glu	Pro	Trp	Leu	Val	Ala	Thr	Arg	Leu	Gly	Arg	Pro
	130					135					140				

His	Val	Thr	Leu	Lys	Phe	Ala	Ser	Thr	Val	Asp	Gly	Phe	Ala	Gly	Ala
145					150					155					160

Thr	Asp	Gly	Thr	Ser	Gln	Trp	Ile	Thr	Gly	Pro	Asp	Ala	Arg	Ala	Phe
				165					170					175	

Val	His	Glu	Asp	Arg	Ser	Lys	Arg	Asp	Ala	Ile	Ile	Val	Gly	Thr	Gly
			180					185					190		

Thr	Ala	Leu	Thr	Asp	Asn	Pro	Ser	Leu	Thr	Ala	Arg	Thr	Asp	Thr	Gly
		195				200						205			

Leu	Tyr	Glu	Asn	Gln	Pro	Arg	Arg	Val	Val	Ile	Gly	Ser	Arg	Glu	Val
	210					215					220				

Pro	Ala	Asp	Ser	Asn	Leu	Ala	Arg	Leu	Gly	Tyr	Glu	Gln	Tyr	Ala	Gly
225					230					235					240

Ile	Pro	Glu	Ala	Leu	Ser	Ala	Leu	Trp	Asp	Lys	Gly	Cys	Arg	Asp	Ile
				245					250					255	

Leu Ile Glu Gly Gly Pro Thr Leu Ala Gly Ala Ala Leu Arg Leu Gly  
                   260                                  265                                  270  
 Ile Val Asp Gln Val Gln Ala Tyr Val Ala Pro Ala Leu Leu Gly Ala  
                   275                                  280                                  285  
 Gly Arg Ser Val Ile Asn Trp Pro Gln Glu Thr Thr Met Asp Gln Ile  
                   290                                  295                                  300  
 Met Arg Phe Asp Thr Thr Ser Val Arg Gln Leu Gly Ser Asp Val Leu  
                   305                                  310                                  315                                  320  
 Ile Glu Met Met Arg Lys Glu His  
                                   325

<210> 557  
 <211> 756  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(733)  
 <223> RXA02247

<400> 557  
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 ttcagatgta ttgatagaaa tgatgagaaa ggaacactaa atg ttc aca ggt att 115  
   Met Phe Thr Gly Ile  
   1  5  
 gtc gag gag ctt ggc tcc gtt gca ggc gtg gaa cat ctg gga gat tcc 163  
 Val Glu Glu Leu Gly Ser Val Ala Gly Val Glu His Leu Gly Asp Ser  
                                   10                                  15                                  20  
 atc cgg atg cag att tcc gcg tcc acc gtt tta gag ggt gtg cat ttg 211  
 Ile Arg Met Gln Ile Ser Ala Ser Thr Val Leu Glu Gly Val His Leu  
                                   25                                  30                                  35  
 ggg gat tcc att tct gtc aat ggt gtg tgc ttg aca gtg gcg tcc ttt 259  
 Gly Asp Ser Ile Ser Val Asn Gly Val Cys Leu Thr Val Ala Ser Phe  
                                   40                                  45                                  50  
 ggc gag gga cat ttc act gca gac ctc atg cag gaa acc tta gat cgc 307  
 Gly Glu Gly His Phe Thr Ala Asp Leu Met Gln Glu Thr Leu Asp Arg  
                                   55                                  60                                  65  
 agc tcc ctg ggc gca tta tcc acc ggt agc aaa gtc aac ctt gag cgc 355  
 Ser Ser Leu Gly Ala Leu Ser Thr Gly Ser Lys Val Asn Leu Glu Arg  
                                   70                                  75                                  80                                  85  
 gcc atg gca gcc gat ggc cgt ctg ggt gga cac atc atg caa ggc cat 403  
 Ala Met Ala Ala Asp Gly Arg Leu Gly Gly His Ile Met Gln Gly His  
                                   90                                  95                                  100  
 gtt gat gcc acc acc tcg ctg atc aag cgc acc agc tca gag aac tgg 451  
 Val Asp Ala Thr Thr Ser Leu Ile Lys Arg Thr Ser Ser Glu Asn Trp  
                                   105                                  110                                  115



gat gtt ctg cgt ttt gag ctg cca gct gat ttg gct cgc tat gtg gtg 499  
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 Glu Lys Gly Ser Ile Ala Leu Asn Gly Thr Ser Leu Thr Val Ser Ser  
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 Leu Gly Asp Asp Trp Phe Glu Val Ser Leu Ile Pro Thr Thr Leu Arg  
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 Asp Thr Thr His Gly Glu Leu Ala Val Gly Asp Ile Val Asn Ile Glu  
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 gtt gat gtg atc gct aag tac gtc gaa cgc atg atg acg cgc ggc gtg 691  
 Val Asp Val Ile Ala Lys Tyr Val Glu Arg Met Met Thr Arg Gly Val  
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 gct gga aac act ccc aat gac tac acc gat ttc acg aga gac 733  
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 Thr Val Ala Ser Phe Gly Glu Gly His Phe Thr Ala Asp Leu Met Gln  
 50 55 60  
 Glu Thr Leu Asp Arg Ser Ser Leu Gly Ala Leu Ser Thr Gly Ser Lys  
 65 70 75 80  
 Val Asn Leu Glu Arg Ala Met Ala Ala Asp Gly Arg Leu Gly Gly His  
 85 90 95  
 Ile Met Gln Gly His Val Asp Ala Thr Thr Ser Leu Ile Lys Arg Thr  
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 Ser Ser Glu Asn Trp Asp Val Leu Arg Phe Glu Leu Pro Ala Asp Leu  
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 Ala Arg Tyr Val Val Glu Lys Gly Ser Ile Ala Leu Asn Gly Thr Ser  
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Leu Thr Val Ser Ser Leu Gly Asp Asp Trp Phe Glu Val Ser Leu Ile  
 145 150 155 160  
 Pro Thr Thr Leu Arg Asp Thr Thr His Gly Glu Leu Ala Val Gly Asp  
 165 170 175  
 Ile Val Asn Ile Glu Val Asp Val Ile Ala Lys Tyr Val Glu Arg Met  
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 <223> RXN02248

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 Val Ser Glu His Glu  
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cag gca cac agc caa tta gat tct gtt gaa gag gcc atc gct gac atc 163  
 Gln Ala His Ser Gln Leu Asp Ser Val Glu Glu Ala Ile Ala Asp Ile  
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gct gcg ggt aaa gcc gtc gtg gtg gta gat gat gaa gat cgt gaa aat 211  
 Ala Ala Gly Lys Ala Val Val Val Val Asp Asp Glu Asp Arg Glu Asn  
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gaa ggc gac atc atc ttt gcc gcc gaa tta gcc act cca gaa tta gtc 259  
 Glu Gly Asp Ile Ile Phe Ala Ala Glu Leu Ala Thr Pro Glu Leu Val  
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gct ttc atg gtg cgt tat tcc tcg gga tac atc tgt gcg cca tta acc 307  
 Ala Phe Met Val Arg Tyr Ser Ser Gly Tyr Ile Cys Ala Pro Leu Thr  
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gca aag gat gca gat cgt ctt gat ctg cct ccg atg acc gcg cac aat 355  
 Ala Lys Asp Ala Asp Arg Leu Asp Leu Pro Pro Met Thr Ala His Asn  
 70 75 80 85

cag gat gcc cgc ggc acc gct tac acc gtg acc gtt gat gcc aac acc 403  
 Gln Asp Ala Arg Gly Thr Ala Tyr Thr Val Thr Val Asp Ala Asn Thr  
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ggc acc aca ggc att tct gca aca gac cgc gcc cac act ttg cgc ttg 451  
 Gly Thr Thr Gly Ile Ser Ala Thr Asp Arg Ala His Thr Leu Arg Leu  
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ctt gct gat cca gaa gcc gac cgc acg gat ttc acc cgt ccc gga cac	499
Leu Ala Asp Pro Glu Ala Asp Arg Thr Asp Phe Thr Arg Pro Gly His	
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Val Val Pro Leu Arg Ala Arg Glu Gly Gly Val Leu Val Arg Ala Gly	
135 140 145	
cac acc gaa gca gct gtc gat ttg gct cgc gct gca ggc ctg cgc cca	595
His Thr Glu Ala Ala Val Asp Leu Ala Arg Ala Ala Gly Leu Arg Pro	
150 155 160 165	
gca ggt gtt atc tgc gaa gtg gtc agt gaa gag gac ccc acc ggc atg	643
Ala Gly Val Ile Cys Glu Val Val Ser Glu Glu Asp Pro Thr Gly Met	
170 175 180	
gct cgg gtt cct gag ctg cgc cgc ttc tgc gat gag cac gat ctg aag	691
Ala Arg Val Pro Glu Leu Arg Arg Phe Cys Asp Glu His Asp Leu Lys	
185 190 195	
ctg atc tct att gag cag ctc att gag tgg cgt cgc aag aat gaa att	739
Leu Ile Ser Ile Glu Gln Leu Ile Glu Trp Arg Arg Lys Asn Glu Ile	
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Leu Val Glu Arg Gln Val Glu Thr Val Leu Pro Thr Asp Phe Gly Thr	
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Phe Lys Ala Val Gly Tyr Arg Ser Ile Ile Asp Gly Thr Glu Leu Val	
230 235 240 245	
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Ala Ile Val Ala Gly Asp Val Ala Ser Asp Gly Gly Glu Asn Val Leu	
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Val Arg Val His Ser Glu Cys Leu Thr Gly Asp Val Phe Gly Ser Arg	
265 270 275	
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Arg Cys Asp Cys Gly Gln Gln Leu His Glu Ser Leu Arg Leu Ile Gln	
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Glu Ala Gly Arg Gly Val Val Val Tyr Met Arg Gly His Glu Gly Arg	
295 300 305	
ggc att ggt ctg ctc gcc aag cta cgc gcc tac caa ctc cag gat gaa	
1075	
Gly Ile Gly Leu Leu Ala Lys Leu Arg Ala Tyr Gln Leu Gln Asp Glu	
310 315 320 325	
ggt gcc gac acc gtc gat gcc aac ctc gca ctt ggt ctt cca gcc gat	
1123	
Gly Ala Asp Thr Val Asp Ala Asn Leu Ala Leu Gly Leu Pro Ala Asp	
330 335 340	
gcc cgc gaa ttt ggc acc agc gcc cag att ctc tac gac ttg ggt gtg	
1171	

Ala Arg Glu Phe Gly Thr Ser Ala Gln Ile Leu Tyr Asp Leu Gly Val  
 345 350 355

cgc tcg ctc aac ttg atc agc aac aac cca gcc aag aag gtg gga ctt  
 1219

Arg Ser Leu Asn Leu Ile Ser Asn Asn Pro Ala Lys Lys Val Gly Leu  
 360 365 370

gaa ggc cac ggc att tcc att gcc agc cga acc ccc atc cct gtt gct  
 1267

Glu Gly His Gly Ile Ser Ile Ala Ser Arg Thr Pro Ile Pro Val Ala  
 375 380 385

gtt cat gaa gac aat gtt cga tac ctg aaa acc aag cgt gac cgc atg  
 1315

Val His Glu Asp Asn Val Arg Tyr Leu Lys Thr Lys Arg Asp Arg Met  
 390 395 400 405

gga cat gac ctc cca gat gtc gca ctg tgg gaa caa gag cac cca gaa  
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Gly His Asp Leu Pro Asp Val Ala Leu Trp Glu Gln Glu His Pro Glu  
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1389

Asn

<210> 560

<211> 422

<212> PRT

<213> Corynebacterium glutamicum

<400> 560

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Glu Asp Arg Glu Asn Glu Gly Asp Ile Ile Phe Ala Ala Glu Leu Ala  
 35 40 45

Thr Pro Glu Leu Val Ala Phe Met Val Arg Tyr Ser Ser Gly Tyr Ile  
 50 55 60

Cys Ala Pro Leu Thr Ala Lys Asp Ala Asp Arg Leu Asp Leu Pro Pro  
 65 70 75 80

Met Thr Ala His Asn Gln Asp Ala Arg Gly Thr Ala Tyr Thr Val Thr  
 85 90 95

Val Asp Ala Asn Thr Gly Thr Thr Gly Ile Ser Ala Thr Asp Arg Ala  
 100 105 110

His Thr Leu Arg Leu Leu Ala Asp Pro Glu Ala Asp Arg Thr Asp Phe  
 115 120 125

Thr Arg Pro Gly His Val Val Pro Leu Arg Ala Arg Glu Gly Gly Val  
 130 135 140

Leu Val Arg Ala Gly His Thr Glu Ala Ala Val Asp Leu Ala Arg Ala  
 145 150 155 160  
 Ala Gly Leu Arg Pro Ala Gly Val Ile Cys Glu Val Val Ser Glu Glu  
 165 170 175  
 Asp Pro Thr Gly Met Ala Arg Val Pro Glu Leu Arg Arg Phe Cys Asp  
 180 185 190  
 Glu His Asp Leu Lys Leu Ile Ser Ile Glu Gln Leu Ile Glu Trp Arg  
 195 200 205  
 Arg Lys Asn Glu Ile Leu Val Glu Arg Gln Val Glu Thr Val Leu Pro  
 210 215 220  
 Thr Asp Phe Gly Thr Phe Lys Ala Val Gly Tyr Arg Ser Ile Ile Asp  
 225 230 235 240  
 Gly Thr Glu Leu Val Ala Ile Val Ala Gly Asp Val Ala Ser Asp Gly  
 245 250 255  
 Gly Glu Asn Val Leu Val Arg Val His Ser Glu Cys Leu Thr Gly Asp  
 260 265 270  
 Val Phe Gly Ser Arg Arg Cys Asp Cys Gly Gln Gln Leu His Glu Ser  
 275 280 285  
 Leu Arg Leu Ile Gln Glu Ala Gly Arg Gly Val Val Val Tyr Met Arg  
 290 295 300  
 Gly His Glu Gly Arg Gly Ile Gly Leu Leu Ala Lys Leu Arg Ala Tyr  
 305 310 315 320  
 Gln Leu Gln Asp Glu Gly Ala Asp Thr Val Asp Ala Asn Leu Ala Leu  
 325 330 335  
 Gly Leu Pro Ala Asp Ala Arg Glu Phe Gly Thr Ser Ala Gln Ile Leu  
 340 345 350  
 Tyr Asp Leu Gly Val Arg Ser Leu Asn Leu Ile Ser Asn Asn Pro Ala  
 355 360 365  
 Lys Lys Val Gly Leu Glu Gly His Gly Ile Ser Ile Ala Ser Arg Thr  
 370 375 380  
 Pro Ile Pro Val Ala Val His Glu Asp Asn Val Arg Tyr Leu Lys Thr  
 385 390 395 400  
 Lys Arg Asp Arg Met Gly His Asp Leu Pro Asp Val Ala Leu Trp Glu  
 405 410 415  
 Gln Glu His Pro Glu Asn  
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&lt;210&gt; 561

&lt;211&gt; 1389

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1366)

&lt;223&gt; FRXA02248

&lt;400&gt; 561

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				Val	Ser	Glu	His	Glu	
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Gln	Ala	His	Ser	Gln	Leu	Asp	Ser	Val	Glu	Glu	Ala	Ile	Ala	Asp	Ile	
				10					15					20		

gct	gcg	ggc	aaa	gcc	gtc	gtg	gtg	gta	gat	gat	gaa	gat	cgt	gaa	aat	211
Ala	Ala	Gly	Lys	Ala	Val	Val	Val	Val	Asp	Asp	Glu	Asp	Arg	Glu	Asn	
			25					30					35			

gaa	ggc	gac	atc	atc	ttt	gcc	gcc	gaa	tta	gcc	act	cca	gaa	tta	gtc	259
Glu	Gly	Asp	Ile	Ile	Phe	Ala	Ala	Glu	Leu	Ala	Thr	Pro	Glu	Leu	Val	
		40					45					50				

gct	ttc	atg	gtg	cgt	tat	tcc	tcg	gga	tac	atc	tgt	gcg	cca	tta	acc	307
Ala	Phe	Met	Val	Arg	Tyr	Ser	Ser	Gly	Tyr	Ile	Cys	Ala	Pro	Leu	Thr	
	55					60					65					

gca	aag	gat	gca	gat	cgt	ctt	gat	ctg	cct	ccg	atg	acc	gcg	cac	aat	355
Ala	Lys	Asp	Ala	Asp	Arg	Leu	Asp	Leu	Pro	Pro	Met	Thr	Ala	His	Asn	
	70				75					80					85	

cag	gat	gcc	cg	ggc	acc	gct	tac	acc	gtg	acc	gtt	gat	gcc	aac	acc	403
Gln	Asp	Ala	Arg	Gly	Thr	Ala	Tyr	Thr	Val	Thr	Val	Asp	Ala	Asn	Thr	
				90					95					100		

ggc	acc	aca	ggc	att	tct	gca	aca	gac	cg	gcc	cac	act	ttg	cg	ttg	451
Gly	Thr	Thr	Gly	Ile	Ser	Ala	Thr	Asp	Arg	Ala	His	Thr	Leu	Arg	Leu	
			105					110					115			

ctt	gct	gat	cca	gaa	gcc	gac	cg	acg	gat	ttc	acc	cgt	ccc	gga	cac	499
Leu	Ala	Asp	Pro	Glu	Ala	Asp	Arg	Thr	Asp	Phe	Thr	Arg	Pro	Gly	His	
		120					125					130				

gtt	gtg	cca	ctg	cgt	gct	cgt	gaa	ggc	ggc	gtc	ttg	gtg	cg	gct	gga	547
Val	Val	Pro	Leu	Arg	Ala	Arg	Glu	Gly	Gly	Val	Leu	Val	Arg	Ala	Gly	
		135				140					145					

cac	acc	gaa	gca	gct	gtc	gat	ttg	gct	cg	gct	gca	ggc	ctg	cg	cca	595
His	Thr	Glu	Ala	Ala	Val	Asp	Leu	Ala	Arg	Ala	Ala	Gly	Leu	Arg	Pro	
		150			155				160						165	

gca	ggc	gtt	atc	tgc	gaa	gtg	gtc	agt	gaa	gag	gac	ccc	acc	ggc	atg	643
Ala	Gly	Val	Ile	Cys	Glu	Val	Val	Ser	Glu	Glu	Asp	Pro	Thr	Gly	Met	
				170					175					180		

gct	cg	gtt	cct	gag	ctg	cg	cg	ttc	tgc	gat	gag	cac	gat	ctg	aag	691
Ala	Arg	Val	Pro	Glu	Leu	Arg	Arg	Phe	Cys	Asp	Glu	His	Asp	Leu	Lys	
			185					190					195			

ctg	atc	tct	att	gag	cag	ctc	att	gag	tgg	cgt	cg	aag	aat	gaa	att	739
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Leu	Ile	Ser	Ile	Glu	Gln	Leu	Ile	Glu	Trp	Arg	Arg	Lys	Asn	Glu	Ile		
		200					205					210					
ttg	gtg	gag	cgc	cag	gtg	gaa	act	gtg	ctg	cct	acc	gat	ttc	ggc	acg	787	
Leu	Val	Glu	Arg	Gln	Val	Glu	Thr	Val	Leu	Pro	Thr	Asp	Phe	Gly	Thr		
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ttc	aag	gct	gtt	ggc	tac	cgt	tcc	atc	atc	gat	ggc	acc	gag	ctt	gtt	835	
Phe	Lys	Ala	Val	Gly	Tyr	Arg	Ser	Ile	Ile	Asp	Gly	Thr	Glu	Leu	Val		
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gcc	att	gtt	gcc	ggc	gac	gtg	gca	tcc	gac	ggc	ggc	gaa	aac	gtc	ctg	883	
Ala	Ile	Val	Ala	Gly	Asp	Val	Ala	Ser	Asp	Gly	Gly	Glu	Asn	Val	Leu		
				250					255					260			
gtt	cga	gtc	cac	tct	gag	tgc	ttg	act	ggc	gat	gtt	ttt	gga	tcc	cgg	931	
Val	Arg	Val	His	Ser	Glu	Cys	Leu	Thr	Gly	Asp	Val	Phe	Gly	Ser	Arg		
			265					270					275				
cgc	tgc	gac	tgt	gga	cag	cag	ctg	cac	gag	tct	ttg	cgc	ctg	atc	cag	979	
Arg	Cys	Asp	Cys	Gly	Gln	Gln	Leu	His	Glu	Ser	Leu	Arg	Leu	Ile	Gln		
		280					285					290					
gaa	gct	ggc	cgg	gga	gta	gtg	gtg	tac	atg	cgt	ggg	cat	gag	gga	cga		
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Glu	Ala	Gly	Arg	Gly	Val	Val	Val	Tyr	Met	Arg	Gly	His	Glu	Gly	Arg		
	295					300					305						
ggc	att	ggc	ctg	ctc	gcc	aag	cta	cgc	gcc	tac	caa	ctc	cag	gat	gaa		
1075																	
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cgc	tcg	ctc	aac	ttg	atc	agc	aac	aac	cca	gcc	aag	aag	gtg	gga	ctt		
1219																	
Arg	Ser	Leu	Asn	Leu	Ile	Ser	Asn	Asn	Pro	Ala	Lys	Lys	Val	Gly	Leu		
		360					365					370					
gaa	ggc	cac	ggc	att	tcc	att	gcc	agc	cga	acc	ccc	atc	cct	gtt	gct		
1267																	
Glu	Gly	His	Gly	Ile	Ser	Ile	Ala	Ser	Arg	Thr	Pro	Ile	Pro	Val	Ala		
	375					380					385						
gtt	cat	gaa	gac	aat	gtt	cga	tac	ctg	aaa	acc	aag	cgt	gac	cgc	atg		
1315																	
Val	His	Glu	Asp	Asn	Val	Arg	Tyr	Leu	Lys	Thr	Lys	Arg	Asp	Arg	Met		
390				395					400						405		
gga	cat	gac	ctc	cca	gat	gtc	gca	ctg	tgg	gaa	caa	gag	cac	cca	gaa		
1363																	
Gly	His	Asp	Leu	Pro	Asp	Val	Ala	Leu	Trp	Glu	Gln	Glu	His	Pro	Glu		

410

415

420

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1389  
Asn

&lt;210&gt; 562

&lt;211&gt; 422

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 562

Val Ser Glu His Glu Gln Ala His Ser Gln Leu Asp Ser Val Glu Glu  
1 5 10 15

Ala Ile Ala Asp Ile Ala Ala Gly Lys Ala Val Val Val Val Asp Asp  
20 25 30

Glu Asp Arg Glu Asn Glu Gly Asp Ile Ile Phe Ala Ala Glu Leu Ala  
35 40 45

Thr Pro Glu Leu Val Ala Phe Met Val Arg Tyr Ser Ser Gly Tyr Ile  
50 55 60

Cys Ala Pro Leu Thr Ala Lys Asp Ala Asp Arg Leu Asp Leu Pro Pro  
65 70 75 80

Met Thr Ala His Asn Gln Asp Ala Arg Gly Thr Ala Tyr Thr Val Thr  
85 90 95

Val Asp Ala Asn Thr Gly Thr Thr Gly Ile Ser Ala Thr Asp Arg Ala  
100 105 110

His Thr Leu Arg Leu Leu Ala Asp Pro Glu Ala Asp Arg Thr Asp Phe  
115 120 125

Thr Arg Pro Gly His Val Val Pro Leu Arg Ala Arg Glu Gly Gly Val  
130 135 140

Leu Val Arg Ala Gly His Thr Glu Ala Ala Val Asp Leu Ala Arg Ala  
145 150 155 160

Ala Gly Leu Arg Pro Ala Gly Val Ile Cys Glu Val Val Ser Glu Glu  
165 170 175

Asp Pro Thr Gly Met Ala Arg Val Pro Glu Leu Arg Arg Phe Cys Asp  
180 185 190

Glu His Asp Leu Lys Leu Ile Ser Ile Glu Gln Leu Ile Glu Trp Arg  
195 200 205

Arg Lys Asn Glu Ile Leu Val Glu Arg Gln Val Glu Thr Val Leu Pro  
210 215 220

Thr Asp Phe Gly Thr Phe Lys Ala Val Gly Tyr Arg Ser Ile Ile Asp  
225 230 235 240

Gly Thr Glu Leu Val Ala Ile Val Ala Gly Asp Val Ala Ser Asp Gly  
245 250 255



Gly Glu Asn Val Leu Val Arg Val His Ser Glu Cys Leu Thr Gly Asp  
 260 265 270  
 Val Phe Gly Ser Arg Arg Cys Asp Cys Gly Gln Gln Leu His Glu Ser  
 275 280 285  
 Leu Arg Leu Ile Gln Glu Ala Gly Arg Gly Val Val Val Tyr Met Arg  
 290 295 300  
 Gly His Glu Gly Arg Gly Ile Gly Leu Leu Ala Lys Leu Arg Ala Tyr  
 305 310 315 320  
 Gln Leu Gln Asp Glu Gly Ala Asp Thr Val Asp Ala Asn Leu Ala Leu  
 325 330 335  
 Gly Leu Pro Ala Asp Ala Arg Glu Phe Gly Thr Ser Ala Gln Ile Leu  
 340 345 350  
 Tyr Asp Leu Gly Val Arg Ser Leu Asn Leu Ile Ser Asn Asn Pro Ala  
 355 360 365  
 Lys Lys Val Gly Leu Glu Gly His Gly Ile Ser Ile Ala Ser Arg Thr  
 370 375 380  
 Pro Ile Pro Val Ala Val His Glu Asp Asn Val Arg Tyr Leu Lys Thr  
 385 390 395 400  
 Lys Arg Asp Arg Met Gly His Asp Leu Pro Asp Val Ala Leu Trp Glu  
 405 410 415  
 Gln Glu His Pro Glu Asn  
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 <213> Corynebacterium glutamicum

<220>  
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 <223> RXN02249

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 Met Ala Lys Glu Gly  
 1 5  
 ttg ccg gca gtc gaa ctc ccc gac gcc agc gga tta aaa gtc gcc gta 163  
 Leu Pro Ala Val Glu Leu Pro Asp Ala Ser Gly Leu Lys Val Ala Val  
 10 15 20  
 gtc acc gca cgg tgg aac gca gaa atc tgc gac cgc ctg cac aag cac 211  
 Val Thr Ala Arg Trp Asn Ala Glu Ile Cys Asp Arg Leu His Lys His  
 25 30 35  
 gca gta gat gcg gga cgt gca gca gga gca acg gtg agc gaa tac cgc 259

Ala	Val	Asp	Ala	Gly	Arg	Ala	Ala	Gly	Ala	Thr	Val	Ser	Glu	Tyr	Arg		
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gtc	atc	ggc	gcc	ctg	gaa	ctt	cca	gtc	gta	gtg	caa	gaa	ctg	gca	cgc	307	
Val	Ile	Gly	Ala	Leu	Glu	Leu	Pro	Val	Val	Val	Gln	Glu	Leu	Ala	Arg		
	55					60					65						
acc	cat	gac	gca	gta	gtt	gcc	ttg	ggc	tgt	gtc	gtt	cgt	ggc	ggc	acc	355	
Thr	His	Asp	Ala	Val	Val	Ala	Leu	Gly	Cys	Val	Val	Arg	Gly	Gly	Thr		
70					75					80					85		
cca	cac	ttt	gat	tac	gtg	tgc	gac	tct	gtc	acc	gaa	ggc	ctc	acc	cgc	403	
Pro	His	Phe	Asp	Tyr	Val	Cys	Asp	Ser	Val	Thr	Glu	Gly	Leu	Thr	Arg		
				90					95						100		
att	gct	ctt	gat	act	tcc	acc	cca	atc	ggc	aac	ggc	gtg	ttg	act	acc	451	
Ile	Ala	Leu	Asp	Thr	Ser	Thr	Pro	Ile	Gly	Asn	Gly	Val	Leu	Thr	Thr		
			105					110					115				
aac	acc	gaa	gag	caa	gcc	gtg	gaa	cgc	tcc	ggc	gga	gaa	ggc	tct	gta	499	
Asn	Thr	Glu	Glu	Gln	Ala	Val	Glu	Arg	Ser	Gly	Gly	Glu	Gly	Ser	Val		
		120					125					130					
gag	gac	aaa	ggc	gca	gag	gca	atg	gtc	gct	gca	ctc	gat	act	gcc	ctc	547	
Glu	Asp	Lys	Gly	Ala	Glu	Ala	Met	Val	Ala	Ala	Leu	Asp	Thr	Ala	Leu		
	135					140					145						
gtg	ctt	tct	caa	att	cgt	gca	act	gag	ggc	tagactgttc	tttaaaaggt					597	
Val	Leu	Ser	Gln	Ile	Arg	Ala	Thr	Glu	Gly								
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ttg																600	

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			20					25					30				
Arg	Leu	His	Lys	His	Ala	Val	Asp	Ala	Gly	Arg	Ala	Ala	Gly	Ala	Thr		
		35					40					45					
Val	Ser	Glu	Tyr	Arg	Val	Ile	Gly	Ala	Leu	Glu	Leu	Pro	Val	Val	Val		
	50					55					60						
Gln	Glu	Leu	Ala	Arg	Thr	His	Asp	Ala	Val	Val	Ala	Leu	Gly	Cys	Val		
65					70					75					80		
Val	Arg	Gly	Gly	Thr	Pro	His	Phe	Asp	Tyr	Val	Cys	Asp	Ser	Val	Thr		
				85					90					95			
Glu	Gly	Leu	Thr	Arg	Ile	Ala	Leu	Asp	Thr	Ser	Thr	Pro	Ile	Gly	Asn		
			100					105					110				

Gly Val Leu Thr Thr Asn Thr Glu Glu Gln Ala Val Glu Arg Ser Gly  
115 120 125

Gly Glu Gly Ser Val Glu Asp Lys Gly Ala Glu Ala Met Val Ala Ala  
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Leu Asp Thr Ala Leu Val Leu Ser Gln Ile Arg Ala Thr Glu Gly  
145 150 155

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<223> FRXA02249

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tgtgggaaca agagcaccca gaaaactaag gagcacaaca atg gct aaa gaa gga 115  
Met Ala Lys Glu Gly  
1 5

ttg ccg gca gtc gaa ctc ccc gac gcc agc gga tta aaa gtc gcc gta 163  
Leu Pro Ala Val Glu Leu Pro Asp Ala Ser Gly Leu Lys Val Ala Val  
10 15 20

gtc acc gca cgg tgg aac gca gaa atc tgc gac cgc ctg cac aag cac 211  
Val Thr Ala Arg Trp Asn Ala Glu Ile Cys Asp Arg Leu His Lys His  
25 30 35

gca gta gat gcg gga cgt gca gca gga gca acg gtg agc gaa tac cgc 259  
Ala Val Asp Ala Gly Arg Ala Ala Gly Ala Thr Val Ser Glu Tyr Arg  
40 45 50

gtc atc ggc gcc ctg gaa ctt cca gtc gta gtg caa gaa ctg gca cgc 307  
Val Ile Gly Ala Leu Glu Leu Pro Val Val Val Gln Glu Leu Ala Arg  
55 60 65

acc cat gac gca gta gtt gcc ttg ggc tgt gtc gtt cgt ggc ggc acc 355  
Thr His Asp Ala Val Val Ala Leu Gly Cys Val Val Arg Gly Gly Thr  
70 75 80 85

cca cac ttt gat tac gtg tgc gac tct gtc acc gaa ggc ctc acc cgc 403  
Pro His Phe Asp Tyr Val Cys Asp Ser Val Thr Glu Gly Leu Thr Arg  
90 95 100

att gct ctt gat act tcc acc cca atc ggc aac ggt gtg ttg act acc 451  
Ile Ala Leu Asp Thr Ser Thr Pro Ile Gly Asn Gly Val Leu Thr Thr  
105 110 115

aac acc gaa gag caa gcc gtg gaa cgc tcc ggt gga gaa ggc tct gta 499  
Asn Thr Glu Glu Gln Ala Val Glu Arg Ser Gly Gly Glu Gly Ser Val  
120 125 130

gag gac aaa ggc gca gag gca atg gtc gct gca ctc gat act gcc ctc 547  
Glu Asp Lys Gly Ala Glu Ala Met Val Ala Ala Leu Asp Thr Ala Leu

135 140 145

gtg ctt tct caa att cgt gca act gag ggt tagactgttc tttaaaagg 597  
 Val Leu Ser Gln Ile Arg Ala Thr Glu Gly  
 150 155

ttg 600

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 <213> Corynebacterium glutamicum

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 Arg Leu His Lys His Ala Val Asp Ala Gly Arg Ala Ala Gly Ala Thr  
 35 40 45  
 Val Ser Glu Tyr Arg Val Ile Gly Ala Leu Glu Leu Pro Val Val Val  
 50 55 60  
 Gln Glu Leu Ala Arg Thr His Asp Ala Val Val Ala Leu Gly Cys Val  
 65 70 75 80  
 Val Arg Gly Gly Thr Pro His Phe Asp Tyr Val Cys Asp Ser Val Thr  
 85 90 95  
 Glu Gly Leu Thr Arg Ile Ala Leu Asp Thr Ser Thr Pro Ile Gly Asn  
 100 105 110  
 Gly Val Leu Thr Thr Asn Thr Glu Glu Gln Ala Val Glu Arg Ser Gly  
 115 120 125  
 Gly Glu Gly Ser Val Glu Asp Lys Gly Ala Glu Ala Met Val Ala Ala  
 130 135 140  
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 <223> RXA02250

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 Val Thr Thr Asn Ala

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ccc gac gga gca acg aac aac atc aac aac gca cat tcg ggc gct gtc			163
Pro Asp Gly Ala Thr Asn Asn Ile Asn Asn Ala His Ser Gly Ala Val			
	10	15	20
ggg aag cca aag gta cag ctc agc gat gcg gaa att cag gaa tac acc			211
Gly Lys Pro Lys Val Gln Leu Ser Asp Ala Glu Ile Gln Glu Tyr Thr			
	25	30	35
gca gct ttc gct ggc acc acc aca acc aag cca tgg gag ctg gag gtg			259
Ala Ala Phe Ala Gly Thr Thr Thr Thr Lys Pro Trp Glu Leu Glu Val			
	40	45	50
acc aca aag ttt ctg aaa aag atc gcg tgg gta gcc gtg gtt gtc atc			307
Thr Thr Lys Phe Leu Lys Lys Ile Ala Trp Val Ala Val Val Val Ile			
	55	60	65
atg gcc gtt cac atc ttc atg ggt gcc gtg gtg gac gtc gat ttc acc			355
Met Ala Val His Ile Phe Met Gly Ala Val Val Asp Val Asp Phe Thr			
	70	75	85
ggt gca gcg gtc acc ttt gtt gac act ctg gca ttc cca gcg ttg ggc			403
Gly Ala Ala Val Thr Phe Val Asp Thr Leu Ala Phe Pro Ala Leu Gly			
	90	95	100
atc atc ttc tcc gtt ctt gtg ttc ttg gga ctg act cgc cct cgc gtg			451
Ile Ile Phe Ser Val Leu Val Phe Leu Gly Leu Thr Arg Pro Arg Val			
	105	110	115
cgt gcc aac gaa gac ggc gtt gag gtg cgt aac ttc atc gga act cgt			499
Arg Ala Asn Glu Asp Gly Val Glu Val Arg Asn Phe Ile Gly Thr Arg			
	120	125	130
ttc tac cca tgg gtt gtc atc tac ggc atg tct ttc ccc aag ggc agc			547
Phe Tyr Pro Trp Val Val Ile Tyr Gly Met Ser Phe Pro Lys Gly Ser			
	135	140	145
agc gtg gca cgt ttg gag ctt cca gac ttt gaa ttc gtt ccc atg tgg			595
Ser Val Ala Arg Leu Glu Leu Pro Asp Phe Glu Phe Val Pro Met Trp			
	150	155	165
gct ttc cag tcc cgc gat gga gaa gat gtg gtg cgc gcg gtt gcg acc			643
Ala Phe Gln Ser Arg Asp Gly Glu Asp Val Val Arg Ala Val Ala Thr			
	170	175	180
ttc cgc gac ctc gaa aac aag tac atg cca gag gac taattaagct			689
Phe Arg Asp Leu Glu Asn Lys Tyr Met Pro Glu Asp			
	185	190	
gtggctgac caa			702

&lt;210&gt; 568

&lt;211&gt; 193

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 568

Val	Thr	Thr	Asn	Ala	Pro	Asp	Gly	Ala	Thr	Asn	Asn	Ile	Asn	Asn	Ala
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His	Ser	Gly	Ala	Val	Gly	Lys	Pro	Lys	Val	Gln	Leu	Ser	Asp	Ala	Glu
			20					25					30		
Ile	Gln	Glu	Tyr	Thr	Ala	Ala	Phe	Ala	Gly	Thr	Thr	Thr	Thr	Lys	Pro
		35					40					45			
Trp	Glu	Leu	Glu	Val	Thr	Thr	Lys	Phe	Leu	Lys	Lys	Ile	Ala	Trp	Val
	50					55					60				
Ala	Val	Val	Val	Ile	Met	Ala	Val	His	Ile	Phe	Met	Gly	Ala	Val	Val
65					70					75					80
Asp	Val	Asp	Phe	Thr	Gly	Ala	Ala	Val	Thr	Phe	Val	Asp	Thr	Leu	Ala
				85					90					95	
Phe	Pro	Ala	Leu	Gly	Ile	Ile	Phe	Ser	Val	Leu	Val	Phe	Leu	Gly	Leu
			100					105					110		
Thr	Arg	Pro	Arg	Val	Arg	Ala	Asn	Glu	Asp	Gly	Val	Glu	Val	Arg	Asn
		115					120					125			
Phe	Ile	Gly	Thr	Arg	Phe	Tyr	Pro	Trp	Val	Val	Ile	Tyr	Gly	Met	Ser
	130					135					140				
Phe	Pro	Lys	Gly	Ser	Ser	Val	Ala	Arg	Leu	Glu	Leu	Pro	Asp	Phe	Glu
145					150					155					160
Phe	Val	Pro	Met	Trp	Ala	Phe	Gln	Ser	Arg	Asp	Gly	Glu	Asp	Val	Val
				165					170					175	
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Asp

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<212> DNA
<213> Corynebacterium glutamicum
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                                         Val Asp Ile Trp Ser
                                         1                               5

gga cta gac agc gtt ccg gct gat ctt caa gga tca gta gtc acc att 163
Gly Leu Asp Ser Val Pro Ala Asp Leu Gln Gly Ser Val Val Thr Ile
                        10                               15                               20

ggt gtg ttt gat ggg ctc cac cgg ggg cat caa agt tta atc ggc gag 211
Gly Val Phe Asp Gly Leu His Arg Gly His Gln Ser Leu Ile Gly Glu

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25				30				35								
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ttt Phe	gac Asp 55	ccg Pro	cat His	ccg Pro	atc Ile	gct Ala 60	gtg Val	ttt Phe	ttg Leu	cca Pro	ggg Gly 65	aaa Lys	gag Glu	cca Pro	acc Thr	307
cgt Arg 70	ttg Leu	gct Ala	cct Pro	ttg Leu	gat Asp 75	tat Tyr	cgc Arg	ctt Leu	aat Asn	ttg Leu 80	gct Ala	gcg Ala	gaa Glu	tgt Cys	ggc Gly 85	355
gtc Val	gat Asp	gct Ala	gcg Ala	ttg Leu 90	gtt Val	att Ile	gat Asp	ttc Phe	act Thr 95	aaa Lys	gaa Glu	ctc Leu	gca Ala	ggg Gly 100	ctg Leu	403
agc Ser	gct Ala	gaa Glu	gag Glu 105	tat Tyr	ttc Phe	aca Thr	acc Thr 110	atg Met	atc Ile	gtg Val	gat Asp	acg Thr	ctg Leu 115	cat His	gcg Ala	451
cgt Arg	tca Ser 120	gtt Val	gtg Val	gtg Val	ggg Gly	gag Glu	aac Asn 125	ttc Phe	acc Thr	ttc Phe	ggg Gly	gtc Val 130	aat Asn	ggc Gly	gct Ala	499
ggc Gly	act Thr 135	gag Glu	tcc Ser	acg Thr	atg Met	cgg Arg 140	gaa Glu	ttg Leu	gga Gly	caa Gln	aag Lys 145	ttt Phe	ggc Gly	gtg Val	aat Asn	547
gtc Val 150	acg Thr	att Ile	gct Ala	ccg Pro	ctg Leu 155	ctg Leu	cat His	gat Asp	gat Asp	gac Asp 160	cag Gln	cgt Arg	att Ile	tgc Cys	tcc Ser 165	595
acc Thr	ttg Leu	gtg Val	cgc Arg 170	gat Asp	tac Tyr	ttg Leu	gat Asp	cag Gln	ggc Gly 175	gag Glu	gtt Val	gag Glu	cgc Arg	gcg Ala 180	aac Asn	643
tgg Trp	gcg Ala	ctt Leu	ggg Gly 185	cga Arg	cgc Arg	tat Tyr	gcc Ala	gtg Val 190	cgc Arg	ggc Gly	gaa Glu	gtt Val	gtc Val 195	cgt Arg	ggg Gly	691
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ctg Leu 215	ccg Pro	acc Thr	tct Ser	gtg Val	gcg Ala	ctg Leu 220	ccc Pro	gcc Ala	gat Asp	ggc Gly	gtg Val 225	tat Tyr	gca Ala	ggc Gly	tgg Trp	787
ttc Phe 230	acc Thr	atc Ile	acc Thr	gat Asp	gac Asp 235	cgc Arg	gaa Glu	atc Ile	gac Asp	aag Lys 240	gaa Glu	atc Ile	tcc Ser	cgc Arg	gat Asp 245	835
atc Ile	gac Asp	ggc Gly	acc Thr	atg Met 250	gtt Val	cca Pro	ggc Gly	gtg Val	cgt Arg 255	tac Tyr	caa Gln	act Thr	gcc Ala	att Ile 260	tcc Ser	883
gtg Val	ggc Gly	acc Thr	aat Asn 265	ccc Pro	acc Thr	ttc Phe	ggc Gly	gat Asp 270	gag Glu	cga Arg	cgc Arg	agc Ser	gtc Val 275	gag Glu	gca Ala	931

ttc atc ctc gac cag gaa gcc gac ctg tac ggt cac cat gtc atg gtg 979  
 Phe Ile Leu Asp Gln Glu Ala Asp Leu Tyr Gly His His Val Met Val  
                   280                                  285                                  290

gaa ttc gtg gga cac ttg cgc gac atg gtc aaa ttc aac ggc gtc gac  
 1027  
 Glu Phe Val Gly His Leu Arg Asp Met Val Lys Phe Asn Gly Val Asp  
                   295                                  300                                  305

gag cta cta gac gcc atg gcc cga gat gtc acc aac gcc cgc gac atc  
 1075  
 Glu Leu Leu Asp Ala Met Ala Arg Asp Val Thr Asn Ala Arg Asp Ile  
 310                                  315                                  320                                  325

ctt gcc aaa gac aaa ttg ctt ctc gac gcc gac acc cag ccc agc gct  
 1123  
 Leu Ala Lys Asp Lys Leu Leu Leu Asp Ala Asp Thr Gln Pro Ser Ala  
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 1146

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<211> 341

<212> PRT

<213> Corynebacterium glutamicum

<400> 570

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Ser Val Val Thr Ile Gly Val Phe Asp Gly Leu His Arg Gly His Gln  
                   20                                  25                                  30

Ser Leu Ile Gly Glu Ala Lys Lys Gln Ala Glu Glu Leu Gly Val Pro  
                   35                                  40                                  45

Cys Val Met Val Thr Phe Asp Pro His Pro Ile Ala Val Phe Leu Pro  
                   50                                  55                                  60

Gly Lys Glu Pro Thr Arg Leu Ala Pro Leu Asp Tyr Arg Leu Asn Leu  
   65                                  70                                  75                                  80

Ala Ala Glu Cys Gly Val Asp Ala Ala Leu Val Ile Asp Phe Thr Lys  
                                   85                                  90                                  95

Glu Leu Ala Gly Leu Ser Ala Glu Glu Tyr Phe Thr Thr Met Ile Val  
                   100                                  105                                  110

Asp Thr Leu His Ala Arg Ser Val Val Val Gly Glu Asn Phe Thr Phe  
                   115                                  120                                  125

Gly Val Asn Gly Ala Gly Thr Glu Ser Thr Met Arg Glu Leu Gly Gln  
                   130                                  135                                  140

Lys Phe Gly Val Asn Val Thr Ile Ala Pro Leu Leu His Asp Asp Asp  
 145                                  150                                  155                                  160

Gln Arg Ile Cys Ser Thr Leu Val Arg Asp Tyr Leu Asp Gln Gly Glu



165										170				175			
Val	Glu	Arg	Ala	Asn	Trp	Ala	Leu	Gly	Arg	Arg	Tyr	Ala	Val	Arg	Gly		
			180					185					190				
Glu	Val	Val	Arg	Gly	Ala	Gly	Arg	Gly	Gly	Lys	Glu	Leu	Gly	Tyr	Pro		
		195					200					205					
Thr	Ala	Asn	Leu	Tyr	Leu	Pro	Thr	Ser	Val	Ala	Leu	Pro	Ala	Asp	Gly		
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Val	Tyr	Ala	Gly	Trp	Phe	Thr	Ile	Thr	Asp	Asp	Arg	Glu	Ile	Asp	Lys		
225					230					235					240		
Glu	Ile	Ser	Arg	Asp	Ile	Asp	Gly	Thr	Met	Val	Pro	Gly	Val	Arg	Tyr		
				245					250					255			
Gln	Thr	Ala	Ile	Ser	Val	Gly	Thr	Asn	Pro	Thr	Phe	Gly	Asp	Glu	Arg		
		260						265					270				
Arg	Ser	Val	Glu	Ala	Phe	Ile	Leu	Asp	Gln	Glu	Ala	Asp	Leu	Tyr	Gly		
		275					280					285					
His	His	Val	Met	Val	Glu	Phe	Val	Gly	His	Leu	Arg	Asp	Met	Val	Lys		
	290					295					300						
Phe	Asn	Gly	Val	Asp	Glu	Leu	Leu	Asp	Ala	Met	Ala	Arg	Asp	Val	Thr		
305					310					315					320		
Asn	Ala	Arg	Asp	Ile	Leu	Ala	Lys	Asp	Lys	Leu	Leu	Leu	Asp	Ala	Asp		
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 Met Val Pro Ala Glu  
 1 5  
 ctt ttt gcg cgt gtg gaa ttt ccg gat cat aaa atc ctg gct cag acg 163  
 Leu Phe Ala Arg Val Glu Phe Pro Asp His Lys Ile Leu Ala Gln Thr  
 10 15 20  
 aag gat ttc cat gac tcc ctc acc aag cca ccc gga tct ttg ggc aag 211  
 Lys Asp Phe His Asp Ser Leu Thr Lys Pro Pro Gly Ser Leu Gly Lys  
 25 30 35

ttg gag cag atc ggc tgt ttc att tcc gca tgc cag ggc cag att ccg	259
Leu Glu Gln Ile Gly Cys Phe Ile Ser Ala Cys Gln Gly Gln Ile Pro	
40 45 50	
cca cgt cca ctc aac aac tca aag atc gtt gtt ttc gct ggc gat cac	307
Pro Arg Pro Leu Asn Asn Ser Lys Ile Val Val Phe Ala Gly Asp His	
55 60 65	
ggc gtt gca act aaa ggc gtg tcc gcg tac cca tcc tca gta agc ttg	355
Gly Val Ala Thr Lys Gly Val Ser Ala Tyr Pro Ser Ser Val Ser Leu	
70 75 80 85	
cag atg gct gaa aac att aca aac ggt ggc gcc gcc atc aac gtg att	403
Gln Met Ala Glu Asn Ile Thr Asn Gly Gly Ala Ala Ile Asn Val Ile	
90 95 100	
gca cgc acc acc ggc acg tcc gtc cga ctt att gat acc tcc ctc gac	451
Ala Arg Thr Thr Gly Thr Ser Val Arg Leu Ile Asp Thr Ser Leu Asp	
105 110 115	
cac gaa gca tgg ggc gac gag cgc gta tct agg tcc tgc gga tcc atc	499
His Glu Ala Trp Gly Asp Glu Arg Val Ser Arg Ser Cys Gly Ser Ile	
120 125 130	
gat gtt gaa gac gcc atg acc caa gaa cag gtc gaa cgc gca ctg aag	547
Asp Val Glu Asp Ala Met Thr Gln Glu Gln Val Glu Arg Ala Leu Lys	
135 140 145	
atc ggt aag cgc att gcg gat caa gaa gtg gac gca ggc gcc gac att	595
Ile Gly Lys Arg Ile Ala Asp Gln Glu Val Asp Ala Gly Ala Asp Ile	
150 155 160 165	
tta atc ccc ggc gat tta gga att ggc aac acc acc acc gcc gct gcc	643
Leu Ile Pro Gly Asp Leu Gly Ile Gly Asn Thr Thr Thr Ala Ala Ala	
170 175 180	
ctc gtt gga acg ttc acc ctc gca gag cct gtt gtt gtc gta ggc cgc	691
Leu Val Gly Thr Phe Thr Leu Ala Glu Pro Val Val Val Val Gly Arg	
185 190 195	
ggc acc gga atc gac gat gaa gcc tgg aaa ctc aaa gtc tcc gcg atc	739
Gly Thr Gly Ile Asp Asp Glu Ala Trp Lys Leu Lys Val Ser Ala Ile	
200 205 210	
cgc gac gcc atg ttc cgc gcc cgc gac ctg cgc caa gac ccc atc gcc	787
Arg Asp Ala Met Phe Arg Ala Arg Asp Leu Arg Gln Asp Pro Ile Ala	
215 220 225	
atc gcc cgg aaa atc tct tcc cca gac ctt gca gcc atg gca gca ttc	835
Ile Ala Arg Lys Ile Ser Ser Pro Asp Leu Ala Ala Met Ala Ala Phe	
230 235 240 245	
att gcc caa gca gca gtt cga cgc acc ccc gtg ctt ctc gac ggc gtt	883
Ile Ala Gln Ala Ala Val Arg Arg Thr Pro Val Leu Leu Asp Gly Val	
250 255 260	
gta gtc acc gcc gca gcc ctc cta gcc aac aaa ctg gcc cca ggt gcc	931
Val Val Thr Ala Ala Ala Leu Leu Ala Asn Lys Leu Ala Pro Gly Ala	
265 270 275	
agg cgt tgg ttc atc gca gga cac cgc tcc acc gaa cca gcg cat tcc	979

Arg Arg Trp Phe Ile Ala Gly His Arg Ser Thr Glu Pro Ala His Ser  
280 285 290

gta gct cta aac gca ctg gcc ctt gat ccc atc ctg gaa ctt gga atg  
1027

Val Ala Leu Asn Ala Leu Ala Leu Asp Pro Ile Leu Glu Leu Gly Met  
295 300 305

tcc ctt ggc gaa ggc tcc ggc gca gcc acc gca ctc ccc ctg gtc aag  
1075

Ser Leu Gly Glu Gly Ser Gly Ala Ala Thr Ala Leu Pro Leu Val Lys  
310 315 320 325

att gcc gtt gac ctg atg aac gac atg tcg aca ttt tct tcc gcc ggc  
1123

Ile Ala Val Asp Leu Met Asn Asp Met Ser Thr Phe Ser Ser Ala Gly  
330 335 340

gtc gat gga ccc cta aac gcc tct tcc gaa gcg ccc gag caa aac acg  
1171

Val Asp Gly Pro Leu Asn Ala Ser Ser Glu Ala Pro Glu Gln Asn Thr  
345 350 355

gag taactttcta agcgatgtcc ggc  
1197  
Glu

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<211> 358

<212> PRT

<213> Corynebacterium glutamicum

<400> 572

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Ile Leu Ala Gln Thr Lys Asp Phe His Asp Ser Leu Thr Lys Pro Pro  
20 25 30

Gly Ser Leu Gly Lys Leu Glu Gln Ile Gly Cys Phe Ile Ser Ala Cys  
35 40 45

Gln Gly Gln Ile Pro Pro Arg Pro Leu Asn Asn Ser Lys Ile Val Val  
50 55 60

Phe Ala Gly Asp His Gly Val Ala Thr Lys Gly Val Ser Ala Tyr Pro  
65 70 75 80

Ser Ser Val Ser Leu Gln Met Ala Glu Asn Ile Thr Asn Gly Gly Ala  
85 90 95

Ala Ile Asn Val Ile Ala Arg Thr Thr Gly Thr Ser Val Arg Leu Ile  
100 105 110

Asp Thr Ser Leu Asp His Glu Ala Trp Gly Asp Glu Arg Val Ser Arg  
115 120 125

Ser Cys Gly Ser Ile Asp Val Glu Asp Ala Met Thr Gln Glu Gln Val  
130 135 140

Glu Arg Ala Leu Lys Ile Gly Lys Arg Ile Ala Asp Gln Glu Val Asp  
 145 150 155 160  
 Ala Gly Ala Asp Ile Leu Ile Pro Gly Asp Leu Gly Ile Gly Asn Thr  
 165 170 175  
 Thr Thr Ala Ala Ala Leu Val Gly Thr Phe Thr Leu Ala Glu Pro Val  
 180 185 190  
 Val Val Val Gly Arg Gly Thr Gly Ile Asp Asp Glu Ala Trp Lys Leu  
 195 200 205  
 Lys Val Ser Ala Ile Arg Asp Ala Met Phe Arg Ala Arg Asp Leu Arg  
 210 215 220  
 Gln Asp Pro Ile Ala Ile Ala Arg Lys Ile Ser Ser Pro Asp Leu Ala  
 225 230 235 240  
 Ala Met Ala Ala Phe Ile Ala Gln Ala Ala Val Arg Arg Thr Pro Val  
 245 250 255  
 Leu Leu Asp Gly Val Val Val Thr Ala Ala Ala Leu Leu Ala Asn Lys  
 260 265 270  
 Leu Ala Pro Gly Ala Arg Arg Trp Phe Ile Ala Gly His Arg Ser Thr  
 275 280 285  
 Glu Pro Ala His Ser Val Ala Leu Asn Ala Leu Ala Leu Asp Pro Ile  
 290 295 300  
 Leu Glu Leu Gly Met Ser Leu Gly Glu Gly Ser Gly Ala Ala Thr Ala  
 305 310 315 320  
 Leu Pro Leu Val Lys Ile Ala Val Asp Leu Met Asn Asp Met Ser Thr  
 325 330 335  
 Phe Ser Ser Ala Gly Val Asp Gly Pro Leu Asn Ala Ser Ser Glu Ala  
 340 345 350  
 Pro Glu Gln Asn Thr Glu  
 355  
  
 <210> 573  
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 <212> DNA  
 <213> Corynebacterium glutamicum  
  
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 <222> (101)..(1123)  
 <223> RXA01489  
  
 <400> 573  
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 agcattcatg tctgttgagt ctatgccgta gtctaaaaca gtg gat att tgg agt 115  
 Val Asp Ile Trp Ser  
 1 5

gga cta gac agc gtt ccg gct gat ctt caa gga tca gta gtc acc att	163
Gly Leu Asp Ser Val Pro Ala Asp Leu Gln Gly Ser Val Val Thr Ile	
10 15 20	
ggt gtg ttt gat ggg ctc cac cgg ggg cat caa agt tta atc ggc gag	211
Gly Val Phe Asp Gly Leu His Arg Gly His Gln Ser Leu Ile Gly Glu	
25 30 35	
gcc aag aag cag gcc gag gag ctg ggt gtg cct tgt gtc atg gtg acc	259
Ala Lys Lys Gln Ala Glu Glu Leu Gly Val Pro Cys Val Met Val Thr	
40 45 50	
ttt gac ccg cat ccg atc gct gtg ttt ttg cca ggt aaa gag cca acc	307
Phe Asp Pro His Pro Ile Ala Val Phe Leu Pro Gly Lys Glu Pro Thr	
55 60 65	
cgt ttg gct cct ttg gat tat cgc ctt aat ttg gct gcg gaa tgt ggc	355
Arg Leu Ala Pro Leu Asp Tyr Arg Leu Asn Leu Ala Ala Glu Cys Gly	
70 75 80 85	
gtc gat gct gcg ttg gtt att gat ttc act aaa gaa ctc gca ggt ctg	403
Val Asp Ala Ala Leu Val Ile Asp Phe Thr Lys Glu Leu Ala Gly Leu	
90 95 100	
agc gct gaa gag tat ttc aca acc atg atc gtg gat acg ctg cat gcg	451
Ser Ala Glu Glu Tyr Phe Thr Thr Met Ile Val Asp Thr Leu His Ala	
105 110 115	
cgt tca gtt gtg gtg ggg gag aac ttc acc ttc ggt gtc aat ggc gct	499
Arg Ser Val Val Val Gly Glu Asn Phe Thr Phe Gly Val Asn Gly Ala	
120 125 130	
ggc act gag tcc acg atg cgg gaa ttg gga caa aag ttt ggc gtg aat	547
Gly Thr Glu Ser Thr Met Arg Glu Leu Gly Gln Lys Phe Gly Val Asn	
135 140 145	
gtc acg att gct ccg ctg ctg cat gat gat gac cag cgt att tgc tcc	595
Val Thr Ile Ala Pro Leu Leu His Asp Asp Asp Gln Arg Ile Cys Ser	
150 155 160 165	
acc ttg gtg cgc gat tac ttg gat cag ggc gag gtt gag cgc gcg aac	643
Thr Leu Val Arg Asp Tyr Leu Asp Gln Gly Glu Val Glu Arg Ala Asn	
170 175 180	
tgg gcg ctt ggt cga cgc tat gcc gtg cgc ggc gaa gtt gtc cgt ggt	691
Trp Ala Leu Gly Arg Arg Tyr Ala Val Arg Gly Glu Val Val Arg Gly	
185 190 195	
gct ggc cgt ggc ggc aaa gaa ttg ggc tat ccc acc gcg aat ctc tac	739
Ala Gly Arg Gly Gly Lys Glu Leu Gly Tyr Pro Thr Ala Asn Leu Tyr	
200 205 210	
ctg ccg acc tct gtg gcg ctg ccc gcc gat ggc gtg tat gca ggc tgg	787
Leu Pro Thr Ser Val Ala Leu Pro Ala Asp Gly Val Tyr Ala Gly Trp	
215 220 225	
ttc acc atc acc gat gac cgc gaa atc gac aag gaa atc tcc cgc gat	835
Phe Thr Ile Thr Asp Asp Arg Glu Ile Asp Lys Glu Ile Ser Arg Asp	
230 235 240 245	
atc gac ggc acc atg gtt cca ggc gtg cgt tac caa act gcc att tcc	883

Ile	Asp	Gly	Thr	Met	Val	Pro	Gly	Val	Arg	Tyr	Gln	Thr	Ala	Ile	Ser	
				250					255					260		
gtg	ggc	acc	aat	ccc	acc	ttc	ggc	gat	gag	cga	cgc	agc	gtc	gag	gca	931
Val	Gly	Thr	Asn	Pro	Thr	Phe	Gly	Asp	Glu	Arg	Arg	Ser	Val	Glu	Ala	
			265					270					275			
ttc	atc	ctc	gac	cag	gaa	gcc	gac	ctg	tac	ggc	cac	cat	gtc	atg	gtg	979
Phe	Ile	Leu	Asp	Gln	Glu	Ala	Asp	Leu	Tyr	Gly	His	His	Val	Met	Val	
		280					285					290				
gaa	ttc	gtg	gga	cac	ttg	cgc	gac	atg	gtc	aaa	ttc	aac	ggc	gtc	gac	
1027																
Glu	Phe	Val	Gly	His	Leu	Arg	Asp	Met	Val	Lys	Phe	Asn	Gly	Val	Asp	
	295					300					305					
gag	cta	cta	gac	gcc	atg	gcc	cga	gat	gtc	acc	aac	gcc	cgc	gac	atc	
1075																
Glu	Leu	Leu	Asp	Ala	Met	Ala	Arg	Asp	Val	Thr	Asn	Ala	Arg	Asp	Ile	
310					315					320					325	
ctt	gcc	aaa	gac	aaa	ttg	ctt	ctc	gac	gcc	gac	acc	cag	ccc	agc	gct	
1123																
Leu	Ala	Lys	Asp	Lys	Leu	Leu	Leu	Asp	Ala	Asp	Thr	Gln	Pro	Ser	Ala	
				330					335					340		
taaggccggt caccggccat caa																
1146																
<210> 574																
<211> 341																
<212> PRT																
<213> Corynebacterium glutamicum																
<400> 574																
Val	Asp	Ile	Trp	Ser	Gly	Leu	Asp	Ser	Val	Pro	Ala	Asp	Leu	Gln	Gly	
1				5					10					15		
Ser	Val	Val	Thr	Ile	Gly	Val	Phe	Asp	Gly	Leu	His	Arg	Gly	His	Gln	
			20					25					30			
Ser	Leu	Ile	Gly	Glu	Ala	Lys	Lys	Gln	Ala	Glu	Glu	Leu	Gly	Val	Pro	
		35					40					45				
Cys	Val	Met	Val	Thr	Phe	Asp	Pro	His	Pro	Ile	Ala	Val	Phe	Leu	Pro	
	50					55					60					
Gly	Lys	Glu	Pro	Thr	Arg	Leu	Ala	Pro	Leu	Asp	Tyr	Arg	Leu	Asn	Leu	
65					70					75				80		
Ala	Ala	Glu	Cys	Gly	Val	Asp	Ala	Ala	Leu	Val	Ile	Asp	Phe	Thr	Lys	
				85					90					95		
Glu	Leu	Ala	Gly	Leu	Ser	Ala	Glu	Glu	Tyr	Phe	Thr	Thr	Met	Ile	Val	
			100					105					110			
Asp	Thr	Leu	His	Ala	Arg	Ser	Val	Val	Val	Gly	Glu	Asn	Phe	Thr	Phe	
		115					120					125				
Gly	Val	Asn	Gly	Ala	Gly	Thr	Glu	Ser	Thr	Met	Arg	Glu	Leu	Gly	Gln	

130					135					140					
Lys	Phe	Gly	Val	Asn	Val	Thr	Ile	Ala	Pro	Leu	Leu	His	Asp	Asp	Asp
145					150					155					160
Gln	Arg	Ile	Cys	Ser	Thr	Leu	Val	Arg	Asp	Tyr	Leu	Asp	Gln	Gly	Glu
				165					170					175	
Val	Glu	Arg	Ala	Asn	Trp	Ala	Leu	Gly	Arg	Arg	Tyr	Ala	Val	Arg	Gly
			180					185					190		
Glu	Val	Val	Arg	Gly	Ala	Gly	Arg	Gly	Gly	Lys	Glu	Leu	Gly	Tyr	Pro
		195					200					205			
Thr	Ala	Asn	Leu	Tyr	Leu	Pro	Thr	Ser	Val	Ala	Leu	Pro	Ala	Asp	Gly
	210					215					220				
Val	Tyr	Ala	Gly	Trp	Phe	Thr	Ile	Thr	Asp	Asp	Arg	Glu	Ile	Asp	Lys
225					230					235					240
Glu	Ile	Ser	Arg	Asp	Ile	Asp	Gly	Thr	Met	Val	Pro	Gly	Val	Arg	Tyr
				245					250					255	
Gln	Thr	Ala	Ile	Ser	Val	Gly	Thr	Asn	Pro	Thr	Phe	Gly	Asp	Glu	Arg
			260					265					270		
Arg	Ser	Val	Glu	Ala	Phe	Ile	Leu	Asp	Gln	Glu	Ala	Asp	Leu	Tyr	Gly
		275					280					285			
His	His	Val	Met	Val	Glu	Phe	Val	Gly	His	Leu	Arg	Asp	Met	Val	Lys
		290				295					300				
Phe	Asn	Gly	Val	Asp	Glu	Leu	Leu	Asp	Ala	Met	Ala	Arg	Asp	Val	Thr
305					310					315					320
Asn	Ala	Arg	Asp	Ile	Leu	Ala	Lys	Asp	Lys	Leu	Leu	Leu	Asp	Ala	Asp
				325					330					335	
Thr	Gln	Pro	Ser	Ala											
				340											

&lt;210&gt; 575

&lt;211&gt; 805

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (87)..(782)

&lt;223&gt; RXN01712

&lt;400&gt; 575

gccggccttag gctcctccga ccagaacccc actggcacct ttggataaca ccattccgtg 60

taaacaagct ggcctagact tgaaacatg gtc gat atc ttg gaa ctc atc ggt 113

Met Val Asp Ile Leu Glu Leu Ile Gly

1

5

ccc cta cct ttt gtg tct acg cca gag tta agg gca att gtc gtg act 161

Pro Leu Pro Phe Val Ser Thr Pro Glu Leu Arg Ala Ile Val Val Thr

10	15	20	25	
gcc att aat ggt tcc acc act att aat ggc acg tct ggt cag ctt gga				209
Ala Ile Asn Gly Ser Thr Thr Ile Asn Gly Thr Ser Gly Gln Leu Gly				
	30	35	40	
aat tcc acg gat acg gaa ctt ctg ttg gcg ctt cgc agg tgg tcg gac				257
Asn Ser Thr Asp Thr Glu Leu Leu Leu Ala Leu Arg Arg Trp Ser Asp				
	45	50	55	
gtg gtg ttg gtt ggg tcg agc acg gtg aag gct gaa aat tat ggt ggc				305
Val Val Leu Val Gly Ser Ser Thr Val Lys Ala Glu Asn Tyr Gly Gly				
	60	65	70	
gtg gag gtt tcg cct gaa atc cag aag caa cgc cag gag ttg ggt cag				353
Val Glu Val Ser Pro Glu Ile Gln Lys Gln Arg Gln Glu Leu Gly Gln				
	75	80	85	
gaa gcg att ccg ccg att gcg gtg atg tca ggg tcg ttg aat ttt gat				401
Glu Ala Ile Pro Pro Ile Ala Val Met Ser Gly Ser Leu Asn Phe Asp				
	90	95	100	105
gtg gat act cgc ttt ttc ctt gag gcc gaa gtg ccg ccg atc atc atc				449
Val Asp Thr Arg Phe Phe Leu Glu Ala Glu Val Pro Pro Ile Ile Ile				
	110	115	120	
acg gat aat tcc gat caa gca aag cag cag cgc ctt gtg gat gct ggg				497
Thr Asp Asn Ser Asp Gln Ala Lys Gln Gln Arg Leu Val Asp Ala Gly				
	125	130	135	
gct cag gtt att gag gtg gag acg ttg acg gcg gag gtt ggc gtc gaa				545
Ala Gln Val Ile Glu Val Glu Thr Leu Thr Ala Glu Val Gly Val Glu				
	140	145	150	
aag ctt agg tct ttg ggt tac gcc cgc att gat tgt gag ggc ggt gca				593
Lys Leu Arg Ser Leu Gly Tyr Ala Arg Ile Asp Cys Glu Gly Gly Ala				
	155	160	165	
acg ttg tat ggg cag atg ttg gcc gcc gat ctt gtt gat gtg tgg cat				641
Thr Leu Tyr Gly Gln Met Leu Ala Ala Asp Leu Val Asp Val Trp His				
	170	175	180	185
cac acg att gat ccg acg ttg tcg ggc agc gtg gag cgc ccc acg gtg				689
His Thr Ile Asp Pro Thr Leu Ser Gly Ser Val Glu Arg Pro Thr Val				
	190	195	200	
aag ggc ggc gat gat gcg ccg cgc cga ttc gcg ttg gag cac gtc ttt				737
Lys Gly Gly Asp Asp Ala Pro Arg Arg Phe Ala Leu Glu His Val Phe				
	205	210	215	
gtc gat gat gac agc acc cta ttc ttg cgg tat aag cgc gcc aag				782
Val Asp Asp Asp Ser Thr Leu Phe Leu Arg Tyr Lys Arg Ala Lys				
	220	225	230	
tgagtgttgg actctccgga tct				805

&lt;210&gt; 576

&lt;211&gt; 232

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum



&lt;400&gt; 576

Met Val Asp Ile Leu Glu Leu Ile Gly Pro Leu Pro Phe Val Ser Thr  
 1 5 10 15

Pro Glu Leu Arg Ala Ile Val Val Thr Ala Ile Asn Gly Ser Thr Thr  
 20 25 30

Ile Asn Gly Thr Ser Gly Gln Leu Gly Asn Ser Thr Asp Thr Glu Leu  
 35 40 45

Leu Leu Ala Leu Arg Arg Trp Ser Asp Val Val Leu Val Gly Ser Ser  
 50 55 60

Thr Val Lys Ala Glu Asn Tyr Gly Gly Val Glu Val Ser Pro Glu Ile  
 65 70 75 80

Gln Lys Gln Arg Gln Glu Leu Gly Gln Glu Ala Ile Pro Pro Ile Ala  
 85 90 95

Val Met Ser Gly Ser Leu Asn Phe Asp Val Asp Thr Arg Phe Phe Leu  
 100 105 110

Glu Ala Glu Val Pro Pro Ile Ile Ile Thr Asp Asn Ser Asp Gln Ala  
 115 120 125

Lys Gln Gln Arg Leu Val Asp Ala Gly Ala Gln Val Ile Glu Val Glu  
 130 135 140

Thr Leu Thr Ala Glu Val Gly Val Glu Lys Leu Arg Ser Leu Gly Tyr  
 145 150 155 160

Ala Arg Ile Asp Cys Glu Gly Gly Ala Thr Leu Tyr Gly Gln Met Leu  
 165 170 175

Ala Ala Asp Leu Val Asp Val Trp His His Thr Ile Asp Pro Thr Leu  
 180 185 190

Ser Gly Ser Val Glu Arg Pro Thr Val Lys Gly Gly Asp Asp Ala Pro  
 195 200 205

Arg Arg Phe Ala Leu Glu His Val Phe Val Asp Asp Asp Ser Thr Leu  
 210 215 220

Phe Leu Arg Tyr Lys Arg Ala Lys  
 225 230

&lt;210&gt; 577

&lt;211&gt; 578

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (55)..(555)

&lt;223&gt; FRXA01712

&lt;400&gt; 577

cttctgttgg cgcttcgcag gtggtcggac gtgggtgttgg ttgggtcgag cacggtg 57  
 Val

1

aag gct gaa aat tat ggt ggc gtg gag gtt tcg cct gaa atc cag aag 105  
Lys Ala Glu Asn Tyr Gly Gly Val Glu Val Ser Pro Glu Ile Gln Lys  
5 10 15

caa cgc cag gag ttg ggt cag gaa gcg att ccg ccg att gcg gtg atg 153  
Gln Arg Gln Glu Leu Gly Gln Glu Ala Ile Pro Pro Ile Ala Val Met  
20 25 30

tca ggg tcg ttg aat ttt gat gtg gat act cgc ttt ttc ctt gag gcc 201  
Ser Gly Ser Leu Asn Phe Asp Val Asp Thr Arg Phe Phe Leu Glu Ala  
35 40 45

gaa gtg ccg ccg atc atc atc acg gat aat tcc gat caa gca aag cag 249  
Glu Val Pro Pro Ile Ile Ile Thr Asp Asn Ser Asp Gln Ala Lys Gln  
50 55 60 65

cag cgg ctt gtg gat gct ggg gct cag gtt att gag gtg gag acg ttg 297  
Gln Arg Leu Val Asp Ala Gly Ala Gln Val Ile Glu Val Glu Thr Leu  
70 75 80

acg gcg gag gtt ggc gtc gaa aag ctt agg tct ttg ggt tac gcc cgc 345  
Thr Ala Glu Val Gly Val Glu Lys Leu Arg Ser Leu Gly Tyr Ala Arg  
85 90 95

att gat tgt gag ggc ggt gca acg ttg tat ggg cag atg ttg gcc gcc 393  
Ile Asp Cys Glu Gly Gly Ala Thr Leu Tyr Gly Gln Met Leu Ala Ala  
100 105 110

gat ctt gtt gat gtg tgg cat cac acg att gat ccg acg ttg tcg ggc 441  
Asp Leu Val Asp Val Trp His His Thr Ile Asp Pro Thr Leu Ser Gly  
115 120 125

agc gtg gag cgc ccc acg gtg aag ggc ggc gat gat gcg ccg cgc cga 489  
Ser Val Glu Arg Pro Thr Val Lys Gly Gly Asp Asp Ala Pro Arg Arg  
130 135 140 145

ttc gcg ttg gag cac gtc ttt gtc gat gat gac agc acc cta ttc ttg 537  
Phe Ala Leu Glu His Val Phe Val Asp Asp Asp Ser Thr Leu Phe Leu  
150 155 160

cgg tat aag cgc gcc aag tgagtgttgg actctccgga tct 578  
Arg Tyr Lys Arg Ala Lys  
165

&lt;210&gt; 578

&lt;211&gt; 167

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 578

Val Lys Ala Glu Asn Tyr Gly Gly Val Glu Val Ser Pro Glu Ile Gln  
1 5 10 15

Lys Gln Arg Gln Glu Leu Gly Gln Glu Ala Ile Pro Pro Ile Ala Val  
20 25 30

Met Ser Gly Ser Leu Asn Phe Asp Val Asp Thr Arg Phe Phe Leu Glu  
35 40 45

Ala Glu Val Pro Pro Ile Ile Ile Thr Asp Asn Ser Asp Gln Ala Lys  
 50 55 60

Gln Gln Arg Leu Val Asp Ala Gly Ala Gln Val Ile Glu Val Glu Thr  
 65 70 75 80

Leu Thr Ala Glu Val Gly Val Glu Lys Leu Arg Ser Leu Gly Tyr Ala  
 85 90 95

Arg Ile Asp Cys Glu Gly Gly Ala Thr Leu Tyr Gly Gln Met Leu Ala  
 100 105 110

Ala Asp Leu Val Asp Val Trp His His Thr Ile Asp Pro Thr Leu Ser  
 115 120 125

Gly Ser Val Glu Arg Pro Thr Val Lys Gly Gly Asp Asp Ala Pro Arg  
 130 135 140

Arg Phe Ala Leu Glu His Val Phe Val Asp Asp Asp Ser Thr Leu Phe  
 145 150 155 160

Leu Arg Tyr Lys Arg Ala Lys  
 165

<210> 579  
 <211> 831  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(808)  
 <223> RXN02384

<400> 579  
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aatacgagcc tggctacgag gacgattaag aggtagtcct gtg act cgt cgc ctg 115  
 Val Thr Arg Arg Leu  
 1 5

att ctg ctc cga cac ggg cag act gaa tac aac gcc acg tcc cga atg 163  
 Ile Leu Leu Arg His Gly Gln Thr Glu Tyr Asn Ala Thr Ser Arg Met  
 10 15 20

cag gga caa ttg gac aca gag ctg tct gac ctg ggc ttt caa cag gcg 211  
 Gln Gly Gln Leu Asp Thr Glu Leu Ser Asp Leu Gly Phe Gln Gln Ala  
 25 30 35

gcc agc gca gcc tca gtg ctg gtt caa aaa aac atc acc cat gtg ttc 259  
 Ala Ser Ala Ala Ser Val Leu Val Gln Lys Asn Ile Thr His Val Phe  
 40 45 50

agc tcg gat ctt tcc cgc gcc ttc aac acc gca agc gcg gtt gcg gcg 307  
 Ser Ser Asp Leu Ser Arg Ala Phe Asn Thr Ala Ser Ala Val Ala Ala  
 55 60 65

ctg att gac gcg gag gtg cgc gtc gat aag cgt ctt cgg gaa acg cat 355  
 Leu Ile Asp Ala Glu Val Arg Val Asp Lys Arg Leu Arg Glu Thr His

70	75	80	85	
ttg ggt gag tgg cag gcc aaa acc cac act gag gtg gat tcc gaa tat				403
Leu Gly Glu Trp Gln Ala Lys Thr His Thr Glu Val Asp Ser Glu Tyr	90	95	100	
cca ggt gcg cgc gct caa tgg cgc cac gat ccg cag tgg gca cca ccc				451
Pro Gly Ala Arg Ala Gln Trp Arg His Asp Pro Gln Trp Ala Pro Pro	105	110	115	
ggc ggc gaa tcg cgc gtg gat gtt gcg cgc cgg gca cgc caa gtt gtc				499
Gly Gly Glu Ser Arg Val Asp Val Ala Arg Arg Ala Arg Gln Val Val	120	125	130	
gac gag ttg atg gtg tcg ctt gat gat tgg gat gaa ggc acc gtg ctc				547
Asp Glu Leu Met Val Ser Leu Asp Asp Trp Asp Glu Gly Thr Val Leu	135	140	145	
atc gtg gct cac ggt ggc acg att aat gcg ctg acc tcg aat ctt ttg				595
Ile Val Ala His Gly Gly Thr Ile Asn Ala Leu Thr Ser Asn Leu Leu	150	155	160	165
gac ctg gcg tat gat cag tac ccc atg ttc tct gga ctt gga aat acc				643
Asp Leu Ala Tyr Asp Gln Tyr Pro Met Phe Ser Gly Leu Gly Asn Thr	170	175	180	
tgt tgg gca caa ttg acc gcc cga cct cgc tat tat gca ggt agt gag				691
Cys Trp Ala Gln Leu Thr Ala Arg Pro Arg Tyr Tyr Ala Gly Ser Glu	185	190	195	
aac cca gaa gat gac ctc aag att tct tcg gcg gtt tcc aac agc cct				739
Asn Pro Glu Asp Asp Leu Lys Ile Ser Ser Ala Val Ser Asn Ser Pro	200	205	210	
cat ttt gag ggc aac aat gtg gaa aac gcc cag tgg tat ctt gac ggc				787
His Phe Glu Gly Asn Asn Val Glu Asn Ala Gln Trp Tyr Leu Asp Gly	215	220	225	
tgg aac atg ggt gtt acg cag taaagaagat ggcaataaaaa atg				831
Trp Asn Met Gly Val Thr Gln	230	235		

&lt;210&gt; 580

&lt;211&gt; 236

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 580

Val Thr Arg Arg Leu Ile Leu Leu Arg His Gly Gln Thr Glu Tyr Asn	
1 5 10 15	

Ala Thr Ser Arg Met Gln Gly Gln Leu Asp Thr Glu Leu Ser Asp Leu	
20 25 30	

Gly Phe Gln Gln Ala Ala Ser Ala Ala Ser Val Leu Val Gln Lys Asn	
35 40 45	

Ile Thr His Val Phe Ser Ser Asp Leu Ser Arg Ala Phe Asn Thr Ala	
50 55 60	

Ser Ala Val Ala Ala Leu Ile Asp Ala Glu Val Arg Val Asp Lys Arg  
 65 70 75 80  
 Leu Arg Glu Thr His Leu Gly Glu Trp Gln Ala Lys Thr His Thr Glu  
 85 90 95  
 Val Asp Ser Glu Tyr Pro Gly Ala Arg Ala Gln Trp Arg His Asp Pro  
 100 105 110  
 Gln Trp Ala Pro Pro Gly Gly Glu Ser Arg Val Asp Val Ala Arg Arg  
 115 120 125  
 Ala Arg Gln Val Val Asp Glu Leu Met Val Ser Leu Asp Asp Trp Asp  
 130 135 140  
 Glu Gly Thr Val Leu Ile Val Ala His Gly Gly Thr Ile Asn Ala Leu  
 145 150 155 160  
 Thr Ser Asn Leu Leu Asp Leu Ala Tyr Asp Gln Tyr Pro Met Phe Ser  
 165 170 175  
 Gly Leu Gly Asn Thr Cys Trp Ala Gln Leu Thr Ala Arg Pro Arg Tyr  
 180 185 190  
 Tyr Ala Gly Ser Glu Asn Pro Glu Asp Asp Leu Lys Ile Ser Ser Ala  
 195 200 205  
 Val Ser Asn Ser Pro His Phe Glu Gly Asn Asn Val Glu Asn Ala Gln  
 210 215 220  
 Trp Tyr Leu Asp Gly Trp Asn Met Gly Val Thr Gln  
 225 230 235

<210> 581  
 <211> 453  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(430)  
 <223> RXN01560

<400> 581  
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 tgcattcagta agcgatgcgt tttaggcaca tctgcgatcc gtg ggc gtg tcc tac 115  
 Val Gly Val Ser Tyr  
 1 5  
 atc atc gcc ggc gat gag cag ctg gat atg gca gaa gcc gtt cgc aaa 163  
 Ile Ile Ala Gly Asp Glu Gln Leu Asp Met Ala Glu Ala Val Arg Lys  
 10 15 20  
 att ggg gag acc ttt aaa act gag gaa att atc ctt ggt ggc gga gga 211  
 Ile Gly Glu Thr Phe Lys Thr Glu Glu Ile Ile Leu Gly Gly Gly Gly  
 25 30 35  
 acc ctg aac tgg tcc atg ctc cgc gac ggt ttg tgc gac gag gtt agc 259  
 Thr Leu Asn Trp Ser Met Leu Arg Asp Gly Leu Cys Asp Glu Val Ser

40	45	50	
atc gtg atg atg cca atc gcc gat ggt gaa aag cac acc cac tct ttg			307
Ile Val Met Met Pro Ile Ala Asp Gly Glu Lys His Thr His Ser Leu			
55	60	65	
ttc gaa gcc gat gaa aaa tac tca gca ccg ttg ccg atc ggt ttt tca			355
Phe Glu Ala Asp Glu Lys Tyr Ser Ala Pro Leu Pro Ile Gly Phe Ser			
70	75	80	85
ctc gcc agc gtt gaa cca cta gaa gat gga agc gtt tgg atg cgt tac			403
Leu Ala Ser Val Glu Pro Leu Glu Asp Gly Ser Val Trp Met Arg Tyr			
90	95	100	
ggg gtc aat ggc cca gtg gac gcg aac taggtagcaa atactcgctc			450
Gly Val Asn Gly Pro Val Asp Ala Asn			
105	110		
ttt			453

<210> 582  
 <211> 110  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 582  
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 1 5 10 15  
 Glu Ala Val Arg Lys Ile Gly Glu Thr Phe Lys Thr Glu Glu Ile Ile  
 20 25 30  
 Leu Gly Gly Gly Gly Thr Leu Asn Trp Ser Met Leu Arg Asp Gly Leu  
 35 40 45  
 Cys Asp Glu Val Ser Ile Val Met Met Pro Ile Ala Asp Gly Glu Lys  
 50 55 60  
 His Thr His Ser Leu Phe Glu Ala Asp Glu Lys Tyr Ser Ala Pro Leu  
 65 70 75 80  
 Pro Ile Gly Phe Ser Leu Ala Ser Val Glu Pro Leu Glu Asp Gly Ser  
 85 90 95  
 Val Trp Met Arg Tyr Gly Val Asn Gly Pro Val Asp Ala Asn  
 100 105 110

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tcc Ser	atg Met	tct Ser	aac Asn 10	agg Arg	gta Val	gta Val	caa Gln	aag Lys	cca Pro 15	aaa Lys	atg Met	aaa Lys	gcg Ala	ccg Pro 20	cta Leu	163
ccc Pro	atc Ile	cgc Arg	gac Asp 25	ggc Gly	ctc Leu	aac Asn	cct Pro	tcc Ser 30	cgt Arg	gtg Val	cgc Arg	ttg Leu	ccg Pro 35	ctc Leu	gac Asp	211
gcg Ala	gcg Ala	ccg Pro 40	atc Ile	cgc Arg	gcc Ala	atc Ile	gat Asp 45	ttt Phe	gtt Val	gaa Glu	tac Tyr	ctc Leu 50	att Ile	tcc Ser	acg Thr	259
cag Gln	cgc Arg 55	cac His	cgc Arg	aat Asn	ccg Pro	gcc Ala 60	gac Asp	aac Asn	gcc Ala	gaa Glu	gcg Ala 65	ctt Leu	caa Gln	gcg Ala	cgt Arg	307
ttc Phe 70	gac Asp	gcc Ala	gac Asp	ctt Leu	gtt Val 75	gtc Val	aac Asn	cac His	tac Tyr	ggc Gly 80	gag Glu	ccc Pro	tac Tyr	gcc Ala	ccc Pro 85	355
gac Asp	acc Thr	atg Met	gtt Val	cag Gln 90	ccc Pro	gac Asp	gac Asp	gac Asp	att Ile 95	tgg Trp	ttc Phe	tac Tyr	cgc Arg	atg Met 100	ccc Pro	403
gcc Ala	gcc Ala	gaa Glu	cgg Arg 105	ccg Pro	atc Ile	cct Pro	tac Tyr	aaa Lys 110	att Ile	cat His	gtc Val	att Ile	cac His 115	gaa Glu	gac Asp	451
gat Asp	gac Asp	atc Ile 120	ctc Leu	gtc Val	att Ile	gac Asp	aag Lys 125	cca Pro	ccc Pro	tac Tyr	cta Leu	gca Ala 130	acc Thr	atg Met	cct Pro	499
cgt Arg	ggc Gly 135	cgc Arg	cac His	atc Ile	acc Thr	gaa Glu 140	acc Thr	gct Ala	ctg Leu	gtg Val	aaa Lys 145	atg Met	cgt Arg	gtg Val	ctg Leu	547
act Thr 150	gga Gly	aac Asn	aac Asn	gat Asp	ctc Leu 155	acc Thr	cca Pro	gct Ala	cac His	cgc Arg 160	ctc Leu	gat Asp	cgc Arg	ctg Leu	act Thr 165	595
tcc Ser	ggc Gly	gtg Val	tta Leu	gtc Val 170	atg Met	gtg Val	aaa Lys	aaa Lys	cca Pro 175	gaa Glu	ctc Leu	cgt Arg	ggc Gly 180	gct Ala	tac Tyr	643
caa Gln	acc Thr	ttg Leu	ttt Phe 185	gcc Ala	cga Arg	cgt Arg	gag Glu	gcg Ala 190	tcc Ser	aaa Lys	acc Thr	tat Tyr	gag Glu 195	gca Ala	atc Ile	691
gca Ala	gaa Glu	ttc Phe 200	gtt Val	cca Pro	ggg Gly	cta Leu	ctt Leu 205	gat Asp	gat Asp	ggc Gly	ccc Pro	gcg Ala 210	att Ile	tgg Trp	gaa Glu	739
tcc Ser	cgc Arg 215	atc Ile	gaa Glu	aaa Lys	gaa Glu	cgc Arg 220	ggc Gly	atc Ile	gtg Val	caa Gln	gcc Ala 225	ttc Phe	gtc Val	gtg Val	gaa Glu	787

ggc ccc gtc aac gca cgc act gaa ctg gtg tca gtc acc cca gtc gaa 835  
 Gly Pro Val Asn Ala Arg Thr Glu Leu Val Ser Val Thr Pro Val Glu  
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gac gcc gaa cag agc atc ctc gaa gaa atg cac ggg cca ctc ccc cgc 883  
 Asp Ala Glu Gln Ser Ile Leu Glu Glu Met His Gly Pro Leu Pro Arg  
 250 255 260

caa gcg cgc tac gtt cta gcc ccc tca aca ggc aaa acc cac cag ctg 931  
 Gln Ala Arg Tyr Val Leu Ala Pro Ser Thr Gly Lys Thr His Gln Leu  
 265 270 275

cgc atc cac atg cgc gac ttc gca gcc ccc atc ctc ggc gac ccc ctc 979  
 Arg Ile His Met Arg Asp Phe Ala Ala Pro Ile Leu Gly Asp Pro Leu  
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 Tyr Pro Val Leu His Ala Val Asp Asp Glu Asp Tyr Thr Thr Pro Met  
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 His Leu Ile Ala Arg Thr Leu Thr Phe Val Asp Pro Gln Thr Asn Glu  
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<400> 584

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Tyr Leu Ile Ser Thr Gln Arg His Arg Asn Pro Ala Asp Asn Ala Glu  
 50 55 60

Ala Leu Gln Ala Arg Phe Asp Ala Asp Leu Val Val Asn His Tyr Gly  
 65 70 75 80

Glu Pro Tyr Ala Pro Asp Thr Met Val Gln Pro Asp Asp Asp Ile Trp  
 85 90 95

Phe Tyr Arg Met Pro Ala Ala Glu Arg Pro Ile Pro Tyr Lys Ile His  
 100 105 110



Val Ile His Glu Asp Asp Asp Ile Leu Val Ile Asp Lys Pro Pro Tyr  
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 Leu Ala Thr Met Pro Arg Gly Arg His Ile Thr Glu Thr Ala Leu Val  
 130 135 140  
 Lys Met Arg Val Leu Thr Gly Asn Asn Asp Leu Thr Pro Ala His Arg  
 145 150 155 160  
 Leu Asp Arg Leu Thr Ser Gly Val Leu Val Met Val Lys Lys Pro Glu  
 165 170 175  
 Leu Arg Gly Ala Tyr Gln Thr Leu Phe Ala Arg Arg Glu Ala Ser Lys  
 180 185 190  
 Thr Tyr Glu Ala Ile Ala Glu Phe Val Pro Gly Leu Leu Asp Asp Gly  
 195 200 205  
 Pro Ala Ile Trp Glu Ser Arg Ile Glu Lys Glu Arg Gly Ile Val Gln  
 210 215 220  
 Ala Phe Val Val Glu Gly Pro Val Asn Ala Arg Thr Glu Leu Val Ser  
 225 230 235 240  
 Val Thr Pro Val Glu Asp Ala Glu Gln Ser Ile Leu Glu Glu Met His  
 245 250 255  
 Gly Pro Leu Pro Arg Gln Ala Arg Tyr Val Leu Ala Pro Ser Thr Gly  
 260 265 270  
 Lys Thr His Gln Leu Arg Ile His Met Arg Asp Phe Ala Ala Pro Ile  
 275 280 285  
 Leu Gly Asp Pro Leu Tyr Pro Val Leu His Ala Val Asp Asp Glu Asp  
 290 295 300  
 Tyr Thr Thr Pro Met His Leu Ile Ala Arg Thr Leu Thr Phe Val Asp  
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 Ser Leu

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His	Arg	Phe	Phe	Val	Leu	Ala	Ile	Asn	Gly	Ala	Val	Thr	Asp	Asp	Phe		
				10					15					20			
acg	acg	gtt	tat	agt	gct	tta	cga	cgt	ttc	gtt	gaa	ggc	att	ccg	gtc		211
Thr	Thr	Val	Tyr	Ser	Ala	Leu	Arg	Arg	Phe	Val	Glu	Gly	Ile	Pro	Val		
			25					30					35				
tac	aac	gag	gtc	tac	cac	ttc	gtc	gat	ccg	cac	tac	ctc	tat	aac	ccg		259
Tyr	Asn	Glu	Val	Tyr	His	Phe	Val	Asp	Pro	His	Tyr	Leu	Tyr	Asn	Pro		
		40					45					50					
ggc	gcc	acc	ctc	cta	ttg	gca	cca	ttg	gga	tat	atc	acc	cat	ttc	acg		307
Gly	Ala	Thr	Leu	Leu	Leu	Ala	Pro	Leu	Gly	Tyr	Ile	Thr	His	Phe	Thr		
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ttg	gct	cgg	tgg	atg	ttc	atc	gcg	gtg	aac	ctc	ctt	gcc	att	gtt	tta		355
Leu	Ala	Arg	Trp	Met	Phe	Ile	Ala	Val	Asn	Leu	Leu	Ala	Ile	Val	Leu		
70					75					80					85		
gcg	ttc	ggg	ctg	ctg	acc	aga	ctc	tcc	ggc	tgg	gcg	ctg	cgc	agc	atg		403
Ala	Phe	Gly	Leu	Leu	Thr	Arg	Leu	Ser	Gly	Trp	Ala	Leu	Arg	Ser	Met		
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gtg	tgg	ccg	att	gcg	atc	gcc	ttg	gcg	atg	ctg	aca	gaa	acc	gtg	caa		451
Val	Trp	Pro	Ile	Ala	Ile	Ala	Leu	Ala	Met	Leu	Thr	Glu	Thr	Val	Gln		
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aac	acc	ctc	att	ttc	tcc	aac	atc	aac	ggc	atc	ctg	ctg	ctc	atg	ttg		499
Asn	Thr	Leu	Ile	Phe	Ser	Asn	Ile	Asn	Gly	Ile	Leu	Leu	Leu	Met	Leu		
		120					125					130					
gcg	att	ttc	ctg	tgg	tgc	gtg	gtg	cac	aaa	aaa	tcc	tgg	ttg	ggc	gga		547
Ala	Ile	Phe	Leu	Trp	Cys	Val	Val	His	Lys	Lys	Ser	Trp	Leu	Gly	Gly		
	135					140					145						
cta	gtc	att	ggc	ttg	gcc	att	ttg	atc	aaa	ccc	atg	ttc	ctg	cca	ctt		595
Leu	Val	Ile	Gly	Leu	Ala	Ile	Leu	Ile	Lys	Pro	Met	Phe	Leu	Pro	Leu		
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ctc	ttc	cta	cct	ttg	gtg	aaa	aag	caa	tgg	gga	tcg	ctc	atc	ctc	ggc		643
Leu	Phe	Leu	Pro	Leu	Val	Lys	Lys	Gln	Trp	Gly	Ser	Leu	Ile	Leu	Gly		
			170						175					180			
att	tta	acc	cca	gtg	att	ttc	aat	gca	gtg	gcc	tgg	ttc	tta	gtt	ccg		691
Ile	Leu	Thr	Pro	Val	Ile	Phe	Asn	Ala	Val	Ala	Trp	Phe	Leu	Val	Pro		
			185				190						195				
gga	gca	tct	gaa	tac	gtc	acc	cgc	acg	atg	ccc	tac	ctt	ggc	gaa	act		739
Gly	Ala	Ser	Glu	Tyr	Val	Thr	Arg	Thr	Met	Pro	Tyr	Leu	Gly	Glu	Thr		
		200					205					210					
cga	gat	ttt	gcc	aac	agc	tca	ctc	cca	ggc	ttg	gcc	atc	tat	ttc	gga		787
Arg	Asp	Phe	Ala	Asn	Ser	Ser	Leu	Pro	Gly	Leu	Ala	Ile	Tyr	Phe	Gly		
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atg	ccc	acc	tgg	atg	gaa	atc	acc	tgg	ttc	ctc	atc	ttc	ggc	gca	atg		835
Met	Pro	Thr	Trp	Met	Glu	Ile	Thr	Trp	Phe	Leu	Ile	Phe	Gly	Ala	Met		

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gtc ggc ctc gca gtg ctg gca ctc ctg aga ttc cgt aac acc gag cca				883
Val Gly Leu Ala Val Leu Ala Leu Leu Arg Phe Arg Asn Thr Glu Pro	250	255	260	
tac ttc tgg gca gca acc acc acc ggt gta ctc ctg act ggc gta ttc				931
Tyr Phe Trp Ala Ala Thr Thr Thr Gly Val Leu Leu Thr Gly Val Phe	265	270	275	
ttc ctg tcc tca ctg gga cag atg tac tac tcc atg atg atc ttc cct				979
Phe Leu Ser Ser Leu Gly Gln Met Tyr Tyr Ser Met Met Ile Phe Pro	280	285	290	
atg atc ttc acc ctg ctc gga agc cga tcc gta ttc cac aac tgg gtt				
1027 Met Ile Phe Thr Leu Leu Gly Ser Arg Ser Val Phe His Asn Trp Val	295	300	305	
gcc tgg gtc gcc gcc tac ttc tta cta tcc cct gac act ttc acc tcc				
1075 Ala Trp Val Ala Ala Tyr Phe Leu Leu Ser Pro Asp Thr Phe Thr Ser	310	315	320	325
cag cga cta ccc gat gta gcc cgc tgg atg gaa ttt ttc agc gcg acc				
1123 Gln Arg Leu Pro Asp Val Ala Arg Trp Met Glu Phe Phe Ser Ala Thr	330	335	340	
gtt ggt tgg gga cta ttg ata gtg gtt aca ttt gtc tcg gcg cta atc				
1171 Val Gly Trp Gly Leu Leu Ile Val Val Thr Phe Val Ser Ala Leu Ile	345	350	355	
tgg ttt att ggt gat atc cga gcc aag gga act ccg agc tca ccc att				
1219 Trp Phe Ile Gly Asp Ile Arg Ala Lys Gly Thr Pro Ser Ser Pro Ile	360	365	370	
acc act gat cca acg cac gac cat ctt gag agg aca gca tgacagactt				
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Val Thr Asp Asp Phe Thr Thr Val Tyr Ser Ala Leu Arg Arg Phe Val	20	25	30	
Glu Gly Ile Pro Val Tyr Asn Glu Val Tyr His Phe Val Asp Pro His				

35					40					45					
Tyr	Leu	Tyr	Asn	Pro	Gly	Ala	Thr	Leu	Leu	Leu	Ala	Pro	Leu	Gly	Tyr
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Ile	Thr	His	Phe	Thr	Leu	Ala	Arg	Trp	Met	Phe	Ile	Ala	Val	Asn	Leu
65					70					75					80
Leu	Ala	Ile	Val	Leu	Ala	Phe	Gly	Leu	Leu	Thr	Arg	Leu	Ser	Gly	Trp
				85					90					95	
Ala	Leu	Arg	Ser	Met	Val	Trp	Pro	Ile	Ala	Ile	Ala	Leu	Ala	Met	Leu
			100					105					110		
Thr	Glu	Thr	Val	Gln	Asn	Thr	Leu	Ile	Phe	Ser	Asn	Ile	Asn	Gly	Ile
		115					120					125			
Leu	Leu	Leu	Met	Leu	Ala	Ile	Phe	Leu	Trp	Cys	Val	Val	His	Lys	Lys
	130					135					140				
Ser	Trp	Leu	Gly	Gly	Leu	Val	Ile	Gly	Leu	Ala	Ile	Leu	Ile	Lys	Pro
145					150					155					160
Met	Phe	Leu	Pro	Leu	Leu	Phe	Leu	Pro	Leu	Val	Lys	Lys	Gln	Trp	Gly
				165					170					175	
Ser	Leu	Ile	Leu	Gly	Ile	Leu	Thr	Pro	Val	Ile	Phe	Asn	Ala	Val	Ala
			180					185					190		
Trp	Phe	Leu	Val	Pro	Gly	Ala	Ser	Glu	Tyr	Val	Thr	Arg	Thr	Met	Pro
		195					200					205			
Tyr	Leu	Gly	Glu	Thr	Arg	Asp	Phe	Ala	Asn	Ser	Ser	Leu	Pro	Gly	Leu
	210					215					220				
Ala	Ile	Tyr	Phe	Gly	Met	Pro	Thr	Trp	Met	Glu	Ile	Thr	Trp	Phe	Leu
225					230					235					240
Ile	Phe	Gly	Ala	Met	Val	Gly	Leu	Ala	Val	Leu	Ala	Leu	Leu	Arg	Phe
				245					250					255	
Arg	Asn	Thr	Glu	Pro	Tyr	Phe	Trp	Ala	Ala	Thr	Thr	Thr	Gly	Val	Leu
			260					265					270		
Leu	Thr	Gly	Val	Phe	Phe	Leu	Ser	Ser	Leu	Gly	Gln	Met	Tyr	Tyr	Ser
		275					280					285			
Met	Met	Ile	Phe	Pro	Met	Ile	Phe	Thr	Leu	Leu	Gly	Ser	Arg	Ser	Val
	290					295					300				
Phe	His	Asn	Trp	Val	Ala	Trp	Val	Ala	Ala	Tyr	Phe	Leu	Leu	Ser	Pro
305					310					315					320
Asp	Thr	Phe	Thr	Ser	Gln	Arg	Leu	Pro	Asp	Val	Ala	Arg	Trp	Met	Glu
				325					330					335	
Phe	Phe	Ser	Ala	Thr	Val	Gly	Trp	Gly	Leu	Leu	Ile	Val	Val	Thr	Phe
			340					345					350		
Val	Ser	Ala	Leu	Ile	Trp	Phe	Ile	Gly	Asp	Ile	Arg	Ala	Lys	Gly	Thr
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Thr Ala  
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 Met Thr Thr Thr Val  
 1 5

aaa cgc cgc gct cgc att ggc atc atg ggt ggc aca ttt gac ccc att 163  
 Lys Arg Arg Ala Arg Ile Gly Ile Met Gly Gly Thr Phe Asp Pro Ile  
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cat aat ggt cac ctt gtg gcg ggc tca gag gta gcg gat cga ttc gat 211  
 His Asn Gly His Leu Val Ala Gly Ser Glu Val Ala Asp Arg Phe Asp  
 25 30 35

ctt gat ctg gtg gtg tac gtt ccc acc gga cag cca tgg caa aag gcg 259  
 Leu Asp Leu Val Val Tyr Val Pro Thr Gly Gln Pro Trp Gln Lys Ala  
 40 45 50

aac aag aaa gtc agc cca gcg gaa gat cgt tac ctg atg acg gtg atc 307  
 Asn Lys Lys Val Ser Pro Ala Glu Asp Arg Tyr Leu Met Thr Val Ile  
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 Ala Thr Ala Ser Asn Pro Arg Phe Met Val Ser Arg Val Asp Ile Asp  
 70 75 80 85

cgg gga ggg gat act tac acg atc gat acc ctg caa gat ttg agc aag 403  
 Arg Gly Gly Asp Thr Tyr Thr Ile Asp Thr Leu Gln Asp Leu Ser Lys  
 90 95 100

caa tac ccg gac gcc cag ctg tac ttc atc acc ggt gcc gat gca ctg 451  
 Gln Tyr Pro Asp Ala Gln Leu Tyr Phe Ile Thr Gly Ala Asp Ala Leu  
 105 110 115

gca cag atc gtg acg tgg cgc gat tgg gag aaa acc ttc gaa ctt gcc 499  
 Ala Gln Ile Val Thr Trp Arg Asp Trp Glu Lys Thr Phe Glu Leu Ala  
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cac ttc gtt gga gtg act cga ccc ggt tat gaa ttg gat gga aac atc 547  
 His Phe Val Gly Val Thr Arg Pro Gly Tyr Glu Leu Asp Gly Asn Ile  
 135 140 145

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 Ile Pro Glu Met His Gln Asp Arg Val Ser Leu Val Asp Ile Pro Ala  
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 Met Ala Ile Ser Ser Thr Asp Cys Arg Glu Arg Ser Ser Glu Glu Arg  
 170 175 180  
  
 cct gtt tgg tat ctt gtc cct gat ggc gtg gtg caa tac att gcc aaa 691  
 Pro Val Trp Tyr Leu Val Pro Asp Gly Val Val Gln Tyr Ile Ala Lys  
 185 190 195  
  
 cgc caa ctc tat cga cct gaa gga tcc gat aag gat atg gat ccc aag 739  
 Arg Gln Leu Tyr Arg Pro Glu Gly Ser Asp Lys Asp Met Asp Pro Lys  
 200 205 210  
  
 ggc caa aac caa gca taaatctagt caaaagtttc aac 777  
 Gly Gln Asn Gln Ala  
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&lt;210&gt; 588

&lt;211&gt; 218

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 588

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 Thr Phe Asp Pro Ile His Asn Gly His Leu Val Ala Gly Ser Glu Val  
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 Ala Asp Arg Phe Asp Leu Asp Leu Val Val Tyr Val Pro Thr Gly Gln  
 35 40 45  
  
 Pro Trp Gln Lys Ala Asn Lys Lys Val Ser Pro Ala Glu Asp Arg Tyr  
 50 55 60  
  
 Leu Met Thr Val Ile Ala Thr Ala Ser Asn Pro Arg Phe Met Val Ser  
 65 70 75 80  
  
 Arg Val Asp Ile Asp Arg Gly Gly Asp Thr Tyr Thr Ile Asp Thr Leu  
 85 90 95  
  
 Gln Asp Leu Ser Lys Gln Tyr Pro Asp Ala Gln Leu Tyr Phe Ile Thr  
 100 105 110  
  
 Gly Ala Asp Ala Leu Ala Gln Ile Val Thr Trp Arg Asp Trp Glu Lys  
 115 120 125  
  
 Thr Phe Glu Leu Ala His Phe Val Gly Val Thr Arg Pro Gly Tyr Glu  
 130 135 140  
  
 Leu Asp Gly Asn Ile Ile Pro Glu Met His Gln Asp Arg Val Ser Leu  
 145 150 155 160  
  
 Val Asp Ile Pro Ala Met Ala Ile Ser Ser Thr Asp Cys Arg Glu Arg  
 165 170 175  
  
 Ser Ser Glu Glu Arg Pro Val Trp Tyr Leu Val Pro Asp Gly Val Val

180	185	190
Gln Tyr Ile Ala Lys Arg Gln Leu Tyr Arg Pro Glu Gly Ser Asp Lys		
195	200	205
Asp Met Asp Pro Lys Gly Gln Asn Gln Ala		
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&lt;210&gt; 589

&lt;211&gt; 777

&lt;212&gt; DNA

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&lt;220&gt;

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&lt;222&gt; (101)..(754)

&lt;223&gt; FRXA02380

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Met Thr Thr Thr Val
1 5

aaa cgc cgc gct cgc att ggc atc atg ggt ggc aca ttt gac ccc att 163
Lys Arg Arg Ala Arg Ile Gly Ile Met Gly Gly Thr Phe Asp Pro Ile
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cat aat ggt cac ctt gtg gcg ggc tca gag gta gcg gat cga ttc gat 211
His Asn Gly His Leu Val Ala Gly Ser Glu Val Ala Asp Arg Phe Asp
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ctt gat ctg gtg gtg tac gtt ccc acc gga cag cca tgg caa aag gcg 259
Leu Asp Leu Val Val Tyr Val Pro Thr Gly Gln Pro Trp Gln Lys Ala
40 45 50

aac aag aaa gtc agc cca gcg gaa gat cgt tac ctg atg acg gtg atc 307
Asn Lys Lys Val Ser Pro Ala Glu Asp Arg Tyr Leu Met Thr Val Ile
55 60 65

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Ala Thr Ala Ser Asn Pro Arg Phe Met Val Ser Arg Val Asp Ile Asp
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cgg gga ggg gat act tac acg atc gat acc ctg caa gat ttg agc aag 403
Arg Gly Gly Asp Thr Tyr Thr Ile Asp Thr Leu Gln Asp Leu Ser Lys
90 95 100

caa tac ccg gac gcc cag ctg tac ttc atc acc ggt gcc gat gca ctg 451
Gln Tyr Pro Asp Ala Gln Leu Tyr Phe Ile Thr Gly Ala Asp Ala Leu
105 110 115

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Ala Gln Ile Val Thr Trp Arg Asp Trp Glu Lys Thr Phe Glu Leu Ala
120 125 130

cac ttc gtt gga gtg act cga ccc ggt tat gaa ttg gat gga aac atc 547
His Phe Val Gly Val Thr Arg Pro Gly Tyr Glu Leu Asp Gly Asn Ile
135 140 145

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 Met Ala Ile Ser Ser Thr Asp Cys Arg Glu Arg Ser Ser Glu Glu Arg  
 170 175 180  
  
 cct gtt tgg tat ctt gtc cct gat ggc gtg gtg caa tac att gcc aaa 691  
 Pro Val Trp Tyr Leu Val Pro Asp Gly Val Val Gln Tyr Ile Ala Lys  
 185 190 195  
  
 cgc caa ctc tat cga cct gaa gga tcc gat aag gat atg gat ccc aag 739  
 Arg Gln Leu Tyr Arg Pro Glu Gly Ser Asp Lys Asp Met Asp Pro Lys  
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&lt;211&gt; 218

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 590

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 Ala Asp Arg Phe Asp Leu Asp Leu Val Val Tyr Val Pro Thr Gly Gln  
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 Pro Trp Gln Lys Ala Asn Lys Lys Val Ser Pro Ala Glu Asp Arg Tyr  
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 Leu Met Thr Val Ile Ala Thr Ala Ser Asn Pro Arg Phe Met Val Ser  
 65 70 75 80  
  
 Arg Val Asp Ile Asp Arg Gly Gly Asp Thr Tyr Thr Ile Asp Thr Leu  
 85 90 95  
  
 Gln Asp Leu Ser Lys Gln Tyr Pro Asp Ala Gln Leu Tyr Phe Ile Thr  
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 Gly Ala Asp Ala Leu Ala Gln Ile Val Thr Trp Arg Asp Trp Glu Lys  
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 Thr Phe Glu Leu Ala His Phe Val Gly Val Thr Arg Pro Gly Tyr Glu  
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 Leu Asp Gly Asn Ile Ile Pro Glu Met His Gln Asp Arg Val Ser Leu  
 145 150 155 160  
  
 Val Asp Ile Pro Ala Met Ala Ile Ser Ser Thr Asp Cys Arg Glu Arg  
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Ser Ser Glu Glu Arg Pro Val Trp Tyr Leu Val Pro Asp Gly Val Val  
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Gln Tyr Ile Ala Lys Arg Gln Leu Tyr Arg Pro Glu Gly Ser Asp Lys  
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 Val Ser Ala Leu Glu  
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 Glu Ser Ile Arg Ile Ala Thr Ile Ala Ala Lys Ala Ala Asp Glu Lys  
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aag gcc gat gac atc gct gtc atc gat gtc tct gac atg atc gca atc 211  
 Lys Ala Asp Asp Ile Ala Val Ile Asp Val Ser Asp Met Ile Ala Ile  
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 Thr Asp Cys Phe Val Val Ala Ser Ala Asp Asn Glu Arg Gln Val Gly  
 40 45 50

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 Ala Ile Val Glu Glu Ile Glu Asp Glu Met Thr Lys Ala Gly Phe Glu  
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 Pro Lys Arg Arg Glu Gly Asn Arg Glu Asn Arg Trp Val Leu Leu Asp  
 70 75 80 85

tac gga ttg gtt gtt atc cac gtt cag cga cag gca gag cgc gag ttc 403  
 Tyr Gly Leu Val Val Ile His Val Gln Arg Gln Ala Glu Arg Glu Phe  
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tac gga ctg gat cgt ctg tac cgc gac tgc cca ctc att gaa att gaa 451  
 Tyr Gly Leu Asp Arg Leu Tyr Arg Asp Cys Pro Leu Ile Glu Ile Glu  
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gga ctt gaa acc ttc aag cgt gaa tcc tcc tgg tct gat gag gcg gat 499  
 Gly Leu Glu Thr Phe Lys Arg Glu Ser Ser Trp Ser Asp Glu Ala Asp  
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 Ile Arg Asn Ile Asp Ser Ile Asp Glu Leu Pro Pro Leu Pro Ala Glu

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 Glu Arg Gln Val Gly Ala Ile Val Glu Glu Ile Glu Asp Glu Met Thr  
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 Lys Ala Gly Phe Glu Pro Lys Arg Arg Glu Gly Asn Arg Glu Asn Arg  
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 Trp Val Leu Leu Asp Tyr Gly Leu Val Val Ile His Val Gln Arg Gln  
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 Ala Glu Arg Glu Phe Tyr Gly Leu Asp Arg Leu Tyr Arg Asp Cys Pro  
 100 105 110  
 Leu Ile Glu Ile Glu Gly Leu Glu Thr Phe Lys Arg Glu Ser Ser Trp  
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 Val Leu Gly Ala Val  
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Ala	Asp	Gly	Gly	Ser	Gly	Phe	Phe	Arg	Arg	Leu	Leu	Thr	Leu	Ser	Val	
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Leu	Thr	Arg	Met	Met	Leu	Ser	Ser	Glu	Gly	Gln	Val	Asn	Val	Val	Met	
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Leu	Phe	Ala	Leu	Phe	Met	Ala	Val	Leu	Asn	Thr	Arg	Glu	Val	Phe	Lys	
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Pro	Gly	Ala	Trp	Ala	Pro	Val	Val	Asn	Asn	Val	Ile	Thr	Leu	Thr	Val	
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Leu	Gly	Val	Tyr	Met	Val	Leu	Pro	Ala	Arg	Leu	His	Pro	His	Glu	Gln	
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Val	Gly	Ile	Phe	Asp	Pro	Gln	Ile	Ile	Phe	Leu	Gly	Val	Gly	Thr	Thr	
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Leu	Gly	Val	Val	Ala	Gln	Cys	Leu	Ile	Met	Ile	Pro	Tyr	Leu	Arg	Arg	
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Gln	Phe	Gly	Gly	Met	Ala	Met	Ala	Ile	Ile	Val	Tyr	Val	Ala	Ile	Ser	
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Gln	Phe	Gly	Tyr	Ile	Ile	Thr	Thr	Arg	Ile	Ala	Ser	Ile	Ala	Asp	Asp	
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gct	gcg	ccg	ttt	att	tat	cag	cag	cac	tgg	atg	ttg	ctg	caa	gtt	cct	787
Ala	Ala	Pro	Phe	Ile	Tyr	Gln	Gln	His	Trp	Met	Leu	Leu	Gln	Val	Pro	
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tat	ggc	atc	atc	ggc	gtc	acc	ttg	ctc	acc	gcg	att	atg	ccg	cga	ctg	835
Tyr	Gly	Ile	Ile	Gly	Val	Thr	Leu	Leu	Thr	Ala	Ile	Met	Pro	Arg	Leu	
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Ser	Arg	Asn	Ala	Ala	Asp	Gly	Asp	Asp	Arg	Ala	Val	Val	Ser	Asp	Leu	
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cag	ttg	ggt	tcc	aag	cta	acc	ttc	atc	gca	ctg	atc	ccc	atc	gtg	gtg	931
Gln	Leu	Gly	Ser	Lys	Leu	Thr	Phe	Ile	Ala	Leu	Ile	Pro	Ile	Val	Val	
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Phe	Phe	Thr	Ala	Phe	Gly	Val	Pro	Ile	Ala	Asn	Gly	Leu	Phe	Ala	Tyr	
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Trp	Ala	Leu	Gly	Ser	Ala	Ala	Val	Gly	Ala	Ala	Ala	Ala	Trp	Ala	Leu	
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ggg	tgg	ctg	att	caa	gcc	gtc	gtg	ggc	gat	ttc	ttg	ctg	ggc	act	cta	
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agc	tcc	gta	ggc	tac	ttg	ttg	aac	ctg	gct	gtg	ttg	ggt	gtc	ttc	ttc	
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 Ile Phe Val Thr Gly Ile Val Leu Ser Arg Ser Gly Leu Pro Glu Val  
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caa aac ttg ggc cag gca ctg acc cgc atc cca ggt ttg agc cgg ttt  
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 Gln Asn Leu Gly Gln Ala Leu Thr Arg Ile Pro Gly Leu Ser Arg Phe  
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att cgc ccg aat acc aag atc tct ttg gat gtc ggc gaa gtc tcc gag  
 1603  
 Ile Arg Pro Asn Thr Lys Ile Ser Leu Asp Val Gly Glu Val Ser Glu  
 490 495 500

cag gat ttc tcc acc cag ctg gtc gcg cca agc gag ttc gca gca acc  
 1651  
 Gln Asp Phe Ser Thr Gln Leu Val Ala Pro Ser Glu Phe Ala Ala Thr  
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cct gtg ccg cca ccg atg tcc gcc ggt att gtc cgc gga cct cgc ctg  
 1699  
 Pro Val Pro Pro Pro Met Ser Ala Gly Ile Val Arg Gly Pro Arg Leu  
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gtt ccc ggc gcc cca gtc ggc gac ggt cgt ttc cgt ctg ctc gcc gat  
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 Val Pro Gly Ala Pro Val Gly Asp Gly Arg Phe Arg Leu Leu Ala Asp  
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 570 575 580

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 Pro Phe Ala Pro Leu Ser Ser Ala Ala Ala Ala Gly Ile Ala Tyr Glu  
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 2083  
 Ala Asp Pro Arg Ala Ala Ala Phe Ala Leu Ala Glu Leu Thr Glu Thr  
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 2131  
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 Cys Arg Ile Arg Ile Asn Thr Asp Gly His Ala Val Leu Ala Leu Pro  
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gcg att ttg ccc gat gcc tca gag ctc cgc gac gcc aag tcc ctg gcc  
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 Ala Ile Leu Pro Asp Ala Ser Glu Leu Arg Asp Ala Lys Ser Leu Ala  
 695 700 705

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 2275  
 Ser Ala Ala Glu Met Leu Ile Asp Ala Thr Leu Ala Pro Ser Asp Val  
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 760 765 770

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gca gcc atc gcc gct gtg gtg atc atc ttg gtt tcc ctg gtg gcc gcc  
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 Ser Pro Leu Ala Ser Val Glu Ala Thr Thr Ser Ala Thr Pro Glu Pro  
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2659

Val Gly Pro Pro Val Tyr Leu Asp Leu Asp Gln Ala Arg Thr Trp Asp  
840 845 850

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Asp Gly Ala Gly Thr Asp Val Thr Asp Val Thr Asp Gly Asn Thr Ser  
855 860 865

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2755

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870 875 880 885

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2899

Ser Pro His Ser Leu Ser Glu Gly Ile Glu Ile Gly Thr Val Asp Tyr  
920 925 930

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2947

Ser Gly Arg Ser Leu Ser His Ser Ile Arg Asp Ser Ser Lys Leu Pro  
935 940 945

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2995

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950 955 960 965

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3043

Gln Thr Ser Asp Thr Asn Pro Gln Met Gln Ile Ala Glu Val Gln Leu  
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Val Gly Trp

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<211> 984

<212> PRT

<213> Corynebacterium glutamicum

<400> 594

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His	Pro	His	Glu	Gln	Val	Gly	Ile	Phe	Asp	Pro	Gln	Ile	Ile	Phe	Leu
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Pro	Tyr	Leu	Arg	Arg	Ala	Gly	Ile	Asp	Met	Arg	Pro	Leu	Trp	Gly	Ile
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Tyr	Val	Ala	Ile	Ser	Gln	Phe	Gly	Tyr	Ile	Ile	Thr	Thr	Arg	Ile	Ala
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Ile	Met	Pro	Arg	Leu	Ser	Arg	Asn	Ala	Ala	Asp	Gly	Asp	Asp	Arg	Ala
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Val	Val	Ser	Asp	Leu	Gln	Leu	Gly	Ser	Lys	Leu	Thr	Phe	Ile	Ala	Leu
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	290					295					300				
Gly	Trp	Thr	Leu	Ser	Phe	Ser	Ala	Phe	Thr	Leu	Ile	Pro	Tyr	Ala	Leu
	305					310					315				320
Val	Leu	Leu	His	Leu	Arg	Val	Phe	Tyr	Ala	Arg	Glu	Glu	Val	Trp	Thr
				325					330					335	
Pro	Thr	Phe	Ile	Ile	Ala	Gly	Ile	Thr	Ala	Thr	Lys	Val	Val	Leu	Ser
			340					345					350		



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 355 360 365  
 Leu Gly Ala Ala Asn Gly Phe Ser Phe Ile Thr Gly Ala Val Ile Gly  
 370 375 380  
 Ala Tyr Leu Leu Arg Asn Lys Leu Gly Leu Leu Gly Met Arg Ser Leu  
 385 390 395 400  
 Ala Lys Thr Ser Leu Trp Ala Leu Gly Ser Ala Ala Val Gly Ala Ala  
 405 410 415  
 Ala Ala Trp Ala Leu Gly Trp Leu Ile Gln Ala Val Val Gly Asp Phe  
 420 425 430  
 Leu Leu Gly Thr Leu Ser Ser Val Gly Tyr Leu Leu Asn Leu Ala Val  
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 Leu Gly Val Phe Phe Ile Phe Val Thr Gly Ile Val Leu Ser Arg Ser  
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 Gly Leu Pro Glu Val Gln Asn Leu Gly Gln Ala Leu Thr Arg Ile Pro  
 465 470 475 480  
 Gly Leu Ser Arg Phe Ile Arg Pro Asn Thr Lys Ile Ser Leu Asp Val  
 485 490 495  
 Gly Glu Val Ser Glu Gln Asp Phe Ser Thr Gln Leu Val Ala Pro Ser  
 500 505 510  
 Glu Phe Ala Ala Thr Pro Val Pro Pro Pro Met Ser Ala Gly Ile Val  
 515 520 525  
 Arg Gly Pro Arg Leu Val Pro Gly Ala Pro Val Gly Asp Gly Arg Phe  
 530 535 540  
 Arg Leu Leu Ala Asp His Gly Gly Val Gln Gly Ala Arg Phe Trp Gln  
 545 550 555 560  
 Ala Arg Glu Ile Ala Thr Gly Lys Glu Val Ala Leu Ile Phe Val Asp  
 565 570 575  
 Thr Ser Gly Asn Ala Pro Phe Ala Pro Leu Ser Ser Ala Ala Ala Ala  
 580 585 590  
 Gly Ile Ala Tyr Glu Val Gln Arg Arg Thr Lys Lys Leu Ala Ser Leu  
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 Gly Ser Leu Ala Val Ala Pro Asn Ile His Ser Glu Ala Tyr Arg Asn  
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 Gly Cys Leu Ile Val Ala Asp Trp Val Pro Gly Ser Ser Leu Ser Ala  
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 Val Ala Glu Ser Gly Ala Asp Pro Arg Ala Ala Ala Phe Ala Leu Ala  
 645 650 655  
 Glu Leu Thr Glu Thr Ile Gly Glu Ala His Glu Met Gly Ile Pro Ala  
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Val	Leu	Ala	Leu	Pro	Ala	Ile	Leu	Pro	Asp	Ala	Ser	Glu	Leu	Arg	Asp	
	690					695					700					
Ala	Lys	Ser	Leu	Ala	Ser	Ala	Ala	Glu	Met	Leu	Ile	Asp	Ala	Thr	Leu	
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Ala	Pro	Ser	Asp	Val	Lys	Ala	Met	Val	Thr	Glu	Ala	Gln	Gly	Leu	Ala	
				725					730					735		
Thr	Glu	Asp	Asn	Pro	Asp	Tyr	Ala	Ser	Leu	Ala	Met	Ala	Met	Arg	Thr	
			740					745					750			
Cys	Gly	Leu	Phe	Thr	Glu	Glu	Pro	Thr	His	Leu	Val	Val	Lys	Lys	Glu	
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Lys	Thr	Pro	Lys	Pro	Ala	Thr	Arg	Asp	Gly	Phe	Gly	Ala	Ser	Asp	Tyr	
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Thr	Val	Lys	Gly	Met	Ala	Ala	Ile	Ala	Ala	Val	Val	Ile	Ile	Leu	Val	
785					790					795					800	
Ser	Leu	Val	Ala	Ala	Gly	Thr	Ala	Phe	Leu	Thr	Ser	Phe	Phe	Gly	Ser	
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Ser	Thr	Asn	Glu	Gln	Ser	Pro	Leu	Ala	Ser	Val	Glu	Ala	Thr	Thr	Ser	
			820					825					830			
Ala	Thr	Pro	Glu	Pro	Val	Gly	Pro	Pro	Val	Tyr	Leu	Asp	Leu	Asp	Gln	
		835					840					845				
Ala	Arg	Thr	Trp	Asp	Asp	Gly	Ala	Gly	Thr	Asp	Val	Thr	Asp	Val	Thr	
	850					855					860					
Asp	Gly	Asn	Thr	Ser	Thr	Ala	Trp	Thr	Ser	Thr	Gly	Gly	Asp	Gly	Leu	
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Leu	Val	Asp	Leu	Ser	Thr	Pro	Ala	Arg	Leu	Asp	Arg	Val	Ile	Leu	Thr	
				885					890					895		
Thr	Gly	Thr	Gly	Ser	Asp	Ser	Asn	Val	Thr	Ser	Thr	Val	Lys	Ile	Tyr	
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Ala	Phe	Asn	Asp	Ala	Ser	Pro	His	Ser	Leu	Ser	Glu	Gly	Ile	Glu	Ile	
		915					920					925				
Gly	Thr	Val	Asp	Tyr	Ser	Gly	Arg	Ser	Leu	Ser	His	Ser	Ile	Arg	Asp	
	930					935					940					
Ser	Ser	Lys	Leu	Pro	Gly	Gln	Val	Glu	Ser	Val	Val	Ile	Leu	Val	Asp	
945					950					955					960	
Glu	Val	Arg	Ser	Ser	Gln	Thr	Ser	Asp	Thr	Asn	Pro	Gln	Met	Gln	Ile	
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Ala	Glu	Val	Gln	Leu	Val	Gly	Trp									
			980													

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 <213> Corynebacterium glutamicum

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 <223> RXA01807

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 Met Pro Ser Ala Gly  
 1 5

gag gag att tta gag cag cgc gca cag ctg gag ttt gat cag cgc cgc 163  
 Glu Glu Ile Leu Glu Gln Arg Ala Gln Leu Glu Phe Asp Gln Arg Arg  
 10 15 20

gcc gat gtg gtg atg atc ggc agc cag gtg gtt tat ggt tcc gtg ggc 211  
 Ala Asp Val Val Met Ile Gly Ser Gln Val Val Tyr Gly Ser Val Gly  
 25 30 35

ctc agt gct gcc att ccg gtg atg cac aac gaa ggc ctc cgc gtg gtc 259  
 Leu Ser Ala Ala Ile Pro Val Met His Asn Glu Gly Leu Arg Val Val  
 40 45 50

gct gtc ccc acc gtg gtg tta agt tcc atg ccg cgt tat gca agt tct 307  
 Ala Val Pro Thr Val Val Leu Ser Ser Met Pro Arg Tyr Ala Ser Ser  
 55 60 65

cac cgc cag ccg atg tcg gac caa tgg ctc gcc gac gcg ctg caa gac 355  
 His Arg Gln Pro Met Ser Asp Gln Trp Leu Ala Asp Ala Leu Gln Asp  
 70 75 80 85

ctg gtg gat ctg ggg att atc gat gag gtt tcc acc att tcc acc ggc 403  
 Leu Val Asp Leu Gly Ile Ile Asp Glu Val Ser Thr Ile Ser Thr Gly  
 90 95 100

tat ttt acc tcc gct tct cag gtg cgt gtg gtc gct gcg tgg ctg cag 451  
 Tyr Phe Thr Ser Ala Ser Gln Val Arg Val Val Ala Ala Trp Leu Gln  
 105 110 115

aaa atc cgc gaa acc cat ccg cat gtg cgc atc gtg gtg gat ccc atc 499  
 Lys Ile Arg Glu Thr His Pro His Val Arg Ile Val Val Asp Pro Ile  
 120 125 130

atg ggg gac agt gac gtg gga att tat gtc gcc gac gag atc gca acc 547  
 Met Gly Asp Ser Asp Val Gly Ile Tyr Val Ala Asp Glu Ile Ala Thr  
 135 140 145

gcc atc tgc cag gac tta tgc cct ctg gct acc gga atc att ccc aat 595  
 Ala Ile Cys Gln Asp Leu Cys Pro Leu Ala Thr Gly Ile Ile Pro Asn  
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gct ttc gag ctc tcc cac atg gtt ggc tcc ggc gat ccg cgc tcg ctg 643  
 Ala Phe Glu Leu Ser His Met Val Gly Ser Gly Asp Pro Arg Ser Leu  
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ctc ggc ccg ttt ggc gag tgg atc atc atc acc agc gcc act gaa act 691  
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 gtg ggc acc acc gtc acc cgc atc gtc acc cgt gac agc gtc cag gaa 739  
 Val Gly Thr Thr Val Thr Arg Ile Val Thr Arg Asp Ser Val Gln Glu  
 200 205 210  
  
 atc gcc tcc gcc acc gtc gat acc acg gcc aaa ggg gca ggc gac gtc 787  
 Ile Ala Ser Ala Thr Val Asp Thr Thr Ala Lys Gly Ala Gly Asp Val  
 215 220 225  
  
 tac gcc gca gca tta atc gcc gcc ctg cat aaa gat ttt tcg ctt atc 835  
 Tyr Ala Ala Ala Leu Ile Ala Ala Leu His Lys Asp Phe Ser Leu Ile  
 230 235 240 245  
  
 gac gcc gcc agc cac gca tcc aac acc gtc tgc gcc ggc ctg cag acc 883  
 Asp Ala Ala Ser His Ala Ser Asn Thr Val Cys Ala Gly Leu Gln Thr  
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 aaa gcg ctt taggtttcgt ccgtctctga cag 915  
 Lys Ala Leu

&lt;210&gt; 596

&lt;211&gt; 264

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 596

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 Phe Asp Gln Arg Arg Ala Asp Val Val Met Ile Gly Ser Gln Val Val  
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 Tyr Gly Ser Val Gly Leu Ser Ala Ala Ile Pro Val Met His Asn Glu  
 35 40 45  
  
 Gly Leu Arg Val Val Ala Val Pro Thr Val Val Leu Ser Ser Met Pro  
 50 55 60  
  
 Arg Tyr Ala Ser Ser His Arg Gln Pro Met Ser Asp Gln Trp Leu Ala  
 65 70 75 80  
  
 Asp Ala Leu Gln Asp Leu Val Asp Leu Gly Ile Ile Asp Glu Val Ser  
 85 90 95  
  
 Thr Ile Ser Thr Gly Tyr Phe Thr Ser Ala Ser Gln Val Arg Val Val  
 100 105 110  
  
 Ala Ala Trp Leu Gln Lys Ile Arg Glu Thr His Pro His Val Arg Ile  
 115 120 125  
  
 Val Val Asp Pro Ile Met Gly Asp Ser Asp Val Gly Ile Tyr Val Ala  
 130 135 140  
  
 Asp Glu Ile Ala Thr Ala Ile Cys Gln Asp Leu Cys Pro Leu Ala Thr  
 145 150 155 160

Gly Ile Ile Pro Asn Ala Phe Glu Leu Ser His Met Val Gly Ser Gly  
 165 170 175  
 Asp Pro Arg Ser Leu Leu Gly Pro Phe Gly Glu Trp Ile Ile Ile Thr  
 180 185 190  
 Ser Ala Thr Glu Thr Val Gly Thr Thr Val Thr Arg Ile Val Thr Arg  
 195 200 205  
 Asp Ser Val Gln Glu Ile Ala Ser Ala Thr Val Asp Thr Thr Ala Lys  
 210 215 220  
 Gly Ala Gly Asp Val Tyr Ala Ala Ala Leu Ile Ala Ala Leu His Lys  
 225 230 235 240  
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 Val Asn Thr Asn Pro  
 1 5  
 tct gaa ttc tcc tca aac cgt tca aca gct ctc ctt act gat aaa tat 163  
 Ser Glu Phe Ser Ser Asn Arg Ser Thr Ala Leu Leu Thr Asp Lys Tyr  
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 Glu Leu Thr Met Leu Gln Ala Ala Leu Ala Asp Gly Ser Ala Glu Arg  
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 Pro Ser Thr Phe Glu Val Phe Ser Arg Arg Leu Pro Asn Glu Arg Arg  
 40 45 50  
 tac ggt gtc gtc gca gga aca gca cga gtg ctg aag gcg att cgt gac 307  
 Tyr Gly Val Val Ala Gly Thr Ala Arg Val Leu Lys Ala Ile Arg Asp  
 55 60 65  
 ttt gta ttc aca gag gaa caa ctc gcc gat ctt gac ttt tta gac gac 355  
 Phe Val Phe Thr Glu Glu Gln Leu Ala Asp Leu Asp Phe Leu Asp Asp  
 70 75 80 85  
 cgt acc ctg gaa tac ctc cgc aac tac cga ttc acc ggc caa gtt gat 403  
 Arg Thr Leu Glu Tyr Leu Arg Asn Tyr Arg Phe Thr Gly Gln Val Asp

90				95				100								
ggc	tac	cgc	gaa	ggc	gaa	atc	tac	ttc	ccg	cag	tcc	cct	ctt	ctg	act	451
Gly	Tyr	Arg	Glu	Gly	Glu	Ile	Tyr	Phe	Pro	Gln	Ser	Pro	Leu	Leu	Thr	
			105					110					115			
gtg	cgt	ggc	acg	ttt	gca	gaa	tgc	gtc	atc	cta	gaa	act	gtc	att	ttg	499
Val	Arg	Gly	Thr	Phe	Ala	Glu	Cys	Val	Ile	Leu	Glu	Thr	Val	Ile	Leu	
			120				125					130				
tcc	atc	atg	aat	gca	gat	tct	gcc	gtc	gct	tcc	gcc	gct	gcg	cgc	atg	547
Ser	Ile	Met	Asn	Ala	Asp	Ser	Ala	Val	Ala	Ser	Ala	Ala	Ala	Arg	Met	
	135					140					145					
gtc	acc	gca	gct	gat	ggg	cgc	ccc	atc	atc	gaa	atg	gga	tcc	agg	cgc	595
Val	Thr	Ala	Ala	Asp	Gly	Arg	Pro	Ile	Ile	Glu	Met	Gly	Ser	Arg	Arg	
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acc	cac	gaa	tac	tcg	gca	gtc	acc	gca	tcc	cgc	gca	gca	tac	ctc	gct	643
Thr	His	Glu	Tyr	Ser	Ala	Val	Thr	Ala	Ser	Arg	Ala	Ala	Tyr	Leu	Ala	
				170					175					180		
gga	ttc	tcc	acc	acc	tcc	aac	ctc	gag	gcg	gcc	tac	cgc	tac	gga	att	691
Gly	Phe	Ser	Thr	Thr	Ser	Asn	Leu	Glu	Ala	Ala	Tyr	Arg	Tyr	Gly	Ile	
			185					190					195			
cca	gca	tcc	gga	acc	tcc	gcc	cac	gca	tgg	act	ttg	ctg	cac	atc	aac	739
Pro	Ala	Ser	Gly	Thr	Ser	Ala	His	Ala	Trp	Thr	Leu	Leu	His	Ile	Asn	
			200				205					210				
gat	gac	ggc	acc	ccc	aac	gaa	gca	gca	gct	ttc	aaa	gca	cag	gtt	gaa	787
Asp	Asp	Gly	Thr	Pro	Asn	Glu	Ala	Ala	Ala	Phe	Lys	Ala	Gln	Val	Glu	
	215					220					225					
tcc	ctc	ggc	gtg	gac	acc	acc	ttg	ctg	gta	gat	act	tat	gac	atc	acc	835
Ser	Leu	Gly	Val	Asp	Thr	Thr	Leu	Leu	Val	Asp	Thr	Tyr	Asp	Ile	Thr	
230					235					240					245	
caa	ggg	gtg	gcc	acc	gcc	att	gaa	gtt	gca	ggg	cca	gac	ctt	ggg	ggc	883
Gln	Gly	Val	Ala	Thr	Ala	Ile	Glu	Val	Ala	Gly	Pro	Asp	Leu	Gly	Gly	
				250					255					260		
gta	cgt	atc	gac	tcc	ggc	gac	cta	ggg	gtg	ctt	gcc	cga	aag	gtc	cgc	931
Val	Arg	Ile	Asp	Ser	Gly	Asp	Leu	Gly	Val	Leu	Ala	Arg	Lys	Val	Arg	
			265					270					275			
aag	cag	ctc	gac	gat	ctc	aac	gcc	cac	aac	acc	aag	att	gtg	gtc	tcc	979
Lys	Gln	Leu	Asp	Asp	Leu	Asn	Ala	His	Asn	Thr	Lys	Ile	Val	Val	Ser	
			280				285					290				
tcc	gac	ctg	gat	gaa	ttc	gcc	atc	gcg	ggg	ctt	cgc	ggc	gaa	cca	gtt	
1027																
Ser	Asp	Leu	Asp	Glu	Phe	Ala	Ile	Ala	Gly	Leu	Arg	Gly	Glu	Pro	Val	
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gac	gtc	ttt	ggc	gtt	ggc	acc	tcc	gtt	gtc	aca	ggg	tct	ggc	gca	cca	
1075																
Asp	Val	Phe	Gly	Val	Gly	Thr	Ser	Val	Val	Thr	Gly	Ser	Gly	Ala	Pro	
310					315					320					325	

acc gct ggc ctc gtg tac aag atc ggg gaa gtt gcc ggt cac cct gtg  
1123  
Thr Ala Gly Leu Val Tyr Lys Ile Gly Glu Val Ala Gly His Pro Val  
330 335 340

gcc aag cgt tcc cga aac aag gaa agc tac ggt ggt ggc aag aag gct  
1171  
Ala Lys Arg Ser Arg Asn Lys Glu Ser Tyr Gly Gly Gly Lys Lys Ala  
345 350 355

gtg cgc acc cac cgc aag tcc ggt acc gca atc gaa gaa atc gtc tac  
1219  
Val Arg Thr His Arg Lys Ser Gly Thr Ala Ile Glu Glu Ile Val Tyr  
360 365 370

cca ttc aat gcc gaa gca cca gat act gga aag ctc gac act ttg agc  
1267  
Pro Phe Asn Ala Glu Ala Pro Asp Thr Gly Lys Leu Asp Thr Leu Ser  
375 380 385

ctg acc atc cca ttg atg cgc gac ggt gaa atc gtt cca ggt ttg cct  
1315  
Leu Thr Ile Pro Leu Met Arg Asp Gly Glu Ile Val Pro Gly Leu Pro  
390 395 400 405

act ttg gaa gat tcc cga gcg tat ttg gcc aag caa ttg gtc tct tta  
1363  
Thr Leu Glu Asp Ser Arg Ala Tyr Leu Ala Lys Gln Leu Val Ser Leu  
410 415 420

cca tgg gaa ggc ctt gca ctg tct cgc gat gag cct gtt ttg cac act  
1411  
Pro Trp Glu Gly Leu Ala Leu Ser Arg Asp Glu Pro Val Leu His Thr  
425 430 435

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Arg Phe Val Gly Phe Pro Pro Ala Ala  
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1461

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<213> Corynebacterium glutamicum

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Gly Ser Ala Glu Arg Pro Ser Thr Phe Glu Val Phe Ser Arg Arg Leu  
35 40 45  
Pro Asn Glu Arg Arg Tyr Gly Val Val Ala Gly Thr Ala Arg Val Leu  
50 55 60

Lys Ala Ile Arg Asp Phe Val Phe Thr Glu Glu Gln Leu Ala Asp Leu  
 65 70 75 80  
 Asp Phe Leu Asp Asp Arg Thr Leu Glu Tyr Leu Arg Asn Tyr Arg Phe  
 85 90 95  
 Thr Gly Gln Val Asp Gly Tyr Arg Glu Gly Glu Ile Tyr Phe Pro Gln  
 100 105 110  
 Ser Pro Leu Leu Thr Val Arg Gly Thr Phe Ala Glu Cys Val Ile Leu  
 115 120 125  
 Glu Thr Val Ile Leu Ser Ile Met Asn Ala Asp Ser Ala Val Ala Ser  
 130 135 140  
 Ala Ala Ala Arg Met Val Thr Ala Ala Asp Gly Arg Pro Ile Ile Glu  
 145 150 155 160  
 Met Gly Ser Arg Arg Thr His Glu Tyr Ser Ala Val Thr Ala Ser Arg  
 165 170 175  
 Ala Ala Tyr Leu Ala Gly Phe Ser Thr Thr Ser Asn Leu Glu Ala Ala  
 180 185 190  
 Tyr Arg Tyr Gly Ile Pro Ala Ser Gly Thr Ser Ala His Ala Trp Thr  
 195 200 205  
 Leu Leu His Ile Asn Asp Asp Gly Thr Pro Asn Glu Ala Ala Ala Phe  
 210 215 220  
 Lys Ala Gln Val Glu Ser Leu Gly Val Asp Thr Thr Leu Leu Val Asp  
 225 230 235 240  
 Thr Tyr Asp Ile Thr Gln Gly Val Ala Thr Ala Ile Glu Val Ala Gly  
 245 250 255  
 Pro Asp Leu Gly Gly Val Arg Ile Asp Ser Gly Asp Leu Gly Val Leu  
 260 265 270  
 Ala Arg Lys Val Arg Lys Gln Leu Asp Asp Leu Asn Ala His Asn Thr  
 275 280 285  
 Lys Ile Val Val Ser Ser Asp Leu Asp Glu Phe Ala Ile Ala Gly Leu  
 290 295 300  
 Arg Gly Glu Pro Val Asp Val Phe Gly Val Gly Thr Ser Val Val Thr  
 305 310 315 320  
 Gly Ser Gly Ala Pro Thr Ala Gly Leu Val Tyr Lys Ile Gly Glu Val  
 325 330 335  
 Ala Gly His Pro Val Ala Lys Arg Ser Arg Asn Lys Glu Ser Tyr Gly  
 340 345 350  
 Gly Gly Lys Lys Ala Val Arg Thr His Arg Lys Ser Gly Thr Ala Ile  
 355 360 365  
 Glu Glu Ile Val Tyr Pro Phe Asn Ala Glu Ala Pro Asp Thr Gly Lys  
 370 375 380



Leu Asp Thr Leu Ser Leu Thr Ile Pro Leu Met Arg Asp Gly Glu Ile  
385 390 395 400

Val Pro Gly Leu Pro Thr Leu Glu Asp Ser Arg Ala Tyr Leu Ala Lys  
405 410 415

Gln Leu Val Ser Leu Pro Trp Glu Gly Leu Ala Leu Ser Arg Asp Glu  
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<210> 599

<211> 871

<212> DNA

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<220>

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<222> (101)..(871)

<223> FRXA02405

<400> 599

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Val Asn Thr Asn Pro  
1 5

tct gaa ttc tcc tca aac cgt tca aca gct ctc ctt act gat aaa tat 163  
Ser Glu Phe Ser Ser Asn Arg Ser Thr Ala Leu Leu Thr Asp Lys Tyr  
10 15 20

gag ctg acc atg ctt caa gca gcg ctc gct gat ggt tct gca gaa cgc 211  
Glu Leu Thr Met Leu Gln Ala Ala Leu Ala Asp Gly Ser Ala Glu Arg  
25 30 35

ccc tca acg ttt gag gtc ttt agc cgc cgc ctc ccc aac gag cgc cga 259  
Pro Ser Thr Phe Glu Val Phe Ser Arg Arg Leu Pro Asn Glu Arg Arg  
40 45 50

tac ggt gtc gtc gca gga aca gca cga gtg ctg aag gcg att cgt gac 307  
Tyr Gly Val Val Ala Gly Thr Ala Arg Val Leu Lys Ala Ile Arg Asp  
55 60 65

ttt gta ttc aca gag gaa caa ctc gcc gat ctt gac ttt tta gac gac 355  
Phe Val Phe Thr Glu Glu Gln Leu Ala Asp Leu Asp Phe Leu Asp Asp  
70 75 80 85

cgt acc ctg gaa tac ctc cgc aac tac cga ttc acc ggc caa gtt gat 403  
Arg Thr Leu Glu Tyr Leu Arg Asn Tyr Arg Phe Thr Gly Gln Val Asp  
90 95 100

ggc tac cgc gaa ggc gaa atc tac ttc ccg cag tcc cct ctt ctg act 451  
Gly Tyr Arg Glu Gly Glu Ile Tyr Phe Pro Gln Ser Pro Leu Leu Thr  
105 110 115

gtg cgt ggc acg ttt gca gaa tgc gtc atc cta gaa act gtc att ttg 499  
Val Arg Gly Thr Phe Ala Glu Cys Val Ile Leu Glu Thr Val Ile Leu  
120 125 130

tcc atc atg aat gca gat tct gcc gtc gct tcc gcc gct gcg cgc atg	547
Ser Ile Met Asn Ala Asp Ser Ala Val Ala Ser Ala Ala Ala Arg Met	
135 140 145	
gtc acc gca gct gat ggt cgc ccc atc atc gaa atg gga tcc agg cgc	595
Val Thr Ala Ala Asp Gly Arg Pro Ile Ile Glu Met Gly Ser Arg Arg	
150 155 160 165	
acc cac gaa tac tcg gca gtc acc gca tcc cgc gca gca tac ctc gct	643
Thr His Glu Tyr Ser Ala Val Thr Ala Ser Arg Ala Ala Tyr Leu Ala	
170 175 180	
gga ttc tcc acc acc tcc aac ctc gag gcg gcc tac cgc tac gga att	691
Gly Phe Ser Thr Thr Ser Asn Leu Glu Ala Ala Tyr Arg Tyr Gly Ile	
185 190 195	
cca gca tcc gga acc tcc gcc cac gca tgg act ttg ctg cac atc aac	739
Pro Ala Ser Gly Thr Ser Ala His Ala Trp Thr Leu Leu His Ile Asn	
200 205 210	
gat gac ggc acc ccc aac gaa gca gca gct ttc aaa gca cag gtt gaa	787
Asp Asp Gly Thr Pro Asn Glu Ala Ala Ala Phe Lys Ala Gln Val Glu	
215 220 225	
tcc ctc ggc gtg gac acc acc ttg ctg gta gat act tat gac atc acc	835
Ser Leu Gly Val Asp Thr Thr Leu Leu Val Asp Thr Tyr Asp Ile Thr	
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caa ggt gtg gcc acc gcc att gaa gtt gca ggt cca	871
Gln Gly Val Ala Thr Ala Ile Glu Val Ala Gly Pro	
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&lt;210&gt; 600

&lt;211&gt; 257

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 600

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Gly Ser Ala Glu Arg Pro Ser Thr Phe Glu Val Phe Ser Arg Arg Leu	
35 40 45	
Pro Asn Glu Arg Arg Tyr Gly Val Val Ala Gly Thr Ala Arg Val Leu	
50 55 60	
Lys Ala Ile Arg Asp Phe Val Phe Thr Glu Glu Gln Leu Ala Asp Leu	
65 70 75 80	
Asp Phe Leu Asp Asp Arg Thr Leu Glu Tyr Leu Arg Asn Tyr Arg Phe	
85 90 95	
Thr Gly Gln Val Asp Gly Tyr Arg Glu Gly Glu Ile Tyr Phe Pro Gln	
100 105 110	

Ser Pro Leu Leu Thr Val Arg Gly Thr Phe Ala Glu Cys Val Ile Leu  
 115 120 125

Glu Thr Val Ile Leu Ser Ile Met Asn Ala Asp Ser Ala Val Ala Ser  
 130 135 140

Ala Ala Ala Arg Met Val Thr Ala Ala Asp Gly Arg Pro Ile Ile Glu  
 145 150 155 160

Met Gly Ser Arg Arg Thr His Glu Tyr Ser Ala Val Thr Ala Ser Arg  
 165 170 175

Ala Ala Tyr Leu Ala Gly Phe Ser Thr Thr Ser Asn Leu Glu Ala Ala  
 180 185 190

Tyr Arg Tyr Gly Ile Pro Ala Ser Gly Thr Ser Ala His Ala Trp Thr  
 195 200 205

Leu Leu His Ile Asn Asp Asp Gly Thr Pro Asn Glu Ala Ala Ala Phe  
 210 215 220

Lys Ala Gln Val Glu Ser Leu Gly Val Asp Thr Thr Leu Leu Val Asp  
 225 230 235 240

Thr Tyr Asp Ile Thr Gln Gly Val Ala Thr Ala Ile Glu Val Ala Gly  
 245 250 255

Pro

<210> 601  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (1)..(486)  
 <223> FRXA02754

<400> 601  
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 Pro Thr Asn Thr Lys Ile Val Val Ser Ser Asp Leu Asp Glu Phe Ala  
 1 5 10 15

atc gcg ggt ctt cgc ggc gaa cca gtt gac gtc ttt ggc gtt ggc acc 96  
 Ile Ala Gly Leu Arg Gly Glu Pro Val Asp Val Phe Gly Val Gly Thr  
 20 25 30

tcc gtt gtc aca ggt tct ggc gca cca acc gct ggc ctc gtg tac aag 144  
 Ser Val Val Thr Gly Ser Gly Ala Pro Thr Ala Gly Leu Val Tyr Lys  
 35 40 45

atc ggg gaa gtt gcc ggt cac cct gtg gcc aag cgt tcc cga aac aag 192  
 Ile Gly Glu Val Ala Gly His Pro Val Ala Lys Arg Ser Arg Asn Lys  
 50 55 60

gaa agc tac ggt ggt ggc aag aag gct gtg cgc acc cac cgc aag tcc 240  
 Glu Ser Tyr Gly Gly Gly Lys Lys Ala Val Arg Thr His Arg Lys Ser  
 65 70 75 80

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ggt acc gca atc gaa gaa atc gtc tac cca ttc aat gcc gaa gca cca 288
Gly Thr Ala Ile Glu Glu Ile Val Tyr Pro Phe Asn Ala Glu Ala Pro
      85                      90                      95

gat act gga aag ctc gac act ttg agc ctg acc atc cca ttg atg cgc 336
Asp Thr Gly Lys Leu Asp Thr Leu Ser Leu Thr Ile Pro Leu Met Arg
      100                      105                      110

gac ggt gaa atc gtt cca ggt ttg cct act ttg gaa gat tcc cga gcg 384
Asp Gly Glu Ile Val Pro Gly Leu Pro Thr Leu Glu Asp Ser Arg Ala
      115                      120                      125

tat ttg gcc aag caa ttg gtc tct tta cca tgg gaa ggc ctt gca ctg 432
Tyr Leu Ala Lys Gln Leu Val Ser Leu Pro Trp Glu Gly Leu Ala Leu
      130                      135                      140

tct cgc gat gag cct gtt ttg cac act cgt ttc gtg ggt ttc ccg ccg 480
Ser Arg Asp Glu Pro Val Leu His Thr Arg Phe Val Gly Phe Pro Pro
145                      150                      155                      160

gcc gct tagacaattc ggtctcacca aac 509
Ala Ala

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&lt;210&gt; 602

&lt;211&gt; 162

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 602

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Pro Thr Asn Thr Lys Ile Val Val Ser Ser Asp Leu Asp Glu Phe Ala
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Ile Ala Gly Leu Arg Gly Glu Pro Val Asp Val Phe Gly Val Gly Thr
      20                      25                      30

Ser Val Val Thr Gly Ser Gly Ala Pro Thr Ala Gly Leu Val Tyr Lys
      35                      40                      45

Ile Gly Glu Val Ala Gly His Pro Val Ala Lys Arg Ser Arg Asn Lys
      50                      55                      60

Glu Ser Tyr Gly Gly Gly Lys Lys Ala Val Arg Thr His Arg Lys Ser
      65                      70                      75                      80

Gly Thr Ala Ile Glu Glu Ile Val Tyr Pro Phe Asn Ala Glu Ala Pro
      85                      90                      95

Asp Thr Gly Lys Leu Asp Thr Leu Ser Leu Thr Ile Pro Leu Met Arg
      100                      105                      110

Asp Gly Glu Ile Val Pro Gly Leu Pro Thr Leu Glu Asp Ser Arg Ala
      115                      120                      125

Tyr Leu Ala Lys Gln Leu Val Ser Leu Pro Trp Glu Gly Leu Ala Leu
      130                      135                      140

Ser Arg Asp Glu Pro Val Leu His Thr Arg Phe Val Gly Phe Pro Pro
145                      150                      155                      160

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Ala Ala

&lt;210&gt; 603

&lt;211&gt; 960

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(937)

&lt;223&gt; RXA02112

&lt;400&gt; 603

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agctcctggtt actcctagct cctcgaagga tgcgtaattt atg act acc cat att 115  
 Met Thr Thr His Ile  
 1 5

gac cgc atc gtt ggc gca gcg tta tcc gag gat gcg cca tgg ggc gac 163  
 Asp Arg Ile Val Gly Ala Ala Leu Ser Glu Asp Ala Pro Trp Gly Asp  
 10 15 20

att acc tcc gac act ttt atc cca gga tcg gcg cag ctg agc gcc aag 211  
 Ile Thr Ser Asp Thr Phe Ile Pro Gly Ser Ala Gln Leu Ser Ala Lys  
 25 30 35

gtt gtt gcc cgg gag cca ggt gtg ttc agc ggg cag gcg ctt tta gac 259  
 Val Val Ala Arg Glu Pro Gly Val Phe Ser Gly Gln Ala Leu Leu Asp  
 40 45 50

gcc tcc ttc cgg ctc gtc gat cct agg ata aac gca tcc ctt aag gtg 307  
 Ala Ser Phe Arg Leu Val Asp Pro Arg Ile Asn Ala Ser Leu Lys Val  
 55 60 65

gct gat ggt gac agc ttt gaa acc ggg gac atc cta gga aca att acc 355  
 Ala Asp Gly Asp Ser Phe Glu Thr Gly Asp Ile Leu Gly Thr Ile Thr  
 70 75 80 85

ggc agt gct aga agc atc ctc cgt tca gag cgc att gct ctc aac ttc 403  
 Gly Ser Ala Arg Ser Ile Leu Arg Ser Glu Arg Ile Ala Leu Asn Phe  
 90 95 100

att cag agg acg tcc ggc atc gct aca ttg aca tcg tgc tat gtt gca 451  
 Ile Gln Arg Thr Ser Gly Ile Ala Thr Leu Thr Ser Cys Tyr Val Ala  
 105 110 115

gag gtt aaa ggc acc aaa gcc cgc att gtt gat acc cgg aaa acc aca 499  
 Glu Val Lys Gly Thr Lys Ala Arg Ile Val Asp Thr Arg Lys Thr Thr  
 120 125 130

ccc ggc ctg cgc atc att gaa cgc caa gct gtc cgt gac ggt ggc gga 547  
 Pro Gly Leu Arg Ile Ile Glu Arg Gln Ala Val Arg Asp Gly Gly Gly  
 135 140 145

ttt aat cac cga gcc acc ttg tcc gat gct gtc atg gtg aaa gat aac 595  
 Phe Asn His Arg Ala Thr Leu Ser Asp Ala Val Met Val Lys Asp Asn  
 150 155 160 165

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cat ctc gca gcc atc gca tcc cag ggg ctc agc atc act gaa gcg ctg 643
His Leu Ala Ala Ile Ala Ser Gln Gly Leu Ser Ile Thr Glu Ala Leu
170 175 180

tcg aat atg aaa gct aaa ctc ccc cac acc acc cat gtg gaa gtc gaa 691
Ser Asn Met Lys Ala Lys Leu Pro His Thr Thr His Val Glu Val Glu
185 190 195

gtt gat cat ata gag cag atc gaa cca gtt ctt gct gct ggt gtg gac 739
Val Asp His Ile Glu Gln Ile Glu Pro Val Leu Ala Ala Gly Val Asp
200 205 210

acc atc atg ttg gat aat ttc acc att gat cag ctc atc gaa ggc gtt 787
Thr Ile Met Leu Asp Asn Phe Thr Ile Asp Gln Leu Ile Glu Gly Val
215 220 225

gat ctc att ggt gga cgt gca ctg gtg gaa gca tct ggc gga gtc aac 835
Asp Leu Ile Gly Gly Arg Ala Leu Val Glu Ala Ser Gly Gly Val Asn
230 235 240 245

ctc aac acc gcg gga aag att gca tca acc ggt gtc gac gtc att tcc 883
Leu Asn Thr Ala Gly Lys Ile Ala Ser Thr Gly Val Asp Val Ile Ser
250 255 260

gtt gga gcg ctt acc cat tct gtg cat gca ctt gac cta gga ctc gat 931
Val Gly Ala Leu Thr His Ser Val His Ala Leu Asp Leu Gly Leu Asp
265 270 275

att ttc taatgctcta ccttgataat gca 960
Ile Phe

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&lt;210&gt; 604

&lt;211&gt; 279

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 604

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Met Thr Thr His Ile Asp Arg Ile Val Gly Ala Ala Leu Ser Glu Asp
1 5 10 15

Ala Pro Trp Gly Asp Ile Thr Ser Asp Thr Phe Ile Pro Gly Ser Ala
20 25 30

Gln Leu Ser Ala Lys Val Val Ala Arg Glu Pro Gly Val Phe Ser Gly
35 40 45

Gln Ala Leu Leu Asp Ala Ser Phe Arg Leu Val Asp Pro Arg Ile Asn
50 55 60

Ala Ser Leu Lys Val Ala Asp Gly Asp Ser Phe Glu Thr Gly Asp Ile
65 70 75 80

Leu Gly Thr Ile Thr Gly Ser Ala Arg Ser Ile Leu Arg Ser Glu Arg
85 90 95

Ile Ala Leu Asn Phe Ile Gln Arg Thr Ser Gly Ile Ala Thr Leu Thr
100 105 110

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Ser Cys Tyr Val Ala Glu Val Lys Gly Thr Lys Ala Arg Ile Val Asp  
 115 120 125  
 Thr Arg Lys Thr Thr Pro Gly Leu Arg Ile Ile Glu Arg Gln Ala Val  
 130 135 140  
 Arg Asp Gly Gly Gly Phe Asn His Arg Ala Thr Leu Ser Asp Ala Val  
 145 150 155 160  
 Met Val Lys Asp Asn His Leu Ala Ala Ile Ala Ser Gln Gly Leu Ser  
 165 170 175  
 Ile Thr Glu Ala Leu Ser Asn Met Lys Ala Lys Leu Pro His Thr Thr  
 180 185 190  
 His Val Glu Val Glu Val Asp His Ile Glu Gln Ile Glu Pro Val Leu  
 195 200 205  
 Ala Ala Gly Val Asp Thr Ile Met Leu Asp Asn Phe Thr Ile Asp Gln  
 210 215 220  
 Leu Ile Glu Gly Val Asp Leu Ile Gly Gly Arg Ala Leu Val Glu Ala  
 225 230 235 240  
 Ser Gly Gly Val Asn Leu Asn Thr Ala Gly Lys Ile Ala Ser Thr Gly  
 245 250 255  
 Val Asp Val Ile Ser Val Gly Ala Leu Thr His Ser Val His Ala Leu  
 260 265 270  
 Asp Leu Gly Leu Asp Ile Phe  
 275

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 <213> Corynebacterium glutamicum

<220>  
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 <223> RXA02111

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 Met Thr Thr Ser Ile  
 1 5

acc cca tct gtc aac ctt gca ttg aaa aat gcc aat agc tgc aac agt 163  
 Thr Pro Ser Val Asn Leu Ala Leu Lys Asn Ala Asn Ser Cys Asn Ser  
 10 15 20

gaa ctc aaa gac gga ccc tgg ttc ctc gac cag ccc gga atg ccg gat 211  
 Glu Leu Lys Asp Gly Pro Trp Phe Leu Asp Gln Pro Gly Met Pro Asp  
 25 30 35

gtc tac ggc ccc ggc gcg tca caa aac gat ccg atc cct gcg cat gct 259  
 Val Tyr Gly Pro Gly Ala Ser Gln Asn Asp Pro Ile Pro Ala His Ala

40						45						50						
ccg	cgc	cag	cag	gtt	ctc	ccc	gag	gag	tac	cag	cgc	gca	agt	gat	gac			307
Pro	Arg	Gln	Gln	Val	Leu	Pro	Glu	Glu	Tyr	Gln	Arg	Ala	Ser	Asp	Asp			
	55					60					65							
gaa	ctg	cat	cgt	agg	atc	cgg	gaa	gcg	aaa	gac	acc	ctg	ggg	gac	aaa			355
Glu	Leu	His	Arg	Arg	Ile	Arg	Glu	Ala	Lys	Asp	Thr	Leu	Gly	Asp	Lys			
	70				75					80					85			
gtg	gtt	atc	cta	gga	cac	ttc	tac	cag	cgc	gat	gaa	gtt	atc	caa	cac			403
Val	Val	Ile	Leu	Gly	His	Phe	Tyr	Gln	Arg	Asp	Glu	Val	Ile	Gln	His			
				90					95					100				
gca	gat	ttt	gtt	ggg	gac	tct	ttc	caa	ctt	gcc	cgc	gct	gcc	aaa	acc			451
Ala	Asp	Phe	Val	Gly	Asp	Ser	Phe	Gln	Leu	Ala	Arg	Ala	Ala	Lys	Thr			
			105					110					115					
cga	ccc	gag	gcg	gaa	gcg	att	gtg	ttc	tgc	ggg	gtg	cac	ttc	atg	gct			499
Arg	Pro	Glu	Ala	Glu	Ala	Ile	Val	Phe	Cys	Gly	Val	His	Phe	Met	Ala			
		120					125					130						
gaa	acc	gct	gat	ctg	tta	tcc	acg	gat	gaa	caa	tca	gtg	atc	ctc	ccc			547
Glu	Thr	Ala	Asp	Leu	Leu	Ser	Thr	Asp	Glu	Gln	Ser	Val	Ile	Leu	Pro			
	135					140					145							
aac	ctt	gcc	gca	ggg	tgc	tcc	atg	gca	gac	atg	gct	gac	ctt	gat	tcc			595
Asn	Leu	Ala	Ala	Gly	Cys	Ser	Met	Ala	Asp	Met	Ala	Asp	Leu	Asp	Ser			
	150				155					160					165			
gtc	gaa	gac	tgc	tgg	gag	caa	ctc	acc	tca	att	tat	ggc	gat	gac	acc			643
Val	Glu	Asp	Cys	Trp	Glu	Gln	Leu	Thr	Ser	Ile	Tyr	Gly	Asp	Asp	Thr			
				170					175					180				
ctg	atc	cct	gtg	acc	tac	atg	aat	tcc	tct	gca	gcg	ctc	aaa	ggg	ttc			691
Leu	Ile	Pro	Val	Thr	Tyr	Met	Asn	Ser	Ser	Ala	Ala	Leu	Lys	Gly	Phe			
			185					190					195					
gtg	ggg	gag	cac	ggc	gga	att	gta	tgc	acc	tcc	tca	aat	gca	cgt	tcc			739
Val	Gly	Glu	His	Gly	Gly	Ile	Val	Cys	Thr	Ser	Ser	Asn	Ala	Arg	Ser			
		200					205					210						
gta	ttg	gag	tgg	gcg	ttt	gaa	cgc	ggc	caa	cga	gtc	ctg	ttc	ttc	ccc			787
Val	Leu	Glu	Trp	Ala	Phe	Glu	Arg	Gly	Gln	Arg	Val	Leu	Phe	Phe	Pro			
	215					220					225							
gat	cag	cac	ttg	ggg	cga	aac	acc	gcg	aaa	gcc	atg	ggc	att	ggg	atc			835
Asp	Gln	His	Leu	Gly	Arg	Asn	Thr	Ala	Lys	Ala	Met	Gly	Ile	Gly	Ile			
	230				235					240					245			
gat	caa	atg	ccc	ctg	tgg	aat	ccc	aac	aaa	cca	ctg	ggg	ggc	aac	acc			883
Asp	Gln	Met	Pro	Leu	Trp	Asn	Pro	Asn	Lys	Pro	Leu	Gly	Gly	Asn	Thr			
				250					255					260				
gtt	tcc	gag	cta	gaa	aac	gca	aag	gta	ctg	ctc	tgg	cat	ggg	ttc	tgc			931
Val	Ser	Glu	Leu	Glu	Asn	Ala	Lys	Val	Leu	Leu	Trp	His	Gly	Phe	Cys			
			265					270					275					
tct	gta	cac	aag	cgc	ttt	act	gtc	gag	cag	atc	aac	aaa	gcc	cgc	gcc			979
Ser	Val	His	Lys	Arg	Phe	Thr	Val	Glu	Gln	Ile	Asn	Lys	Ala	Arg	Ala			
		280					285					290						



gag tac ccc gac gtt cac gtc atc gtg cac cct gaa tcc ccc atg cca  
 1027  
 Glu Tyr Pro Asp Val His Val Ile Val His Pro Glu Ser Pro Met Pro  
 295 300 305

gtt gtt gac gcc gcc gac tca tcc gga tcc act gac ttc att gtg aaa  
 1075  
 Val Val Asp Ala Ala Asp Ser Ser Gly Ser Thr Asp Phe Ile Val Lys  
 310 315 320 325

gcc att caa gca gca ccg gca gga tct acc ttt gcg atc ggc acc gaa  
 1123  
 Ala Ile Gln Ala Ala Pro Ala Gly Ser Thr Phe Ala Ile Gly Thr Glu  
 330 335 340

atc aac ttg gtt cag cgc ctg gca gcc cag tac ccg cag cac acc atc  
 1171  
 Ile Asn Leu Val Gln Arg Leu Ala Ala Gln Tyr Pro Gln His Thr Ile  
 345 350 355

ttc tgc ctc gac cct gtc atc tgc cca tgc tcc acc atg tat cgc att  
 1219  
 Phe Cys Leu Asp Pro Val Ile Cys Pro Cys Ser Thr Met Tyr Arg Ile  
 360 365 370

cac cct ggt tac ctg gcc tgg gca ctt gag gag ttg gtg gct gga aac  
 1267  
 His Pro Gly Tyr Leu Ala Trp Ala Leu Glu Glu Leu Val Ala Gly Asn  
 375 380 385

gtg att aac cag att tct gtc tct gaa tcc gtg gcg gca ccg gcg cga  
 1315  
 Val Ile Asn Gln Ile Ser Val Ser Glu Ser Val Ala Ala Pro Ala Arg  
 390 395 400 405

gtc gct ttg gaa agg atg cta tct gtt gtt cca gca gct cct gtt act  
 1363  
 Val Ala Leu Glu Arg Met Leu Ser Val Val Pro Ala Ala Pro Val Thr  
 410 415 420

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 1407  
 Pro Ser Ser Ser Lys Asp Ala  
 425

<210> 606

<211> 428

<212> PRT

<213> Corynebacterium glutamicum

<400> 606

Met Thr Thr Ser Ile Thr Pro Ser Val Asn Leu Ala Leu Lys Asn Ala  
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Asn Ser Cys Asn Ser Glu Leu Lys Asp Gly Pro Trp Phe Leu Asp Gln  
 20 25 30

Pro Gly Met Pro Asp Val Tyr Gly Pro Gly Ala Ser Gln Asn Asp Pro  
 35 40 45

Ile	Pro 50	Ala	His	Ala	Pro	Arg 55	Gln	Gln	Val	Leu	Pro 60	Glu	Glu	Tyr	Gln
Arg 65	Ala	Ser	Asp	Asp	Glu 70	Leu	His	Arg	Arg	Ile 75	Arg	Glu	Ala	Lys	Asp 80
Thr	Leu	Gly	Asp	Lys 85	Val	Val	Ile	Leu	Gly 90	His	Phe	Tyr	Gln	Arg 95	Asp
Glu	Val	Ile	Gln 100	His	Ala	Asp	Phe	Val 105	Gly	Asp	Ser	Phe	Gln 110	Leu	Ala
Arg	Ala	Ala 115	Lys	Thr	Arg	Pro	Glu 120	Ala	Glu	Ala	Ile	Val 125	Phe	Cys	Gly
Val 130	His	Phe	Met	Ala	Glu	Thr 135	Ala	Asp	Leu	Leu	Ser 140	Thr	Asp	Glu	Gln
Ser 145	Val	Ile	Leu	Pro	Asn 150	Leu	Ala	Ala	Gly	Cys 155	Ser	Met	Ala	Asp	Met 160
Ala	Asp	Leu	Asp	Ser 165	Val	Glu	Asp	Cys	Trp 170	Glu	Gln	Leu	Thr	Ser 175	Ile
Tyr	Gly	Asp	Asp 180	Thr	Leu	Ile	Pro	Val 185	Thr	Tyr	Met	Asn	Ser 190	Ser	Ala
Ala	Leu	Lys 195	Gly	Phe	Val	Gly	Glu 200	His	Gly	Gly	Ile	Val 205	Cys	Thr	Ser
Ser	Asn 210	Ala	Arg	Ser	Val	Leu 215	Glu	Trp	Ala	Phe	Glu 220	Arg	Gly	Gln	Arg
Val 225	Leu	Phe	Phe	Pro	Asp 230	Gln	His	Leu	Gly	Arg 235	Asn	Thr	Ala	Lys	Ala 240
Met	Gly	Ile	Gly	Ile 245	Asp	Gln	Met	Pro	Leu 250	Trp	Asn	Pro	Asn	Lys 255	Pro
Leu	Gly	Gly	Asn 260	Thr	Val	Ser	Glu	Leu 265	Glu	Asn	Ala	Lys	Val 270	Leu	Leu
Trp	His 275	Gly	Phe	Cys	Ser	Val	His 280	Lys	Arg	Phe	Thr	Val 285	Glu	Gln	Ile
Asn 290	Lys	Ala	Arg	Ala	Glu	Tyr 295	Pro	Asp	Val	His	Val 300	Ile	Val	His	Pro
Glu 305	Ser	Pro	Met	Pro	Val 310	Val	Asp	Ala	Ala	Asp 315	Ser	Ser	Gly	Ser	Thr 320
Asp	Phe	Ile	Val	Lys 325	Ala	Ile	Gln	Ala	Ala 330	Pro	Ala	Gly	Ser	Thr 335	Phe
Ala	Ile	Gly	Thr 340	Glu	Ile	Asn	Leu	Val 345	Gln	Arg	Leu	Ala	Ala 350	Gln	Tyr
Pro	Gln	His 355	Thr	Ile	Phe	Cys	Leu 360	Asp	Pro	Val	Ile	Cys 365	Pro	Cys	Ser

Thr Met Tyr Arg Ile His Pro Gly Tyr Leu Ala Trp Ala Leu Glu Glu  
 370 375 380  
 Leu Val Ala Gly Asn Val Ile Asn Gln Ile Ser Val Ser Glu Ser Val  
 385 390 395 400  
 Ala Ala Pro Ala Arg Val Ala Leu Glu Arg Met Leu Ser Val Val Pro  
 405 410 415  
 Ala Ala Pro Val Thr Pro Ser Ser Ser Lys Asp Ala  
 420 425

<210> 607  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(931)  
 <223> RXA01073

<400> 607

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 Met Thr Asn Thr Gln  
 1 5  
 acc gag atc att aat gaa cta aag gtg agc cca gca atc gac gtg gcc 163  
 Thr Glu Ile Ile Asn Glu Leu Lys Val Ser Pro Ala Ile Asp Val Ala  
 10 15 20  
 aag gaa gtt gaa ttc cgt gtg cag ttc ctc gtc gat tac ctg cgg gct 211  
 Lys Glu Val Glu Phe Arg Val Gln Phe Leu Val Asp Tyr Leu Arg Ala  
 25 30 35  
 tcc cat aca aaa ggc ttt gtt ctt ggt att tca ggt ggc cag gat tcc 259  
 Ser His Thr Lys Gly Phe Val Leu Gly Ile Ser Gly Gly Gln Asp Ser  
 40 45 50  
 act ctt gcg gga cga ctc acg cag ctg gca gta gag cgc att cgt gcg 307  
 Thr Leu Ala Gly Arg Leu Thr Gln Leu Ala Val Glu Arg Ile Arg Ala  
 55 60 65  
 gaa gaa aac agc acg gat tat gtc ttc tac gca gtt cgc ctc ccc tac 355  
 Glu Glu Asn Ser Thr Asp Tyr Val Phe Tyr Ala Val Arg Leu Pro Tyr  
 70 75 80 85  
 gcg atc cag gca gat gag gac gat gcg caa gtt gca ttg gaa ttc atc 403  
 Ala Ile Gln Ala Asp Glu Asp Asp Ala Gln Val Ala Leu Glu Phe Ile  
 90 95 100  
 gca cct gac aag agc gtg acc gtc aac gtt aaa gac gca acg gac gcc 451  
 Ala Pro Asp Lys Ser Val Thr Val Asn Val Lys Asp Ala Thr Asp Ala  
 105 110 115  
 acc gaa gca act gtt gca gct gct ttg gaa ctt cct gag ctg acc gac 499  
 Thr Glu Ala Thr Val Ala Ala Ala Leu Glu Leu Pro Glu Leu Thr Asp  
 120 125 130

ttc aat cgg ggc aat att aaa gct cgc caa cgc atg gtt gcc cag tac 547  
 Phe Asn Arg Gly Asn Ile Lys Ala Arg Gln Arg Met Val Ala Gln Tyr  
 135 140 145  
  
 gca atc gca ggc cag ttg ggc ttg ctg gtt att ggc act gat cac gcg 595  
 Ala Ile Ala Gly Gln Leu Gly Leu Leu Val Ile Gly Thr Asp His Ala  
 150 155 160 165  
  
 gct gaa aac gtc acg ggg ttc ttc acc aaa ttc ggt gat ggc gca gct 643  
 Ala Glu Asn Val Thr Gly Phe Phe Thr Lys Phe Gly Asp Gly Ala Ala  
 170 175 180  
  
 gac ctg ctt cct ttg gca ggt ttg agc aag cgt caa gga gct gcc att 691  
 Asp Leu Leu Pro Leu Ala Gly Leu Ser Lys Arg Gln Gly Ala Ala Ile  
 185 190 195  
  
 ctg gag cac ctg ggt gca cct tca agc acg tgg acc aag gtt cct acc 739  
 Leu Glu His Leu Gly Ala Pro Ser Ser Thr Trp Thr Lys Val Pro Thr  
 200 205 210  
  
 gct gat ttg gaa gag gat cgc cca gcg ttg cca gat gag gaa gca ctt 787  
 Ala Asp Leu Glu Glu Asp Arg Pro Ala Leu Pro Asp Glu Glu Ala Leu  
 215 220 225  
  
 ggt gtg tcg tat gcg gac atc gat aat tac ctg gaa aac aag ccc gat 835  
 Gly Val Ser Tyr Ala Asp Ile Asp Asn Tyr Leu Glu Asn Lys Pro Asp  
 230 235 240 245  
  
 gtc agt gaa aaa gcc cag cag cgc att gag cac ctg tgg aag gtg ggc 883  
 Val Ser Glu Lys Ala Gln Gln Arg Ile Glu His Leu Trp Lys Val Gly  
 250 255 260  
  
 cag cac aag cgc cac ctc cct gct acc ccg cag gaa aat tgg tgg cgt 931  
 Gln His Lys Arg His Leu Pro Ala Thr Pro Gln Glu Asn Trp Trp Arg  
 265 270 275  
  
 taatccaaca gtttgagtgt cgc 954

&lt;210&gt; 608

&lt;211&gt; 277

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 608

Met Thr Asn Thr Gln Thr Glu Ile Ile Asn Glu Leu Lys Val Ser Pro  
 1 5 10 15

Ala Ile Asp Val Ala Lys Glu Val Glu Phe Arg Val Gln Phe Leu Val  
 20 25 30

Asp Tyr Leu Arg Ala Ser His Thr Lys Gly Phe Val Leu Gly Ile Ser  
 35 40 45

Gly Gly Gln Asp Ser Thr Leu Ala Gly Arg Leu Thr Gln Leu Ala Val  
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Ala Leu Glu Phe Ile Ala Pro Asp Lys Ser Val Thr Val Asn Val Lys  
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Asp Ala Thr Asp Ala Thr Glu Ala Thr Val Ala Ala Ala Leu Glu Leu  
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Gly Asp Gly Ala Ala Asp Leu Leu Pro Leu Ala Gly Leu Ser Lys Arg  
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Gln Gly Ala Ala Ile Leu Glu His Leu Gly Ala Pro Ser Ser Thr Trp  
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Thr Lys Val Pro Thr Ala Asp Leu Glu Glu Asp Arg Pro Ala Leu Pro  
210 215 220

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Glu Asn Lys Pro Asp Val Ser Glu Lys Ala Gln Gln Arg Ile Glu His  
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Tyr	Gly	Val	Val	Ala	Gly	Thr	Ala	Arg	Val	Leu	Lys	Ala	Ile	Arg	Asp	
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Phe	Val	Phe	Thr	Glu	Glu	Gln	Leu	Ala	Asp	Leu	Asp	Phe	Leu	Asp	Asp	
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Ser	Ile	Met	Asn	Ala	Asp	Ser	Ala	Val	Ala	Ser	Ala	Ala	Ala	Arg	Met	
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Val	Thr	Ala	Ala	Asp	Gly	Arg	Pro	Ile	Ile	Glu	Met	Gly	Ser	Arg	Arg	
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Thr	His	Glu	Tyr	Ser	Ala	Val	Thr	Ala	Ser	Arg	Ala	Ala	Tyr	Leu	Ala	
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Pro	Ala	Ser	Gly	Thr	Ser	Ala	His	Ala	Trp	Thr	Leu	Leu	His	Ile	Asn	
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Asp	Asp	Gly	Thr	Pro	Asn	Glu	Ala	Ala	Ala	Phe	Lys	Ala	Gln	Val	Glu	
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Gln	Gly	Val	Ala	Thr	Ala	Ile	Glu	Val	Ala	Gly	Pro	Asp	Leu	Gly	Gly	
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 Thr Ala Gly Leu Val Tyr Lys Ile Gly Glu Val Ala Gly His Pro Val  
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 Val Arg Thr His Arg Lys Ser Gly Thr Ala Ile Glu Glu Ile Val Tyr  
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 Pro Phe Asn Ala Glu Ala Pro Asp Thr Gly Lys Leu Asp Thr Leu Ser  
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Tyr	Arg	Tyr	Gly	Ile	Pro	Ala	Ser	Gly	Thr	Ser	Ala	His	Ala	Trp	Thr
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Leu	Leu	His	Ile	Asn	Asp	Asp	Gly	Thr	Pro	Asn	Glu	Ala	Ala	Ala	Phe
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Lys	Ile	Val	Val	Ser	Ser	Asp	Leu	Asp	Glu	Phe	Ala	Ile	Ala	Gly	Leu



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Gly	Ser	Gly	Ala	Pro	Thr	Ala	Gly	Leu	Val	Tyr	Lys	Ile	Gly	Glu	Val
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Ala	Gly	His	Pro	Val	Ala	Lys	Arg	Ser	Arg	Asn	Lys	Glu	Ser	Tyr	Gly
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Glu	Glu	Ile	Val	Tyr	Pro	Phe	Asn	Ala	Glu	Ala	Pro	Asp	Thr	Gly	Lys
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Leu	Asp	Thr	Leu	Ser	Leu	Thr	Ile	Pro	Leu	Met	Arg	Asp	Gly	Glu	Ile
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Val	Pro	Gly	Leu	Pro	Thr	Leu	Glu	Asp	Ser	Arg	Ala	Tyr	Leu	Ala	Lys
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Gln	Leu	Val	Ser	Leu	Pro	Trp	Glu	Gly	Leu	Ala	Leu	Ser	Arg	Asp	Glu
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 Met Leu Arg Thr Ile 5  
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 Tyr Val Gly Ser Val Thr Ile Asp Ala Asp Leu Val His Ala Ala Gly 35  
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 Leu Ile Glu Gly Glu Lys Val Ala Ile Val Asp Ile Thr Asn Gly Ala 50  
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 Arg Leu Glu Thr Tyr Val Ile Val Gly Asp Ala Gly Thr Gly Asn Ile

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Cys Ile Asn Gly Ala Ala Ala His Leu Ile Asn Pro Gly Asp Leu Val			
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atc atc atg agc tac ctt cag gca act gat gcg gaa gcc aag gcg tat			403
Ile Ile Met Ser Tyr Leu Gln Ala Thr Asp Ala Glu Ala Lys Ala Tyr			
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Glu Pro Lys Ile Val His Val Asp Ala Asp Asn Arg Ile Val Ala Leu			
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Gly Asn Asp Leu Ala Glu Ala Leu Pro Gly Ser Gly Leu Leu Thr Ser			
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 Gly Thr Gly Asn Ile Cys Ile Asn Gly Ala Ala Ala His Leu Ile Asn  
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 Glu Ala Lys Ala Tyr Glu Pro Lys Ile Val His Val Asp Ala Asp Asn  
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Thr Lys Gln Ala Leu Ile Asp Ala Leu Leu His His Lys Ser Val Gly
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Leu Val Pro Thr Met Gly Ala Leu His Ser Gly His Ala Ser Leu Val
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Lys Ala Ala Arg Ala Glu Asn Asp Thr Val Val Ala Ser Ile Phe Val
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Asn Pro Leu Gln Phe Glu Ala Leu Gly Asp Cys Asp Asp Tyr Arg Asn
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Tyr Pro Arg Gln Leu Asp Ala Asp Leu Ala Leu Leu Glu Glu Ala Gly
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Leu Pro Leu Val Trp Ala Arg Thr Gly Ser Ile Gly Thr Lys Leu Glu
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Gly Ala Ser Arg Pro Gly His Phe Asp Gly Val Ala Thr Val Val Ala
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Lys Leu Phe Asn Leu Val Arg Pro Asp Arg Ala Tyr Phe Gly Gln Lys
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Asp Ala Gln Gln Val Ala Val Ile Arg Arg Leu Val Ala Asp Leu Asp
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Ile Pro Val Glu Ile Arg Pro Val Pro Ile Ile Arg Gly Ala Asp Gly
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Leu Ala Glu Ser Ser Arg Asn Gln Arg Leu Ser Ala Asp Gln Arg Ala
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 Ser Ala Asp Gly Val Arg Leu Asp His Leu Glu Ile Val Asp Pro Ala  
 230 235 240 245

acc ctc gaa cca tta gaa atc gac ggc ctg ctc acc caa cca gcg ttg 883  
 Thr Leu Glu Pro Leu Glu Ile Asp Gly Leu Leu Thr Gln Pro Ala Leu  
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gag ctc tagtaccaac cctgcgttgc agc 960  
 Glu Leu

&lt;210&gt; 614

&lt;211&gt; 279

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 614

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His Lys Ser Val Gly Leu Val Pro Thr Met Gly Ala Leu His Ser Gly  
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His Ala Ser Leu Val Lys Ala Ala Arg Ala Glu Asn Asp Thr Val Val  
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Ala Ser Ile Phe Val Asn Pro Leu Gln Phe Glu Ala Leu Gly Asp Cys  
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Asp Asp Tyr Arg Asn Tyr Pro Arg Gln Leu Asp Ala Asp Leu Ala Leu  
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Leu Glu Glu Ala Gly Val Asp Ile Val Phe Ala Pro Asp Val Glu Glu  
 85 90 95

Met Tyr Pro Gly Gly Leu Pro Leu Val Trp Ala Arg Thr Gly Ser Ile  
 100 105 110

Gly Thr Lys Leu Glu Gly Ala Ser Arg Pro Gly His Phe Asp Gly Val  
 115 120 125

Ala Thr Val Val Ala Lys Leu Phe Asn Leu Val Arg Pro Asp Arg Ala  
 130 135 140

Tyr Phe Gly Gln Lys Asp Ala Gln Gln Val Ala Val Ile Arg Arg Leu  
 145 150 155 160

Val Ala Asp Leu Asp Ile Pro Val Glu Ile Arg Pro Val Pro Ile Ile  
 165 170 175

Arg Gly Ala Asp Gly Leu Ala Glu Ser Ser Arg Asn Gln Arg Leu Ser  
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Ala Asp Gln Arg Ala Gln Ala Leu Val Leu Pro Gln Val Leu Ser Gly  
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Leu Gln Arg Arg Lys Ala Ala Gly Glu Ala Leu Asp Ile Gln Gly Ala  
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Arg Asp Thr Leu Ala Ser Ala Asp Gly Val Arg Leu Asp His Leu Glu  
 225 230 235 240

Ile Val Asp Pro Ala Thr Leu Glu Pro Leu Glu Ile Asp Gly Leu Leu  
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aac ggc cag aaa gtt tcg gtt ctc acc agc tat gat gcg ctt tcg gcg 211  
 Asn Gly Gln Lys Val Ser Val Leu Thr Ser Tyr Asp Ala Leu Ser Ala  
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Arg Ile Val Asp Ala Gly Ile Pro Val Val Gly His Ile Gly Tyr Thr	
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Pro Gln Ser Glu His Ser Leu Gly Gly His Val Val Gln Gly Arg Gly	
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gcg agt tct gga aag ctc atc gcc gat gcc cgc gcg ttg gag cag gcg	643
Ala Ser Ser Gly Lys Leu Ile Ala Asp Ala Arg Ala Leu Glu Gln Ala	
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Gly Ala Phe Ala Val Val Leu Glu Met Val Pro Ala Glu Ala Ala Arg	
185 190 195	
gag gtt acc gag gat ctt tcc atc acc act atc gga atc ggt gcc ggc	739
Glu Val Thr Glu Asp Leu Ser Ile Thr Thr Ile Gly Ile Gly Ala Gly	
200 205 210	
aat ggc aca gat ggg cag gtt ttg gtg tgg cag gat gcc ttc ggc ctc	787
Asn Gly Thr Asp Gly Gln Val Leu Val Trp Gln Asp Ala Phe Gly Leu	
215 220 225	
aac cgc ggc aag aag cca cgc ttc gtc cgc gag tac gcc acc ttg ggc	835
Asn Arg Gly Lys Lys Pro Arg Phe Val Arg Glu Tyr Ala Thr Leu Gly	
230 235 240 245	
gat tcc ttg cac gac gcc gcg cag gcc tac atc gcc gat atc cac gcg	883
Asp Ser Leu His Asp Ala Ala Gln Ala Tyr Ile Ala Asp Ile His Ala	
250 255 260	
ggt acc ttc cca ggc gaa gcg gag tcc ttt taatgcaggt agcaaccaca	933
Gly Thr Phe Pro Gly Glu Ala Glu Ser Phe	
265 270	
aag	936

&lt;210&gt; 616

&lt;211&gt; 271

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 616

Met	Pro	Met	Ser	Gly	Ile	Asp	Ala	Lys	Lys	Ile	Arg	Thr	Arg	His	Phe
1				5					10					15	

Arg Glu Ala Lys Val Asn Gly Gln Lys Val Ser Val Leu Thr Ser Tyr  
                   20                                  25                                  30  
 Asp Ala Leu Ser Ala Arg Ile Phe Asp Glu Ala Gly Val Asp Met Leu  
                   35                                  40                                  45  
 Leu Val Gly Asp Ser Ala Ala Asn Val Val Leu Gly Arg Asp Thr Thr  
                   50                                  55                                  60  
 Leu Ser Ile Thr Leu Asp Glu Met Ile Val Leu Ala Lys Ala Val Thr  
                   65                                  70                                  75                                  80  
 Ile Ala Thr Lys Arg Ala Leu Val Val Val Asp Leu Pro Phe Gly Thr  
                                   85                                  90                                  95  
 Tyr Glu Val Ser Pro Asn Gln Ala Val Glu Ser Ala Ile Arg Val Met  
                   100                                  105                                  110  
 Arg Glu Thr Gly Ala Ala Ala Val Lys Ile Glu Gly Gly Val Glu Ile  
                   115                                  120                                  125  
 Ala Gln Thr Ile Arg Arg Ile Val Asp Ala Gly Ile Pro Val Val Gly  
                   130                                  135                                  140  
 His Ile Gly Tyr Thr Pro Gln Ser Glu His Ser Leu Gly Gly His Val  
                   145                                  150                                  155                                  160  
 Val Gln Gly Arg Gly Ala Ser Ser Gly Lys Leu Ile Ala Asp Ala Arg  
                                   165                                  170                                  175  
 Ala Leu Glu Gln Ala Gly Ala Phe Ala Val Val Leu Glu Met Val Pro  
                   180                                  185                                  190  
 Ala Glu Ala Ala Arg Glu Val Thr Glu Asp Leu Ser Ile Thr Thr Ile  
                   195                                  200                                  205  
 Gly Ile Gly Ala Gly Asn Gly Thr Asp Gly Gln Val Leu Val Trp Gln  
                   210                                  215                                  220  
 Asp Ala Phe Gly Leu Asn Arg Gly Lys Lys Pro Arg Phe Val Arg Glu  
                   225                                  230                                  235                                  240  
 Tyr Ala Thr Leu Gly Asp Ser Leu His Asp Ala Ala Gln Ala Tyr Ile  
                                   245                                  250                                  255  
 Ala Asp Ile His Ala Gly Thr Phe Pro Gly Glu Ala Glu Ser Phe  
                   260                                  265                                  270

&lt;210&gt; 617

&lt;211&gt; 930

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(907)

&lt;223&gt; FRXA01929

&lt;400&gt; 617

tgactccata acgagaactt aatcgagcaa cacccttgaa cagtgaatca aatcggaatt 60

tatttattct	gagctgggtca	tcacatctat	actcatgccc	atg	tca	ggc	att	gat	115
				Met	Ser	Gly	Ile	Asp	
				1				5	
gca aag aaa atc cgc acc cgt cat ttc cgc gaa gct aaa gta aac ggc	163								
Ala Lys Lys Ile Arg Thr Arg His Phe Arg Glu Ala Lys Val Asn Gly									
	10 15 20								
cag aaa gtt tcg gtt ctc acc agc tat gat gcg ctt tcg gcg cgc att	211								
Gln Lys Val Ser Val Leu Thr Ser Tyr Asp Ala Leu Ser Ala Arg Ile									
	25 30 35								
ttt gat gag gct ggc gtc gat atg ctc ctt gtt ggt gat tcc gct gcc	259								
Phe Asp Glu Ala Gly Val Asp Met Leu Leu Val Gly Asp Ser Ala Ala									
	40 45 50								
aac gtt gtg ctg ggt cgc gat acc acc ttg tcg atc acc ttg gat gag	307								
Asn Val Val Leu Gly Arg Asp Thr Thr Leu Ser Ile Thr Leu Asp Glu									
	55 60 65								
atg att gtg ctg gcc aag gcg gtg acg atc gct acg aag cgt gcg ctt	355								
Met Ile Val Leu Ala Lys Ala Val Thr Ile Ala Thr Lys Arg Ala Leu									
	70 75 80 85								
gtg gtg gtt gat ctg ccg ttt ggt acc tat gag gtg agc cca aat cag	403								
Val Val Val Asp Leu Pro Phe Gly Thr Tyr Glu Val Ser Pro Asn Gln									
	90 95 100								
gcg gtg gag tcc gcg atc ccg gtc atg cgt gaa acg ggt gcg gct gcg	451								
Ala Val Glu Ser Ala Ile Arg Val Met Arg Glu Thr Gly Ala Ala Ala									
	105 110 115								
gtg aag atc gag ggt ggc gtg gag atc gcg cag acg att cga cgc att	499								
Val Lys Ile Glu Gly Gly Val Glu Ile Ala Gln Thr Ile Arg Arg Ile									
	120 125 130								
gtt gat gct gga att ccg gtt gtc ggc cac atc ggg tac acc ccg cag	547								
Val Asp Ala Gly Ile Pro Val Val Gly His Ile Gly Tyr Thr Pro Gln									
	135 140 145								
tcc gag cat tcc ttg ggc ggc cac gtg gtt cag ggt cgt ggc gcg agt	595								
Ser Glu His Ser Leu Gly Gly His Val Val Gln Gly Arg Gly Ala Ser									
	150 155 160 165								
tct gga aag ctc atc gcc gat gcc cgc gcg ttg gag cag gcg ggt gcg	643								
Ser Gly Lys Leu Ile Ala Asp Ala Arg Ala Leu Glu Gln Ala Gly Ala									
	170 175 180								
ttt gcg gtt gtg ttg gag atg gtt cca gca gag gca gcg cgc gag gtt	691								
Phe Ala Val Val Leu Glu Met Val Pro Ala Glu Ala Ala Arg Glu Val									
	185 190 195								
acc gag gat ctt tcc atc acc act atc gga atc ggt gcc ggc aat ggc	739								
Thr Glu Asp Leu Ser Ile Thr Thr Ile Gly Ile Gly Ala Gly Asn Gly									
	200 205 210								
aca gat ggg cag gtt ttg gtg tgg cag gat gcc ttc ggc ctc aac cgc	787								
Thr Asp Gly Gln Val Leu Val Trp Gln Asp Ala Phe Gly Leu Asn Arg									
	215 220 225								



ggc aag aag cca cgc ttc gtc cgc gag tac gcc acc ttg ggc gat tcc 835  
 Gly Lys Lys Pro Arg Phe Val Arg Glu Tyr Ala Thr Leu Gly Asp Ser  
 230 235 240 245

ttg cac gac gcc gcg cag gcc tac atc gcc gat atc cac gcg ggt acc 883  
 Leu His Asp Ala Ala Gln Ala Tyr Ile Ala Asp Ile His Ala Gly Thr  
 250 255 260

ttc cca ggc gaa gcg gag tcc ttt taatgcaggt agcaaccaca aag 930  
 Phe Pro Gly Glu Ala Glu Ser Phe  
 265

<210> 618

<211> 269

<212> PRT

<213> Corynebacterium glutamicum

<400> 618

Met Ser Gly Ile Asp Ala Lys Lys Ile Arg Thr Arg His Phe Arg Glu  
 1 5 10 15

Ala Lys Val Asn Gly Gln Lys Val Ser Val Leu Thr Ser Tyr Asp Ala  
 20 25 30

Leu Ser Ala Arg Ile Phe Asp Glu Ala Gly Val Asp Met Leu Leu Val  
 35 40 45

Gly Asp Ser Ala Ala Asn Val Val Leu Gly Arg Asp Thr Thr Leu Ser  
 50 55 60

Ile Thr Leu Asp Glu Met Ile Val Leu Ala Lys Ala Val Thr Ile Ala  
 65 70 75 80

Thr Lys Arg Ala Leu Val Val Val Asp Leu Pro Phe Gly Thr Tyr Glu  
 85 90 95

Val Ser Pro Asn Gln Ala Val Glu Ser Ala Ile Arg Val Met Arg Glu  
 100 105 110

Thr Gly Ala Ala Ala Val Lys Ile Glu Gly Gly Val Glu Ile Ala Gln  
 115 120 125

Thr Ile Arg Arg Ile Val Asp Ala Gly Ile Pro Val Val Gly His Ile  
 130 135 140

Gly Tyr Thr Pro Gln Ser Glu His Ser Leu Gly Gly His Val Val Gln  
 145 150 155 160

Gly Arg Gly Ala Ser Ser Gly Lys Leu Ile Ala Asp Ala Arg Ala Leu  
 165 170 175

Glu Gln Ala Gly Ala Phe Ala Val Val Leu Glu Met Val Pro Ala Glu  
 180 185 190

Ala Ala Arg Glu Val Thr Glu Asp Leu Ser Ile Thr Thr Ile Gly Ile  
 195 200 205

Gly Ala Gly Asn Gly Thr Asp Gly Gln Val Leu Val Trp Gln Asp Ala  
 210 215 220

Phe Gly Leu Asn Arg Gly Lys Lys Pro Arg Phe Val Arg Glu Tyr Ala  
 225 230 235 240  
 Thr Leu Gly Asp Ser Leu His Asp Ala Ala Gln Ala Tyr Ile Ala Asp  
 245 250 255  
 Ile His Ala Gly Thr Phe Pro Gly Glu Ala Glu Ser Phe  
 260 265

<210> 619  
 <211> 921  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(898)  
 <223> RXA01521

<400> 619  
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cgcaagatat tgagctgtgg gcaattcaga aggaggaccg ttg agt ttc acg cat 115  
 Leu Ser Phe Thr His  
 1 5

ggt cag ggc aga gtt ttt gat acc gtc gag cag atc cgc atg ttc ggc 163  
 Gly Gln Gly Arg Val Phe Asp Thr Val Glu Gln Ile Arg Met Phe Gly  
 10 15 20

agc gcc ctg cgc aaa acc ggc aaa cca gtg gtg ctc gta ccc ttg gga 211  
 Ser Ala Leu Arg Lys Thr Gly Lys Pro Val Val Leu Val Pro Leu Gly  
 25 30 35

aat ggc ctc cac gca ggc cat att gcg ctc atc cgc gca gca aaa cgc 259  
 Asn Gly Leu His Ala Gly His Ile Ala Leu Ile Arg Ala Ala Lys Arg  
 40 45 50

atc ccc ggt gcg gtg gtc gtc gtc gcc tat gcc ggc ccg gaa tcg gat 307  
 Ile Pro Gly Ala Val Val Val Val Ala Tyr Ala Gly Pro Glu Ser Asp  
 55 60 65

cac gca cgt tta agg gaa gag ctt atc gac gcg atc ttc ccg ttc aat 355  
 His Ala Arg Leu Arg Glu Glu Leu Ile Asp Ala Ile Phe Pro Phe Asn  
 70 75 80 85

ccc gaa acg cta tgg cct cac ggc atc cgg gtg gaa gtt aca ggt ggc 403  
 Pro Glu Thr Leu Trp Pro His Gly Ile Arg Val Glu Val Thr Gly Gly  
 90 95 100

cca aca ctt acc cca caa ggt gcg gaa gta acc aag gtg ctg ggg ctg 451  
 Pro Thr Leu Thr Pro Gln Gly Ala Glu Val Thr Lys Val Leu Gly Leu  
 105 110 115

ttg gga atc acc gga gca act gat gtg gtg ctc ggt gaa aag gac tat 499  
 Leu Gly Ile Thr Gly Ala Thr Asp Val Val Leu Gly Glu Lys Asp Tyr  
 120 125 130

gag ctg gtg gtt cta gtc cag cgc gcc ctt aat gat ctg cat att cca 547  
 Glu Leu Val Val Leu Val Gln Arg Ala Leu Asn Asp Leu His Ile Pro

135	140	145	
gta aaa ctg cat tct gtt cca acc gtg cgc atg cca gat gga cta gcc Val Lys Leu His Ser Val Pro Thr Val Arg Met Pro Asp Gly Leu Ala 150 155 160 165			595
att tcc ctg cgt aat att tca gtg ccc gaa gac tcc cgc gaa acg gca Ile Ser Leu Arg Asn Ile Ser Val Pro Glu Asp Ser Arg Glu Thr Ala 170 175 180			643
ttg agc ctg gca gca gcc ctc acc gcc ggt gcg cat tcg gca gaa cac Leu Ser Leu Ala Ala Leu Thr Ala Gly Ala His Ser Ala Glu His 185 190 195			691
ggc gag gca gtg gtt aaa gaa aca gtc acg caa gtg ctc aaa gcc gca Gly Glu Ala Val Val Lys Glu Thr Val Thr Gln Val Leu Lys Ala Ala 200 205 210			739
ggc gtg acc ccc gat tat gta gaa atc cgt ggc ctg gat ctt gga cca Gly Val Thr Pro Asp Tyr Val Glu Ile Arg Gly Leu Asp Leu Gly Pro 215 220 225			787
gcc ccc gaa atc gga gac gcc cga ctc ttc gca gcc atc acg ctt ggc Ala Pro Glu Ile Gly Asp Ala Arg Leu Phe Ala Ala Ile Thr Leu Gly 230 235 240 245			835
gat gtc caa ctc cac gac aac gtc ggc cta ccc ctt gga atc ggc ttc Asp Val Gln Leu His Asp Asn Val Gly Leu Pro Leu Gly Ile Gly Phe 250 255 260			883
aaa aac atc gaa ggc tgatcccggt ttacccagtt cgc Lys Asn Ile Glu Gly 265			921

&lt;210&gt; 620

&lt;211&gt; 266

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 620

Leu Ser Phe Thr His Gly Gln Gly Arg Val Phe Asp Thr Val Glu Gln
1 5 10 15

Ile Arg Met Phe Gly Ser Ala Leu Arg Lys Thr Gly Lys Pro Val Val
20 25 30

Leu Val Pro Leu Gly Asn Gly Leu His Ala Gly His Ile Ala Leu Ile
35 40 45

Arg Ala Ala Lys Arg Ile Pro Gly Ala Val Val Val Val Ala Tyr Ala
50 55 60

Gly Pro Glu Ser Asp His Ala Arg Leu Arg Glu Glu Leu Ile Asp Ala
65 70 75 80

Ile Phe Pro Phe Asn Pro Glu Thr Leu Trp Pro His Gly Ile Arg Val
85 90 95

Glu Val Thr Gly Gly Pro Thr Leu Thr Pro Gln Gly Ala Glu Val Thr
100 105 110

Lys Val Leu Gly Leu Leu Gly Ile Thr Gly Ala Thr Asp Val Val Leu  
 115 120 125  
 Gly Glu Lys Asp Tyr Glu Leu Val Val Leu Val Gln Arg Ala Leu Asn  
 130 135 140  
 Asp Leu His Ile Pro Val Lys Leu His Ser Val Pro Thr Val Arg Met  
 145 150 155 160  
 Pro Asp Gly Leu Ala Ile Ser Leu Arg Asn Ile Ser Val Pro Glu Asp  
 165 170 175  
 Ser Arg Glu Thr Ala Leu Ser Leu Ala Ala Ala Leu Thr Ala Gly Ala  
 180 185 190  
 His Ser Ala Glu His Gly Glu Ala Val Val Lys Glu Thr Val Thr Gln  
 195 200 205  
 Val Leu Lys Ala Ala Gly Val Thr Pro Asp Tyr Val Glu Ile Arg Gly  
 210 215 220  
 Leu Asp Leu Gly Pro Ala Pro Glu Ile Gly Asp Ala Arg Leu Phe Ala  
 225 230 235 240  
 Ala Ile Thr Leu Gly Asp Val Gln Leu His Asp Asn Val Gly Leu Pro  
 245 250 255  
 Leu Gly Ile Gly Phe Lys Asn Ile Glu Gly  
 260 265

&lt;210&gt; 621

&lt;211&gt; 1137

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1114)

&lt;223&gt; RXS01145

&lt;400&gt; 621

taatgtagtt gtctgccc aa gcgagttaaa ctcccacgat ttacagtggg gggcagacat 60

cttttcacca aaattttttac gaaaggcgag atttttctccc atg gct att gaa ctg 115  
 Met Ala Ile Glu Leu  
 1 5

ctt tat gat gct gac gct gac ctc tcc ttg atc cag ggc cgt aag gtt 163  
 Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile Gln Gly Arg Lys Val  
 10 15 20

gcc atc gtt ggc tac ggc tcc cag ggc cac gca cac tcc cag aac ctc 211  
 Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala His Ser Gln Asn Leu  
 25 30 35

cgc gat tct ggc gtt gag gtt gtc att ggt ctg cgc gag ggc tcc aag 259  
 Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu Arg Glu Gly Ser Lys  
 40 45 50

tcc gca gag aag gca aag gaa gca ggc ttc gag gtc aag acc acc gct	307
Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu Val Lys Thr Thr Ala	
55 60 65	
gag gct gca gct tgg gct gac gtc atc atg ctc ctg gct cca gac acc	355
Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu Leu Ala Pro Asp Thr	
70 75 80 85	
tcc cag gca gaa atc ttc acc aac gac atc gag cca aac ctg aac gca	403
Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu Pro Asn Leu Asn Ala	
90 95 100	
ggc gac gca ctg ctg ttc ggc cac ggc ctg aac att cac ttc gac ctg	451
Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn Ile His Phe Asp Leu	
105 110 115	
atc aag cca gct gac gac atc atc gtt ggc atg gtt gcg cca aag ggc	499
Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met Val Ala Pro Lys Gly	
120 125 130	
cca ggc cac ttg gtt cgc cgt cag ttc gtt gat ggc aag ggt gtt cct	547
Pro Gly His Leu Val Arg Arg Gln Phe Val Asp Gly Lys Gly Val Pro	
135 140 145	
tgc ctc atc gca gtc gac cag gac cca acc gga acc gca cag gct ctg	595
Cys Leu Ile Ala Val Asp Gln Asp Pro Thr Gly Thr Ala Gln Ala Leu	
150 155 160 165	
acc ctg tcc tac gca gca gca atc ggt ggc gca cgc gca ggc gtt atc	643
Thr Leu Ser Tyr Ala Ala Ala Ile Gly Gly Ala Arg Ala Gly Val Ile	
170 175 180	
cca acc acc ttc gaa gct gag acc gtc acc gac ctc ttc ggc gag cag	691
Pro Thr Thr Phe Glu Ala Glu Thr Val Thr Asp Leu Phe Gly Glu Gln	
185 190 195	
gct gtt ctc tgc ggt ggc acc gag gaa ctg gtc aag gtt ggc ttc gag	739
Ala Val Leu Cys Gly Gly Thr Glu Glu Leu Val Lys Val Gly Phe Glu	
200 205 210	
gtt ctc acc gaa gct ggc tac gag cca gag atg gca tac ttc gag gtt	787
Val Leu Thr Glu Ala Gly Tyr Glu Pro Glu Met Ala Tyr Phe Glu Val	
215 220 225	
ctt cac gag ctc aag ctc atc gtt gac ctc atg ttc gaa ggt ggc atc	835
Leu His Glu Leu Lys Leu Ile Val Asp Leu Met Phe Glu Gly Gly Ile	
230 235 240 245	
agc aac atg aac tac tct gtt tct gac acc gct gag ttc ggt ggc tac	883
Ser Asn Met Asn Tyr Ser Val Ser Asp Thr Ala Glu Phe Gly Gly Tyr	
250 255 260	
ctc tcc ggc cca cgc gtc atc gat gca gac acc aag tcc cgc atg aag	931
Leu Ser Gly Pro Arg Val Ile Asp Ala Asp Thr Lys Ser Arg Met Lys	
265 270 275	
gac atc ctg acc gat atc cag gac ggc acc ttc acc aag cgc ctc atc	979
Asp Ile Leu Thr Asp Ile Gln Asp Gly Thr Phe Thr Lys Arg Leu Ile	
280 285 290	

gca aac gtt gag aac ggc aac acc gag ctt gag ggc ctt cgt gct tcc  
 1027  
 Ala Asn Val Glu Asn Gly Asn Thr Glu Leu Glu Gly Leu Arg Ala Ser  
       295                              300                              305

tac aac aac cac cca atc gag gag acc ggc gct aag ctc cgc gac ctc  
 1075  
 Tyr Asn Asn His Pro Ile Glu Glu Thr Gly Ala Lys Leu Arg Asp Leu  
 310                              315                              320                              325

atg agc tgg gtc aag gtt gac gct cgc gca gaa acc gct taagtttcac  
 1124  
 Met Ser Trp Val Lys Val Asp Ala Arg Ala Glu Thr Ala  
                               330                              335

ccctttgacg gct  
 1137

<210> 622  
 <211> 338  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 622  
 Met Ala Ile Glu Leu Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile  
       1                              5                              10                              15  
 Gln Gly Arg Lys Val Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala  
                               20                              25                              30  
 His Ser Gln Asn Leu Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu  
                               35                              40                              45  
 Arg Glu Gly Ser Lys Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu  
                               50                              55                              60  
 Val Lys Thr Thr Ala Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu  
       65                              70                              75                              80  
 Leu Ala Pro Asp Thr Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu  
                               85                              90                              95  
 Pro Asn Leu Asn Ala Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn  
                               100                              105                              110  
 Ile His Phe Asp Leu Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met  
                               115                              120                              125  
 Val Ala Pro Lys Gly Pro Gly His Leu Val Arg Arg Gln Phe Val Asp  
                               130                              135                              140  
 Gly Lys Gly Val Pro Cys Leu Ile Ala Val Asp Gln Asp Pro Thr Gly  
 145                              150                              155                              160  
 Thr Ala Gln Ala Leu Thr Leu Ser Tyr Ala Ala Ala Ile Gly Gly Ala  
                               165                              170                              175  
 Arg Ala Gly Val Ile Pro Thr Thr Phe Glu Ala Glu Thr Val Thr Asp  
                               180                              185                              190

Leu Phe Gly Glu Gln Ala Val Leu Cys Gly Gly Thr Glu Glu Leu Val  
 195 200 205  
 Lys Val Gly Phe Glu Val Leu Thr Glu Ala Gly Tyr Glu Pro Glu Met  
 210 215 220  
 Ala Tyr Phe Glu Val Leu His Glu Leu Lys Leu Ile Val Asp Leu Met  
 225 230 235 240  
 Phe Glu Gly Gly Ile Ser Asn Met Asn Tyr Ser Val Ser Asp Thr Ala  
 245 250 255  
 Glu Phe Gly Gly Tyr Leu Ser Gly Pro Arg Val Ile Asp Ala Asp Thr  
 260 265 270  
 Lys Ser Arg Met Lys Asp Ile Leu Thr Asp Ile Gln Asp Gly Thr Phe  
 275 280 285  
 Thr Lys Arg Leu Ile Ala Asn Val Glu Asn Gly Asn Thr Glu Leu Glu  
 290 295 300  
 Gly Leu Arg Ala Ser Tyr Asn Asn His Pro Ile Glu Glu Thr Gly Ala  
 305 310 315 320  
 Lys Leu Arg Asp Leu Met Ser Trp Val Lys Val Asp Ala Arg Ala Glu  
 325 330 335

Thr Ala

<210> 623  
 <211> 556  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(556)  
 <223> FRXA01145

<400> 623  
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 cttttcacca aaatttttac gaaaggcgag attttctccc atg gct att gaa ctg 115  
 Met Ala Ile Glu Leu  
 1 5  
 ctt tat gat gct gac gct gac ctc tcc ttg atc cag ggc cgt aag gtt 163  
 Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile Gln Gly Arg Lys Val  
 10 15 20  
 gcc atc gtt ggc tac ggc tcc cag ggc cac gca cac tcc cag aac ctc 211  
 Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala His Ser Gln Asn Leu  
 25 30 35  
 cgc gat tct ggc gtt gag gtt gtc att ggt ctg cgc gag ggc tcc aag 259  
 Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu Arg Glu Gly Ser Lys  
 40 45 50  
 tcc gca gag aag gca aag gaa gca ggc ttc gag gtc aag acc acc gct 307

Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu Val Lys Thr Thr Ala  
 55 60 65

gag gct gca gct tgg gct gac gtc atc atg ctc ctg gct cca gac acc 355  
 Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu Leu Ala Pro Asp Thr  
 70 75 80 85

tcc cag gca gaa atc ttc acc aac gac atc gag cca aac ctg aac gca 403  
 Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu Pro Asn Leu Asn Ala  
 90 95 100

ggc gac gca ctg ctg ttc ggc cac ggc ctg aac att cac ttc gac ctg 451  
 Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn Ile His Phe Asp Leu  
 105 110 115

atc aag cca gct gac gac atc atc gtt ggc atg gtt gcg cca aag ggc 499  
 Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met Val Ala Pro Lys Gly  
 120 125 130

cca ggc cac ttg gtt cgc cgt cag ttc gtt gat ggc aag ggt gtt cct 547  
 Pro Gly His Leu Val Arg Arg Gln Phe Val Asp Gly Lys Gly Val Pro  
 135 140 145

tgc ctc atc 556  
 Cys Leu Ile  
 150

&lt;210&gt; 624

&lt;211&gt; 152

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 624

Met Ala Ile Glu Leu Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile  
 1 5 10 15

Gln Gly Arg Lys Val Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala  
 20 25 30

His Ser Gln Asn Leu Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu  
 35 40 45

Arg Glu Gly Ser Lys Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu  
 50 55 60

Val Lys Thr Thr Ala Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu  
 65 70 75 80

Leu Ala Pro Asp Thr Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu  
 85 90 95

Pro Asn Leu Asn Ala Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn  
 100 105 110

Ile His Phe Asp Leu Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met  
 115 120 125

Val Ala Pro Lys Gly Pro Gly His Leu Val Arg Arg Gln Phe Val Asp  
 130 135 140



Gly Lys Gly Val Pro Cys Leu Ile  
145 150

<210> 625  
<211> 1389  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(1366)  
<223> RXA02239

<400> 625  
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Val Pro Met Thr His  
1 5  
gtt tca agc ccc tcc gca ccc cgc aac gtg gtt gtt ggt gtt gcc ggc 163  
Val Ser Ser Pro Ser Ala Pro Arg Asn Val Val Val Gly Val Ala Gly  
10 15 20  
gga atc gca gcg tac aag gcg tgt cac atc gtg cgc gcg ttt aaa gaa 211  
Gly Ile Ala Ala Tyr Lys Ala Cys His Ile Val Arg Ala Phe Lys Glu  
25 30 35  
gcg ggc gat aat gtg cgg gtg gtt cct acg gaa tcc gcg ttg aag ttt 259  
Ala Gly Asp Asn Val Arg Val Val Pro Thr Glu Ser Ala Leu Lys Phe  
40 45 50  
gtg ggg aag gcg acg ttt gaa gcg ttg tct ggc aat ccg gtg tct aca 307  
Val Gly Lys Ala Thr Phe Glu Ala Leu Ser Gly Asn Pro Val Ser Thr  
55 60 65  
acg gtg ttt gat gcg gtg gat tcc gtg cag cat gtg aaa gtt ggc cag 355  
Thr Val Phe Asp Ala Val Asp Ser Val Gln His Val Lys Val Gly Gln  
70 75 80 85  
gaa gct gat ttg atc gtg att gcg ccg gcg aca gcc gat ttg atg gcg 403  
Glu Ala Asp Leu Ile Val Ile Ala Pro Ala Thr Ala Asp Leu Met Ala  
90 95 100  
cgt gtg gtg gca ggt ctc ggt gac gat ctg ttg gcg gcg acg ctg ctg 451  
Arg Val Val Ala Gly Leu Gly Asp Asp Leu Leu Ala Ala Thr Leu Leu  
105 110 115  
gtg gca acg tgc ccc gtg gtt att gcg ccg gcc atg cat acg gag atg 499  
Val Ala Thr Cys Pro Val Val Ile Ala Pro Ala Met His Thr Glu Met  
120 125 130  
tgg ttt aat ccg gct acc gta gcc aat gtg gca acg ctg agg cag cgg 547  
Trp Phe Asn Pro Ala Thr Val Ala Asn Val Ala Thr Leu Arg Gln Arg  
135 140 145  
ggg att acc gtg att gag cct gcg cat ggt cga ctc acc ggt aaa gat 595  
Gly Ile Thr Val Ile Glu Pro Ala His Gly Arg Leu Thr Gly Lys Asp  
150 155 160 165

aca ggc cct ggc cgg ctg ccg gat cca gag cag att gtt gat tta gcc	643
Thr Gly Pro Gly Arg Leu Pro Asp Pro Glu Gln Ile Val Asp Leu Ala	
170 175 180	
aat gcg gtg cac gcc ggg gcg agg ttg cct cag gat ttg gcg ggc aag	691
Asn Ala Val His Ala Gly Ala Arg Leu Pro Gln Asp Leu Ala Gly Lys	
185 190 195	
aaa gtg ctg atc act gct ggt ggc acg cat gag cat att gat cct gtg	739
Lys Val Leu Ile Thr Ala Gly Gly Thr His Glu His Ile Asp Pro Val	
200 205 210	
cgc ttt att ggc aat agt tcc tcg ggc cgt caa ggt ttt gcg ttg ggt	787
Arg Phe Ile Gly Asn Ser Ser Ser Gly Arg Gln Gly Phe Ala Leu Gly	
215 220 225	
gaa atc gca gca cag cga ggt gct cat gtc agc atc gtg gcg gga aat	835
Glu Ile Ala Ala Gln Arg Gly Ala His Val Ser Ile Val Ala Gly Asn	
230 235 240 245	
gct gcg gag ctg ccc act ccg gca ggc gca gag atc gtg ccg gtg gtg	883
Ala Ala Glu Leu Pro Thr Pro Ala Gly Ala Glu Ile Val Pro Val Val	
250 255 260	
tcc aca caa gac atg ttt gat gca gtc cag gaa cga gct ggc caa tct	931
Ser Thr Gln Asp Met Phe Asp Ala Val Gln Glu Arg Ala Gly Gln Ser	
265 270 275	
gat ttc atc gtc atg gcg gca gcg gta gct gat ttc acg ccc gca tcg	979
Asp Phe Ile Val Met Ala Ala Ala Val Ala Asp Phe Thr Pro Ala Ser	
280 285 290	
cag gcg aca tcg aag ttg aag aag ggc tca gat tct gat gaa gac gca	
1027	
Gln Ala Thr Ser Lys Leu Lys Lys Gly Ser Asp Ser Asp Glu Asp Ala	
295 300 305	
ttg agc acc atc tcg ttg gtg gaa aac ccg gat att ttg gct acc acg	
1075	
Leu Ser Thr Ile Ser Leu Val Glu Asn Pro Asp Ile Leu Ala Thr Thr	
310 315 320 325	
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1123	
Val Lys Arg Arg Glu Ala Gly Glu Leu Asp Ser Asn Pro Val Ile Val	
330 335 340	
ggt ttt gct gcg gaa act gga gac gag cac acc acc gcc ttg gag tat	
1171	
Gly Phe Ala Ala Glu Thr Gly Asp Glu His Thr Thr Ala Leu Glu Tyr	
345 350 355	
gcg cgc aag aaa ctg cag aag aag ggc tgc gac ctc ctc atg tgt aat	
1219	
Ala Arg Lys Lys Leu Gln Lys Lys Gly Cys Asp Leu Leu Met Cys Asn	
360 365 370	
gag gtg ggc atg ggc aaa gtg ttt ggg caa aag cac aat gag ggc tgg	
1267	
Glu Val Gly Met Gly Lys Val Phe Gly Gln Lys His Asn Glu Gly Trp	
375 380 385	

att ttg gat gct cac ggt ggg gta gtc gat gtg gag cac ggc agc aaa  
1315

Ile Leu Asp Ala His Gly Gly Val Val Asp Val Glu His Gly Ser Lys  
390 395 400 405

atc gag gtt gct gcg caa att tgg gac gcg gca ctg gcg tat cgc gaa  
1363

Ile Glu Val Ala Ala Gln Ile Trp Asp Ala Ala Leu Ala Tyr Arg Glu  
410 415 420

gtc tagaaaaatc cagctagacc act

1389

Val

<210> 626

<211> 422

<212> PRT

<213> Corynebacterium glutamicum

<400> 626

Val Pro Met Thr His Val Ser Ser Pro Ser Ala Pro Arg Asn Val Val  
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Val Gly Val Ala Gly Gly Ile Ala Ala Tyr Lys Ala Cys His Ile Val  
20 25 30

Arg Ala Phe Lys Glu Ala Gly Asp Asn Val Arg Val Val Pro Thr Glu  
35 40 45

Ser Ala Leu Lys Phe Val Gly Lys Ala Thr Phe Glu Ala Leu Ser Gly  
50 55 60

Asn Pro Val Ser Thr Thr Val Phe Asp Ala Val Asp Ser Val Gln His  
65 70 75 80

Val Lys Val Gly Gln Glu Ala Asp Leu Ile Val Ile Ala Pro Ala Thr  
85 90 95

Ala Asp Leu Met Ala Arg Val Val Ala Gly Leu Gly Asp Asp Leu Leu  
100 105 110

Ala Ala Thr Leu Leu Val Ala Thr Cys Pro Val Val Ile Ala Pro Ala  
115 120 125

Met His Thr Glu Met Trp Phe Asn Pro Ala Thr Val Ala Asn Val Ala  
130 135 140

Thr Leu Arg Gln Arg Gly Ile Thr Val Ile Glu Pro Ala His Gly Arg  
145 150 155 160

Leu Thr Gly Lys Asp Thr Gly Pro Gly Arg Leu Pro Asp Pro Glu Gln  
165 170 175

Ile Val Asp Leu Ala Asn Ala Val His Ala Gly Ala Arg Leu Pro Gln  
180 185 190

Asp Leu Ala Gly Lys Lys Val Leu Ile Thr Ala Gly Gly Thr His Glu  
195 200 205

His Ile Asp Pro Val Arg Phe Ile Gly Asn Ser Ser Ser Gly Arg Gln  
 210 215 220  
 Gly Phe Ala Leu Gly Glu Ile Ala Ala Gln Arg Gly Ala His Val Ser  
 225 230 235 240  
 Ile Val Ala Gly Asn Ala Ala Glu Leu Pro Thr Pro Ala Gly Ala Glu  
 245 250 255  
 Ile Val Pro Val Val Ser Thr Gln Asp Met Phe Asp Ala Val Gln Glu  
 260 265 270  
 Arg Ala Gly Gln Ser Asp Phe Ile Val Met Ala Ala Ala Val Ala Asp  
 275 280 285  
 Phe Thr Pro Ala Ser Gln Ala Thr Ser Lys Leu Lys Lys Gly Ser Asp  
 290 295 300  
 Ser Asp Glu Asp Ala Leu Ser Thr Ile Ser Leu Val Glu Asn Pro Asp  
 305 310 315 320  
 Ile Leu Ala Thr Thr Val Lys Arg Arg Glu Ala Gly Glu Leu Asp Ser  
 325 330 335  
 Asn Pro Val Ile Val Gly Phe Ala Ala Glu Thr Gly Asp Glu His Thr  
 340 345 350  
 Thr Ala Leu Glu Tyr Ala Arg Lys Lys Leu Gln Lys Lys Gly Cys Asp  
 355 360 365  
 Leu Leu Met Cys Asn Glu Val Gly Met Gly Lys Val Phe Gly Gln Lys  
 370 375 380  
 His Asn Glu Gly Trp Ile Leu Asp Ala His Gly Gly Val Val Asp Val  
 385 390 395 400  
 Glu His Gly Ser Lys Ile Glu Val Ala Ala Gln Ile Trp Asp Ala Ala  
 405 410 415  
 Leu Ala Tyr Arg Glu Val  
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 <212> DNA  
 <213> Corynebacterium glutamicum

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 <223> RXA00581

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 Met Ala Glu Gln Asn  
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gct gca agc aca act ggt gtg aaa cct tcc cca cgc aca cca gat ttc	163
Ala Ala Ser Thr Thr Gly Val Lys Pro Ser Pro Arg Thr Pro Asp Phe	
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agc ccc tac ctt gat ttc gac cgc gca caa tgg cgc gag ctg aga aac	211
Ser Pro Tyr Leu Asp Phe Asp Arg Ala Gln Trp Arg Glu Leu Arg Asn	
25 30 35	
tca atg cct cag gtg ctg acc caa aaa gaa gtc att gaa ctt cga ggc	259
Ser Met Pro Gln Val Leu Thr Gln Lys Glu Val Ile Glu Leu Arg Gly	
40 45 50	
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Ile Gly Glu Asn Ile Asp Leu Ala Glu Val Ala Glu Val Tyr Leu Pro	
55 60 65	
ctg tcc cgt ctg att cac ctc cag gta gcg gcc cga cag caa ctt act	355
Leu Ser Arg Leu Ile His Leu Gln Val Ala Ala Arg Gln Gln Leu Thr	
70 75 80 85	
gca gcc acc gaa acc ttc ctc gga act tcc ccc tct atc tct gtg ccg	403
Ala Ala Thr Glu Thr Phe Leu Gly Thr Ser Pro Ser Ile Ser Val Pro	
90 95 100	
ttt gtc att ggt gtc gcg gga tcc gtc gcc gtc ggt aaa tca acc acc	451
Phe Val Ile Gly Val Ala Gly Ser Val Ala Val Gly Lys Ser Thr Thr	
105 110 115	
gcc cga ctc ctc caa gtt ctg ctt cag cgc tgg aat tcc cac ccc cgc	499
Ala Arg Leu Leu Gln Val Leu Leu Gln Arg Trp Asn Ser His Pro Arg	
120 125 130	
gtg gac ctc gtc acc acc gac gga ttc ctc tat ccc ggc gcg gaa cta	547
Val Asp Leu Val Thr Thr Asp Gly Phe Leu Tyr Pro Gly Ala Glu Leu	
135 140 145	
atc cgc cgc gga tta atg tcc cga aaa gga ttc ccc gaa agc tac gac	595
Ile Arg Arg Gly Leu Met Ser Arg Lys Gly Phe Pro Glu Ser Tyr Asp	
150 155 160 165	
caa cgt gca ctc ctc cgc ttt gtc acc gac gta aaa tcc gga aaa ctc	643
Gln Arg Ala Leu Leu Arg Phe Val Thr Asp Val Lys Ser Gly Lys Leu	
170 175 180	
gaa gtc aac gca cct gtc tac tcc cac acc gcg tac gac cga gtt cca	691
Glu Val Asn Ala Pro Val Tyr Ser His Thr Ala Tyr Asp Arg Val Pro	
185 190 195	
ggc gaa ttc acc aca gtc cgc caa ccc gac att ttg atc gtc gaa ggc	739
Gly Glu Phe Thr Thr Val Arg Gln Pro Asp Ile Leu Ile Val Glu Gly	
200 205 210	
tta aac gtc ctc caa act ggc cca aca ttg atg gtc agt gac ctt ttc	787
Leu Asn Val Leu Gln Thr Gly Pro Thr Leu Met Val Ser Asp Leu Phe	
215 220 225	
gac ttc agc gtc tac gta gat gcc cgc acc gaa gat atc gaa aaa tgg	835
Asp Phe Ser Val Tyr Val Asp Ala Arg Thr Glu Asp Ile Glu Lys Trp	
230 235 240 245	
tac atc gac cgc ttc ctc aaa ctc cgc gac act gca ttc cgt cgc ccc	883

Tyr Ile Asp Arg Phe Leu Lys Leu Arg Asp Thr Ala Phe Arg Arg Pro  
 250 255 260

ggt gcc cac ttc tcc cat tac gcc gac atg gct gat cca gag tcc atc 931  
 Gly Ala His Phe Ser His Tyr Ala Asp Met Ala Asp Pro Glu Ser Ile  
 265 270 275

gcc gtc gct cga gaa ctg tgg caa tcg atc aac ctg ccc aac ttg gtg 979  
 Ala Val Ala Arg Glu Leu Trp Gln Ser Ile Asn Leu Pro Asn Leu Val  
 280 285 290

gag aat att ctt ccc acc cga gtt cgc gcg tcg ttg gta ctg aaa aaa  
 1027  
 Glu Asn Ile Leu Pro Thr Arg Val Arg Ala Ser Leu Val Leu Lys Lys  
 295 300 305

ggt agc gat cac ttg gtg gaa cgg gtg agg atg cgc aag atc  
 1069  
 Gly Ser Asp His Leu Val Glu Arg Val Arg Met Arg Lys Ile  
 310 315 320

taggggttct tgctgggtttt gag  
 1092

<210> 628

<211> 323

<212> PRT

<213> Corynebacterium glutamicum

<400> 628

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Arg Thr Pro Asp Phe Ser Pro Tyr Leu Asp Phe Asp Arg Ala Gln Trp  
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Arg Glu Leu Arg Asn Ser Met Pro Gln Val Leu Thr Gln Lys Glu Val  
 35 40 45

Ile Glu Leu Arg Gly Ile Gly Glu Asn Ile Asp Leu Ala Glu Val Ala  
 50 55 60

Glu Val Tyr Leu Pro Leu Ser Arg Leu Ile His Leu Gln Val Ala Ala  
 65 70 75 80

Arg Gln Gln Leu Thr Ala Ala Thr Glu Thr Phe Leu Gly Thr Ser Pro  
 85 90 95

Ser Ile Ser Val Pro Phe Val Ile Gly Val Ala Gly Ser Val Ala Val  
 100 105 110

Gly Lys Ser Thr Thr Ala Arg Leu Leu Gln Val Leu Leu Gln Arg Trp  
 115 120 125

Asn Ser His Pro Arg Val Asp Leu Val Thr Thr Asp Gly Phe Leu Tyr  
 130 135 140

Pro Gly Ala Glu Leu Ile Arg Arg Gly Leu Met Ser Arg Lys Gly Phe  
 145 150 155 160

Pro Glu Ser Tyr Asp Gln Arg Ala Leu Leu Arg Phe Val Thr Asp Val  
 165 170 175

Lys Ser Gly Lys Leu Glu Val Asn Ala Pro Val Tyr Ser His Thr Ala  
 180 185 190

Tyr Asp Arg Val Pro Gly Glu Phe Thr Thr Val Arg Gln Pro Asp Ile  
 195 200 205

Leu Ile Val Glu Gly Leu Asn Val Leu Gln Thr Gly Pro Thr Leu Met  
 210 215 220

Val Ser Asp Leu Phe Asp Phe Ser Val Tyr Val Asp Ala Arg Thr Glu  
 225 230 235 240

Asp Ile Glu Lys Trp Tyr Ile Asp Arg Phe Leu Lys Leu Arg Asp Thr  
 245 250 255

Ala Phe Arg Arg Pro Gly Ala His Phe Ser His Tyr Ala Asp Met Ala  
 260 265 270

Asp Pro Glu Ser Ile Ala Val Ala Arg Glu Leu Trp Gln Ser Ile Asn  
 275 280 285

Leu Pro Asn Leu Val Glu Asn Ile Leu Pro Thr Arg Val Arg Ala Ser  
 290 295 300

Leu Val Leu Lys Lys Gly Ser Asp His Leu Val Glu Arg Val Arg Met  
 305 310 315 320

Arg Lys Ile

<210> 629  
 <211> 1023  
 <212> DNA  
 <213> Corynebacterium glutamicum

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 <222> (101)..(1000)  
 <223> RXS00838

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tgcttacaaa tcttatctgt gctcaggcaa gatagcaggt atg aaa att gcg atc 115  
 Met Lys Ile Ala Ile  
 1 5

gtt ggc gct ggt gca gtt ggt gga tat ttc gga gcg ttg tta caa gaa 163  
 Val Gly Ala Gly Ala Val Gly Gly Tyr Phe Gly Ala Leu Leu Gln Glu  
 10 15 20

tct ggt gca gat atc acg atg gtt gca cgt gga cga aca tta gaa gcc 211  
 Ser Gly Ala Asp Ile Thr Met Val Ala Arg Gly Arg Thr Leu Glu Ala  
 25 30 35

ttg aag tct aaa gga ctc cac atc aac gat gca aga ggc gaa cgc tac 259  
 Leu Lys Ser Lys Gly Leu His Ile Asn Asp Ala Arg Gly Glu Arg Tyr

40				45				50								
gta	cca	att	cct	gca	gtt	gcg	agc	gtg	caa	gaa	cta	aaa	gat	gca	gat	307
Val	Pro	Ile	Pro	Ala	Val	Ala	Ser	Val	Gln	Glu	Leu	Lys	Asp	Ala	Asp	
	55					60					65					
gta	gtg	atg	att	gct	act	aaa	gca	tta	tcg	cgg	tct	tta	gat	ctc	gct	355
Val	Val	Met	Ile	Ala	Thr	Lys	Ala	Leu	Ser	Arg	Ser	Leu	Asp	Leu	Ala	
70					75					80					85	
gaa	ctt	ttg	ggt	ggg	ata	cct	gcg	aat	tcg	gtg	gtc	gcg	att	act	cag	403
Glu	Leu	Leu	Gly	Gly	Ile	Pro	Ala	Asn	Ser	Val	Val	Ala	Ile	Thr	Gln	
				90					95					100		
aat	tcg	att	gaa	tct	gct	gat	cta	gca	gcg	aag	agt	atc	ggt	gct	gat	451
Asn	Ser	Ile	Glu	Ser	Ala	Asp	Leu	Ala	Ala	Lys	Ser	Ile	Gly	Ala	Asp	
			105					110					115			
cgt	gtg	tgg	cct	ggt	gtg	gtt	cgt	ggg	ttc	ttt	gtt	cat	gag	ggg	cca	499
Arg	Val	Trp	Pro	Gly	Val	Val	Arg	Gly	Phe	Phe	Val	His	Glu	Gly	Pro	
		120					125					130				
gcc	tca	gtg	tca	tac	aag	gga	ggc	cca	ctg	tcc	tac	acg	ttt	ggt	gat	547
Ala	Ser	Val	Ser	Tyr	Lys	Gly	Gly	Pro	Leu	Ser	Tyr	Thr	Phe	Gly	Asp	
	135					140					145					
tct	ggt	gaa	ctt	tct	agg	caa	ttc	gca	agc	act	ctt	gaa	cag	gcc	ggt	595
Ser	Gly	Glu	Leu	Ser	Arg	Gln	Phe	Ala	Ser	Thr	Leu	Glu	Gln	Ala	Gly	
150					155					160					165	
att	gac	gga	gtt	ctg	cat	ccc	gat	att	ttg	gtg	gat	gtg	tgg	gag	aaa	643
Ile	Asp	Gly	Val	Leu	His	Pro	Asp	Ile	Leu	Val	Asp	Val	Trp	Glu	Lys	
				170					175					180		
gcc	atg	ttc	gta	gag	gtt	ttc	ggc	ggg	ttg	ggg	gct	ttc	gtc	gaa	aag	691
Ala	Met	Phe	Val	Glu	Val	Phe	Gly	Gly	Leu	Gly	Ala	Phe	Val	Glu	Lys	
			185					190					195			
caa	tta	ggt	acc	ttg	cgt	acg	cat	ttt	agg	gct	tcc	ctg	gaa	gcc	ttg	739
Gln	Leu	Gly	Thr	Leu	Arg	Thr	His	Phe	Arg	Ala	Ser	Leu	Glu	Ala	Leu	
		200					205					210				
atg	gaa	gag	gtg	gct	gag	gtg	gct	cgc	gcg	gca	ggt	gtt	gcg	ttg	ccg	787
Met	Glu	Glu	Val	Ala	Glu	Val	Ala	Arg	Ala	Ala	Gly	Val	Ala	Leu	Pro	
	215					220					225					
agc	gat	gcg	gtg	gag	cgc	acc	atg	aat	ttt	gcg	gat	cgg	atg	cct	gag	835
Ser	Asp	Ala	Val	Glu	Arg	Thr	Met	Asn	Phe	Ala	Asp	Arg	Met	Pro	Glu	
230					235					240					245	
aat	tcg	acg	agt	tcg	atg	cag	cgt	gat	ttg	gcc	gcg	gga	gtg	gct	agt	883
Asn	Ser	Thr	Ser	Ser	Met	Gln	Arg	Asp	Leu	Ala	Ala	Gly	Val	Ala	Ser	
				250					255					260		
gag	ctt	gag	gct	cag	aca	ggt	gca	att	gtg	cgg	gca	gcg	cac	aaa	gtg	931
Glu	Leu	Glu	Ala	Gln	Thr	Gly	Ala	Ile	Val	Arg	Ala	Ala	His	Lys	Val	
			265					270					275			
ggt	gtg	aaa	act	ccg	ctt	cat	gac	ctt	att	tat	gct	ggt	ctt	aag	ctg	979
Gly	Val	Lys	Thr	Pro	Leu	His	Asp	Leu	Ile	Tyr	Ala	Gly	Leu	Lys	Leu	
		280					285					290				



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1023

Lys Glu Glu Glu Asn Ser Leu  
295 300

<210> 630

<211> 300

<212> PRT

<213> Corynebacterium glutamicum

<400> 630

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20 25 30

Arg Thr Leu Glu Ala Leu Lys Ser Lys Gly Leu His Ile Asn Asp Ala  
35 40 45

Arg Gly Glu Arg Tyr Val Pro Ile Pro Ala Val Ala Ser Val Gln Glu  
50 55 60

Leu Lys Asp Ala Asp Val Val Met Ile Ala Thr Lys Ala Leu Ser Arg  
65 70 75 80

Ser Leu Asp Leu Ala Glu Leu Leu Gly Gly Ile Pro Ala Asn Ser Val  
85 90 95

Val Ala Ile Thr Gln Asn Ser Ile Glu Ser Ala Asp Leu Ala Ala Lys  
100 105 110

Ser Ile Gly Ala Asp Arg Val Trp Pro Gly Val Val Arg Gly Phe Phe  
115 120 125

Val His Glu Gly Pro Ala Ser Val Ser Tyr Lys Gly Gly Pro Leu Ser  
130 135 140

Tyr Thr Phe Gly Asp Ser Gly Glu Leu Ser Arg Gln Phe Ala Ser Thr  
145 150 155 160

Leu Glu Gln Ala Gly Ile Asp Gly Val Leu His Pro Asp Ile Leu Val  
165 170 175

Asp Val Trp Glu Lys Ala Met Phe Val Glu Val Phe Gly Gly Leu Gly  
180 185 190

Ala Phe Val Glu Lys Gln Leu Gly Thr Leu Arg Thr His Phe Arg Ala  
195 200 205

Ser Leu Glu Ala Leu Met Glu Glu Val Ala Glu Val Ala Arg Ala Ala  
210 215 220

Gly Val Ala Leu Pro Ser Asp Ala Val Glu Arg Thr Met Asn Phe Ala  
225 230 235 240

Asp Arg Met Pro Glu Asn Ser Thr Ser Ser Met Gln Arg Asp Leu Ala  
245 250 255

Ala	Gly	Val	Ala	Ser	Glu	Leu	Glu	Ala	Gln	Thr	Gly	Ala	Ile	Val	Arg
			260					265					270		
Ala	Ala	His	Lys	Val	Gly	Val	Lys	Thr	Pro	Leu	His	Asp	Leu	Ile	Tyr
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Ala	Gly	Leu	Lys	Leu	Lys	Glu	Glu	Glu	Asn	Ser	Leu				
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<210> 631
<211> 408
<212> DNA
<213> Corynebacterium glutamicum
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<222> (101) .. (385)  
<223> RXC02238
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Val Thr Asn Val Ser  
1 5

aac gag acc aac gcc acc aag gcc gtc ttc gat ccg cca gtg ggc att 163  
Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp Pro Pro Val Gly Ile  
10 15 20

acc gct cct ccg atc gat gaa ctg ctg gat aag gtc act tcc aag tac 211  
Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys Val Thr Ser Lys Tyr  
25 30 35

gcc ctc gtg atc ttc gca gcc aag cgt gcg cgc cag atc aac agc ttc 259  
Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg Gln Ile Asn Ser Phe  
40 45 50

tac cat cag gca gat gag gga gta ttc gag ttc atc gga cca ttg gtt 307  
Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe Ile Gly Pro Leu Val  
55 60 65

act ccg cag cca ggc gaa aag cca ctt tct att gct ctg cgt gag atc 355  
Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile Ala Leu Arg Glu Ile  
70 75 80 85

aat gca ggt ctg ttg gac cac gag gaa ggt taaaagacct tataacttca 405  
Asn Ala Gly Leu Leu Asp His Glu Glu Gly  
90 95

**cac** 408

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<210> 632
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Pro	Pro	Val	Gly	Ile	Thr	Ala	Pro	Pro	Ile	Asp	Glu	Leu	Leu	Asp	Lys
			20					25					30		
Val	Thr	Ser	Lys	Tyr	Ala	Leu	Val	Ile	Phe	Ala	Ala	Lys	Arg	Ala	Arg
		35					40					45			
Gln	Ile	Asn	Ser	Phe	Tyr	His	Gln	Ala	Asp	Glu	Gly	Val	Phe	Glu	Phe
	50					55					60				
Ile	Gly	Pro	Leu	Val	Thr	Pro	Gln	Pro	Gly	Glu	Lys	Pro	Leu	Ser	Ile
65					70					75					80
Ala	Leu	Arg	Glu	Ile	Asn	Ala	Gly	Leu	Leu	Asp	His	Glu	Glu	Gly	
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&lt;210&gt; 633

&lt;211&gt; 606

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(583)

&lt;223&gt; RXN03058

&lt;400&gt; 633

acgagcttcc gctctgcaca agccgctaga agccccgcat agccctaattg tagagctcat 60

gcccatttgg aatcacaaca ccgcatatcg gccatggctg gtg tca aag ctc aaa 115  
 Val Ser Lys Leu Lys  
 1 5

ggc tca aga tcg ctt ctc gac gtc ggc tcc ggc gat cac tcc ttc gcc 163  
 Gly Ser Arg Ser Leu Leu Asp Val Gly Ser Gly Asp His Ser Phe Ala  
 10 15 20

gac ctg gcc ggc cgc cag gtc gcg cat gtc gat gtc gtg gat cct ctt 211  
 Asp Leu Ala Gly Arg Gln Val Ala His Val Asp Val Val Asp Pro Leu  
 25 30 35

att aat aca acc ttt gaa gaa ttc cag ccg acc caa agc tac gat gcc 259  
 Ile Asn Thr Thr Phe Glu Glu Phe Gln Pro Thr Gln Ser Tyr Asp Ala  
 40 45 50

atc acg ttc atc gcg tcc ctc cat cac atg aac gcg gaa gaa gga ctt 307  
 Ile Thr Phe Ile Ala Ser Leu His His Met Asn Ala Glu Glu Gly Leu  
 55 60 65

aac aaa gca gtc cga atc ctc aat cct ggc ggc aag ctc ctc atc gta 355  
 Asn Lys Ala Val Arg Ile Leu Asn Pro Gly Gly Lys Leu Leu Ile Val  
 70 75 80 85

ggc ctc gcc aaa aac aaa acc gcc tcc gac tgg atc atc tcc gga cta 403  
 Gly Leu Ala Lys Asn Lys Thr Ala Ser Asp Trp Ile Ile Ser Gly Leu  
 90 95 100

caa gct ttt ctc tcc cga cca atc agc ctc atc aat agg gaa caa caa 451  
 Gln Ala Phe Leu Ser Arg Pro Ile Ser Leu Ile Asn Arg Glu Gln Gln

105								110				115				
atc	tac	ccc	ttc	cct	acc	aaa	gaa	ccc	tca	gag	agt	ctc	cac	gaa	ata	499
Ile	Tyr	Pro	Phe	Pro	Thr	Lys	Glu	Pro	Ser	Glu	Ser	Leu	His	Glu	Ile	
		120					125					130				
cga	caa	ctc	acc	aag	cag	ctc	ctc	cct	cac	cgc	cgt	att	cgc	cgt	gga	547
Arg	Gln	Leu	Thr	Lys	Gln	Leu	Leu	Pro	His	Arg	Arg	Ile	Arg	Arg	Gly	
		135				140					145					
atc	cac	ttc	cga	tac	ctc	ctc	gag	tgg	aca	aag	cct	taaacagccc				593
Ile	His	Phe	Arg	Tyr	Leu	Leu	Glu	Trp	Thr	Lys	Pro					
150					155					160						
tataaaccaa aaa															606	

&lt;210&gt; 634

&lt;211&gt; 161

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 634

Val	Ser	Lys	Leu	Lys	Gly	Ser	Arg	Ser	Leu	Leu	Asp	Val	Gly	Ser	Gly
1				5					10					15	

Asp	His	Ser	Phe	Ala	Asp	Leu	Ala	Gly	Arg	Gln	Val	Ala	His	Val	Asp
			20					25					30		

Val	Val	Asp	Pro	Leu	Ile	Asn	Thr	Thr	Phe	Glu	Glu	Phe	Gln	Pro	Thr
		35					40					45			

Gln	Ser	Tyr	Asp	Ala	Ile	Thr	Phe	Ile	Ala	Ser	Leu	His	His	Met	Asn
	50					55					60				

Ala	Glu	Glu	Gly	Leu	Asn	Lys	Ala	Val	Arg	Ile	Leu	Asn	Pro	Gly	Gly
65					70					75					80

Lys	Leu	Leu	Ile	Val	Gly	Leu	Ala	Lys	Asn	Lys	Thr	Ala	Ser	Asp	Trp
				85					90					95	

Ile	Ile	Ser	Gly	Leu	Gln	Ala	Phe	Leu	Ser	Arg	Pro	Ile	Ser	Leu	Ile
			100					105					110		

Asn	Arg	Glu	Gln	Gln	Ile	Tyr	Pro	Phe	Pro	Thr	Lys	Glu	Pro	Ser	Glu
		115					120					125			

Ser	Leu	His	Glu	Ile	Arg	Gln	Leu	Thr	Lys	Gln	Leu	Leu	Pro	His	Arg
	130					135					140				

Arg	Ile	Arg	Arg	Gly	Ile	His	Phe	Arg	Tyr	Leu	Leu	Glu	Trp	Thr	Lys
145					150					155					160

Pro

&lt;210&gt; 635

&lt;211&gt; 606

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(583)

&lt;223&gt; FRXA02903

&lt;400&gt; 635

acgagcttcc gctctgcaca agccgctaga agccccgcat agccctaattg tagagctcat 60

gcccatttgg aatcacaaca ccgcatatcg gccatggctg gtg tca aag ctc aaa 115  
 Val Ser Lys Leu Lys  
 1 5

ggc tca aga tcg ctt ctc gac gtc ggc tcc ggc gat cac tcc ttc gcc 163  
 Gly Ser Arg Ser Leu Leu Asp Val Gly Ser Gly Asp His Ser Phe Ala  
 10 15 20

gac ctg gcc ggc cgc cag gtc gcg cat gtc gat gtc gtg gat cct ctt 211  
 Asp Leu Ala Gly Arg Gln Val Ala His Val Asp Val Val Asp Pro Leu  
 25 30 35

att aat aca acc ttt gaa gaa ttc cag ccg acc caa agc tac gat gcc 259  
 Ile Asn Thr Thr Phe Glu Glu Phe Gln Pro Thr Gln Ser Tyr Asp Ala  
 40 45 50

atc acg ttc atc gcg tcc ctc cat cac atg aac gcg gaa gaa gga ctt 307  
 Ile Thr Phe Ile Ala Ser Leu His His Met Asn Ala Glu Glu Gly Leu  
 55 60 65

aac aaa gca gtc cga atc ctc aat cct ggc ggc aag ctc ctc atc gta 355  
 Asn Lys Ala Val Arg Ile Leu Asn Pro Gly Gly Lys Leu Leu Ile Val  
 70 75 80 85

ggc ctc gcc aaa aac aaa acc gcc tcc gac tgg atc atc tcc gga cta 403  
 Gly Leu Ala Lys Asn Lys Thr Ala Ser Asp Trp Ile Ile Ser Gly Leu  
 90 95 100

caa gct ttt ctc tcc cga cca atc agc ctc atc aat agg gaa caa caa 451  
 Gln Ala Phe Leu Ser Arg Pro Ile Ser Leu Ile Asn Arg Glu Gln Gln  
 105 110 115

atc tac ccc ttc cct acc aaa gaa ccc tca gag agt ctc cac gaa ata 499  
 Ile Tyr Pro Phe Pro Thr Lys Glu Pro Ser Glu Ser Leu His Glu Ile  
 120 125 130

cga caa ctc acc aag cag ctc ctc cct cac cgc cgt att cgc cgt gga 547  
 Arg Gln Leu Thr Lys Gln Leu Leu Pro His Arg Arg Ile Arg Arg Gly  
 135 140 145

atc cac ttc cga tac ctc ctc gag tgg aca aag cct taaacagccc 593  
 Ile His Phe Arg Tyr Leu Leu Glu Trp Thr Lys Pro  
 150 155 160

tataaaccaa aaa 606

&lt;210&gt; 636

&lt;211&gt; 161

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 636

Val Ser Lys Leu Lys Gly Ser Arg Ser Leu Leu Asp Val Gly Ser Gly  
1 5 10 15

Asp His Ser Phe Ala Asp Leu Ala Gly Arg Gln Val Ala His Val Asp  
20 25 30

Val Val Asp Pro Leu Ile Asn Thr Thr Phe Glu Glu Phe Gln Pro Thr  
35 40 45

Gln Ser Tyr Asp Ala Ile Thr Phe Ile Ala Ser Leu His His Met Asn  
50 55 60

Ala Glu Glu Gly Leu Asn Lys Ala Val Arg Ile Leu Asn Pro Gly Gly  
65 70 75 80

Lys Leu Leu Ile Val Gly Leu Ala Lys Asn Lys Thr Ala Ser Asp Trp  
85 90 95

Ile Ile Ser Gly Leu Gln Ala Phe Leu Ser Arg Pro Ile Ser Leu Ile  
100 105 110

Asn Arg Glu Gln Gln Ile Tyr Pro Phe Pro Thr Lys Glu Pro Ser Glu  
115 120 125

Ser Leu His Glu Ile Arg Gln Leu Thr Lys Gln Leu Leu Pro His Arg  
130 135 140

Arg Ile Arg Arg Gly Ile His Phe Arg Tyr Leu Leu Glu Trp Thr Lys  
145 150 155 160

Pro

&lt;210&gt; 637

&lt;211&gt; 783

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(760)

&lt;223&gt; RXA00166

&lt;400&gt; 637

ggcgtttagc gatcttcaac atcgagcaac cagcgccagc gctttttaccc aaggcagcac 60

gacttatcac gatgtccgac ctggatatcc ggctgaggcc gtg gag tta gcc cgt 115  
Val Glu Leu Ala Arg  
1 5

ggg ttt ggc cga gtc ctg gat gtc ggt gca ggt acc gga aaa cta acc 163  
Gly Phe Gly Arg Val Leu Asp Val Gly Ala Gly Thr Gly Lys Leu Thr  
10 15 20

agt gag cta aca gct gat cag gtc cta gcc ctt gat cca agc atg gac 211  
Ser Glu Leu Thr Ala Asp Gln Val Leu Ala Leu Asp Pro Ser Met Asp  
25 30 35

atg ttg cgg gtg ttt cgc tcc gcg ctt ccg gcg gtt ccc tgc tgg caa 259

Met	Leu	Arg	Val	Phe	Arg	Ser	Ala	Leu	Pro	Ala	Val	Pro	Cys	Trp	Gln	
		40					45					50				
gcg	aca	gca	gaa	cac	aca	gga	ata	cgt	gac	aac	gcg	gtt	gat	ctg	att	307
Ala	Thr	Ala	Glu	His	Thr	Gly	Ile	Arg	Asp	Asn	Ala	Val	Asp	Leu	Ile	
	55					60					65					
acg	tgc	gca	caa	acg	tgg	cat	tgg	gtt	gac	gtg	acg	gct	gcc	tca	gcg	355
Thr	Cys	Ala	Gln	Thr	Trp	His	Trp	Val	Asp	Val	Thr	Ala	Ala	Ser	Ala	
	70				75					80					85	
gaa	ttt	gat	cgg	gtg	att	gca	cct	gag	ggt	gca	gtc	ctg	ctc	gtg	tgg	403
Glu	Phe	Asp	Arg	Val	Ile	Ala	Pro	Glu	Gly	Ala	Val	Leu	Leu	Val	Trp	
				90					95					100		
aat	aac	ctg	gac	acc	tcc	atc	gcg	tgg	gta	cac	cga	ctc	agt	cgc	att	451
Asn	Asn	Leu	Asp	Thr	Ser	Ile	Ala	Trp	Val	His	Arg	Leu	Ser	Arg	Ile	
			105					110					115			
atg	cat	gcc	ggc	gat	gta	ctc	aag	ccg	gga	ttc	acc	cca	gaa	acc	gca	499
Met	His	Ala	Gly	Asp	Val	Leu	Lys	Pro	Gly	Phe	Thr	Pro	Glu	Thr	Ala	
		120					125					130				
gct	ccc	tgg	ata	att	gat	cga	gaa	att	cgc	acc	acg	tgg	aat	cag	cac	547
Ala	Pro	Trp	Ile	Ile	Asp	Arg	Glu	Ile	Arg	Thr	Thr	Trp	Asn	Gln	His	
	135					140					145					
ctc	acc	cct	gaa	gaa	atc	atc	cag	ctc	gct	cac	acg	agg	tcc	tac	tgg	595
Leu	Thr	Pro	Glu	Glu	Ile	Ile	Gln	Leu	Ala	His	Thr	Arg	Ser	Tyr	Trp	
	150				155					160					165	
tta	aac	gcg	tca	gag	aaa	atc	aaa	gag	cgt	gtt	gat	cag	aac	ctt	cag	643
Leu	Asn	Ala	Ser	Glu	Lys	Ile	Lys	Glu	Arg	Val	Asp	Gln	Asn	Leu	Gln	
				170				175						180		
tgg	tat	ctc	tac	gag	cat	ttg	ggt	ttc	agt	ccc	gac	aat	cca	gtg	gaa	691
Trp	Tyr	Leu	Tyr	Glu	His	Leu	Gly	Phe	Ser	Pro	Asp	Asn	Pro	Val	Glu	
			185				190						195			
ctt	ccc	tat	cgc	tgt	gat	gca	ttt	tta	ctt	tca	cgt	tcc	ggt	acc	ctg	739
Leu	Pro	Tyr	Arg	Cys	Asp	Ala	Phe	Leu	Leu	Ser	Arg	Ser	Gly	Thr	Leu	
		200					205					210				
gca	ggc	aga	tct	tcc	aat	ctt	taggagccct	cgccatgtac	ctg							783
Ala	Gly	Arg	Ser	Ser	Asn	Leu										
	215					220										

&lt;210&gt; 638

&lt;211&gt; 220

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 638

Val	Glu	Leu	Ala	Arg	Gly	Phe	Gly	Arg	Val	Leu	Asp	Val	Gly	Ala	Gly
1				5					10					15	

Thr	Gly	Lys	Leu	Thr	Ser	Glu	Leu	Thr	Ala	Asp	Gln	Val	Leu	Ala	Leu
		20						25					30		

Asp	Pro	Ser	Met	Asp	Met	Leu	Arg	Val	Phe	Arg	Ser	Ala	Leu	Pro	Ala
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

35					40					45						
Val	Pro	Cys	Trp	Gln	Ala	Thr	Ala	Glu	His	Thr	Gly	Ile	Arg	Asp	Asn	
50					55					60						
Ala	Val	Asp	Leu	Ile	Thr	Cys	Ala	Gln	Thr	Trp	His	Trp	Val	Asp	Val	
65					70					75					80	
Thr	Ala	Ala	Ser	Ala	Glu	Phe	Asp	Arg	Val	Ile	Ala	Pro	Glu	Gly	Ala	
85					90					95						
Val	Leu	Leu	Val	Trp	Asn	Asn	Leu	Asp	Thr	Ser	Ile	Ala	Trp	Val	His	
100					105					110						
Arg	Leu	Ser	Arg	Ile	Met	His	Ala	Gly	Asp	Val	Leu	Lys	Pro	Gly	Phe	
115					120					125						
Thr	Pro	Glu	Thr	Ala	Ala	Pro	Trp	Ile	Ile	Asp	Arg	Glu	Ile	Arg	Thr	
130					135					140						
Thr	Trp	Asn	Gln	His	Leu	Thr	Pro	Glu	Glu	Ile	Ile	Gln	Leu	Ala	His	
145					150					155					160	
Thr	Arg	Ser	Tyr	Trp	Leu	Asn	Ala	Ser	Glu	Lys	Ile	Lys	Glu	Arg	Val	
165					170					175						
Asp	Gln	Asn	Leu	Gln	Trp	Tyr	Leu	Tyr	Glu	His	Leu	Gly	Phe	Ser	Pro	
180					185					190						
Asp	Asn	Pro	Val	Glu	Leu	Pro	Tyr	Arg	Cys	Asp	Ala	Phe	Leu	Leu	Ser	
195					200					205						
Arg	Ser	Gly	Thr	Leu	Ala	Gly	Arg	Ser	Ser	Asn	Leu					
210					215					220						

&lt;210&gt; 639

&lt;211&gt; 1392

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1369)

&lt;223&gt; RXA00633

&lt;400&gt; 639

aaagctgcgg taattaaaaa cacttagcgc caaaaattga acactgttca attaacctat 60

tacactgcag	atatacatcc	aaaccaagtg	acggagga	aaa	atg	gaa	aac	ccc	agc	115
					Met	Glu	Asn	Pro	Ser	
					1				5	

ttg	cgc	gag	ctt	gat	cac	cga	aac	atc	tgg	cac	ccg	tat	gcc	gcg	ccg	163
Leu	Arg	Glu	Leu	Asp	His	Arg	Asn	Ile	Trp	His	Pro	Tyr	Ala	Ala	Pro	
			10					15					20			

ggc	gtg	cgc	aat	aga	ctc	gtc	acc	aaa	acc	gat	gga	gtg	ttt	ttg	acg	211
Gly	Val	Arg	Asn	Arg	Leu	Val	Thr	Lys	Thr	Asp	Gly	Val	Phe	Leu	Thr	
			25					30					35			



ctg	gaa	gat	ggc	agc	acc	gtg	att	gac	gcg	atg	agc	tcc	tgg	tgg	tcg	259
Leu	Glu	Asp	Gly	Ser	Thr	Val	Ile	Asp	Ala	Met	Ser	Ser	Trp	Trp	Ser	
		40					45					50				
gca	att	cat	gga	cac	gga	cac	ccc	cga	ctg	aaa	gct	gcc	gcc	caa	aaa	307
Ala	Ile	His	Gly	His	Gly	His	Pro	Arg	Leu	Lys	Ala	Ala	Ala	Gln	Lys	
	55					60				65						
caa	atc	gac	acc	atg	agt	cac	gtc	atg	ttt	ggc	gga	cta	acc	cac	gag	355
Gln	Ile	Asp	Thr	Met	Ser	His	Val	Met	Phe	Gly	Gly	Leu	Thr	His	Glu	
70					75					80					85	
ccc	gcc	att	aag	ctc	acc	cac	aaa	ctc	ctc	aat	ctc	act	gga	aat	tcc	403
Pro	Ala	Ile	Lys	Leu	Thr	His	Lys	Leu	Leu	Asn	Leu	Thr	Gly	Asn	Ser	
				90				95						100		
ttt	gac	cac	gtc	ttt	tat	tcc	gat	tcg	ggc	tcg	gtc	tca	gtg	gag	gtc	451
Phe	Asp	His	Val	Phe	Tyr	Ser	Asp	Ser	Gly	Ser	Val	Ser	Val	Glu	Val	
			105					110					115			
gcc	atc	aaa	atg	gca	ctg	cag	gcc	tcc	aaa	gga	caa	ggc	cac	ccg	gaa	499
Ala	Ile	Lys	Met	Ala	Leu	Gln	Ala	Ser	Lys	Gly	Gln	Gly	His	Pro	Glu	
		120					125					130				
cgg	aca	aaa	ctc	ctc	acc	tgg	cgg	tcc	ggc	tac	cac	gga	gac	aca	ttc	547
Arg	Thr	Lys	Leu	Leu	Thr	Trp	Arg	Ser	Gly	Tyr	His	Gly	Asp	Thr	Phe	
	135					140					145					
acc	gcg	atg	agc	gtg	tgc	gac	cca	gaa	aat	ggc	atg	cat	agc	ctc	tgg	595
Thr	Ala	Met	Ser	Val	Cys	Asp	Pro	Glu	Asn	Gly	Met	His	Ser	Leu	Trp	
150					155					160					165	
aaa	ggc	aca	ctc	ccc	gag	cag	att	ttc	gcc	ccc	gcc	cca	cca	gtt	cgg	643
Lys	Gly	Thr	Leu	Pro	Glu	Gln	Ile	Phe	Ala	Pro	Ala	Pro	Pro	Val	Arg	
				170				175						180		
ggg	tca	tcg	ccg	cag	gcg	att	tcc	gag	tac	ctg	cgc	agc	atg	gaa	ttg	691
Gly	Ser	Ser	Pro	Gln	Ala	Ile	Ser	Glu	Tyr	Leu	Arg	Ser	Met	Glu	Leu	
			185					190					195			
ctt	atc	gac	gag	gcg	gtc	tcc	gca	atc	atc	atc	gaa	ccg	atc	gtc	caa	739
Leu	Ile	Asp	Glu	Ala	Val	Ser	Ala	Ile	Ile	Ile	Glu	Pro	Ile	Val	Gln	
		200					205					210				
ggc	gct	gga	ggc	atg	cgc	ttt	cac	gat	gtc	gca	ctc	att	gaa	gga	gtc	787
Gly	Ala	Gly	Gly	Met	Arg	Phe	His	Asp	Val	Ala	Leu	Ile	Glu	Gly	Val	
	215					220					225					
gcc	aca	ctg	tgc	aag	aag	cac	gat	cgt	ttc	ttg	atc	gtc	gat	gaa	att	835
Ala	Thr	Leu	Cys	Lys	Lys	His	Asp	Arg	Phe	Leu	Ile	Val	Asp	Glu	Ile	
230					235					240					245	
gcc	act	ggt	ttc	ggc	cgc	acc	ggt	gaa	cta	ttt	gcc	acg	tta	agc	aat	883
Ala	Thr	Gly	Phe	Gly	Arg	Thr	Gly	Glu	Leu	Phe	Ala	Thr	Leu	Ser	Asn	
			250					255						260		
ggc	cta	caa	cca	gac	atc	atg	tgt	gtg	ggc	aag	gcc	ctc	acc	ggt	gga	931
Gly	Leu	Gln	Pro	Asp	Ile	Met	Cys	Val	Gly	Lys	Ala	Leu	Thr	Gly	Gly	
			265					270					275			
ttc	atg	tcc	ttc	gcc	gct	act	tta	tgc	acg	gac	aag	gtg	gct	caa	tta	979

Phe Met Ser Phe Ala Ala Thr Leu Cys Thr Asp Lys Val Ala Gln Leu  
280 285 290

atc agc acc cca aat ggc gga ggt gcg ctg atg cac ggc ccc act ttt  
1027

Ile Ser Thr Pro Asn Gly Gly Gly Ala Leu Met His Gly Pro Thr Phe  
295 300 305

atg gct aat cct ctg gcc tgt gcg gtt tcg cat gct tca tta gaa atc  
1075

Met Ala Asn Pro Leu Ala Cys Ala Val Ser His Ala Ser Leu Glu Ile  
310 315 320 325

att gag acc ggc atg tgg cag aaa cag gta aaa aga atc gaa gcc gaa  
1123

Ile Glu Thr Gly Met Trp Gln Lys Gln Val Lys Arg Ile Glu Ala Glu  
330 335 340

ctt atc gca ggc ctt tcc cca ctt caa cac ctt cca ggg gtt gcc gat  
1171

Leu Ile Ala Gly Leu Ser Pro Leu Gln His Leu Pro Gly Val Ala Asp  
345 350 355

gtc cgg gtt ctc ggc gcg att ggt gtc atc gaa atg gaa caa aat gtc  
1219

Val Arg Val Leu Gly Ala Ile Gly Val Ile Glu Met Glu Gln Asn Val  
360 365 370

aat gtc gaa gaa gct act cag gct gca tta gat cac ggt gtg tgg atc  
1267

Asn Val Glu Glu Ala Thr Gln Ala Ala Leu Asp His Gly Val Trp Ile  
375 380 385

cgc ccc ttt gga cgc ttg ctc tat gtc atg cct cca tat atc acc acg  
1315

Arg Pro Phe Gly Arg Leu Leu Tyr Val Met Pro Pro Tyr Ile Thr Thr  
390 395 400 405

tca gag cag tgc gca cag atc tgc act gcg ctt cat gct gca gtt aaa  
1363

Ser Glu Gln Cys Ala Gln Ile Cys Thr Ala Leu His Ala Ala Val Lys  
410 415 420

ggg aaa taaaccatgc cattttttatt tgt  
1392

Gly Lys

<210> 640

<211> 423

<212> PRT

<213> Corynebacterium glutamicum

<400> 640

Met Glu Asn Pro Ser Leu Arg Glu Leu Asp His Arg Asn Ile Trp His  
1 5 10 15

Pro Tyr Ala Ala Pro Gly Val Arg Asn Arg Leu Val Thr Lys Thr Asp  
20 25 30

Gly Val Phe Leu Thr Leu Glu Asp Gly Ser Thr Val Ile Asp Ala Met  
 35 40 45  
 Ser Ser Trp Trp Ser Ala Ile His Gly His Gly His Pro Arg Leu Lys  
 50 55 60  
 Ala Ala Ala Gln Lys Gln Ile Asp Thr Met Ser His Val Met Phe Gly  
 65 70 75 80  
 Gly Leu Thr His Glu Pro Ala Ile Lys Leu Thr His Lys Leu Leu Asn  
 85 90 95  
 Leu Thr Gly Asn Ser Phe Asp His Val Phe Tyr Ser Asp Ser Gly Ser  
 100 105 110  
 Val Ser Val Glu Val Ala Ile Lys Met Ala Leu Gln Ala Ser Lys Gly  
 115 120 125  
 Gln Gly His Pro Glu Arg Thr Lys Leu Leu Thr Trp Arg Ser Gly Tyr  
 130 135 140  
 His Gly Asp Thr Phe Thr Ala Met Ser Val Cys Asp Pro Glu Asn Gly  
 145 150 155 160  
 Met His Ser Leu Trp Lys Gly Thr Leu Pro Glu Gln Ile Phe Ala Pro  
 165 170 175  
 Ala Pro Pro Val Arg Gly Ser Ser Pro Gln Ala Ile Ser Glu Tyr Leu  
 180 185 190  
 Arg Ser Met Glu Leu Leu Ile Asp Glu Ala Val Ser Ala Ile Ile Ile  
 195 200 205  
 Glu Pro Ile Val Gln Gly Ala Gly Gly Met Arg Phe His Asp Val Ala  
 210 215 220  
 Leu Ile Glu Gly Val Ala Thr Leu Cys Lys Lys His Asp Arg Phe Leu  
 225 230 235 240  
 Ile Val Asp Glu Ile Ala Thr Gly Phe Gly Arg Thr Gly Glu Leu Phe  
 245 250 255  
 Ala Thr Leu Ser Asn Gly Leu Gln Pro Asp Ile Met Cys Val Gly Lys  
 260 265 270  
 Ala Leu Thr Gly Gly Phe Met Ser Phe Ala Ala Thr Leu Cys Thr Asp  
 275 280 285  
 Lys Val Ala Gln Leu Ile Ser Thr Pro Asn Gly Gly Gly Ala Leu Met  
 290 295 300  
 His Gly Pro Thr Phe Met Ala Asn Pro Leu Ala Cys Ala Val Ser His  
 305 310 315 320  
 Ala Ser Leu Glu Ile Ile Glu Thr Gly Met Trp Gln Lys Gln Val Lys  
 325 330 335  
 Arg Ile Glu Ala Glu Leu Ile Ala Gly Leu Ser Pro Leu Gln His Leu  
 340 345 350  
 Pro Gly Val Ala Asp Val Arg Val Leu Gly Ala Ile Gly Val Ile Glu

355		360		365
Met Glu Gln Asn Val Asn Val Glu Glu Ala Thr Gln Ala Ala Leu Asp				
370		375		380
His Gly Val Trp Ile Arg Pro Phe Gly Arg Leu Leu Tyr Val Met Pro				
385		390		395
Pro Tyr Ile Thr Thr Ser Glu Gln Cys Ala Gln Ile Cys Thr Ala Leu				
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				415
His Ala Ala Val Lys Gly Lys				
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 <223> RXA00632

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 Met Pro Phe Leu Phe 5  
 1  
 gtc agc ggt acc gga act ggg gtt ggg aaa acc ttc tcc aca gcc gtt 163  
 Val Ser Gly Thr Gly Thr Gly Val Gly Lys Thr Phe Ser Thr Ala Val 20  
 10 15  
 ttg gtt cga tac tta gcc gat caa gga cac gat gtt ctg ccc gta aag 211  
 Leu Val Arg Tyr Leu Ala Asp Gln Gly His Asp Val Leu Pro Val Lys 35  
 25 30  
 cta gtc caa acc ggt gaa ctt cca ggc gag gga gac atc ttt aac att 259  
 Leu Val Gln Thr Gly Glu Leu Pro Gly Glu Gly Asp Ile Phe Asn Ile 50  
 40 45  
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 Glu Arg Leu Thr Gly Ile Ala Gly Glu Glu Phe Ala Arg Phe Lys Asp 65  
 55 60  
 cct ctt gcg cca aat ctg gca gcc cga cga gag ggg gtc gag cca ata 355  
 Pro Leu Ala Pro Asn Leu Ala Ala Arg Arg Glu Gly Val Glu Pro Ile 85  
 70 75 80  
 cag ttt gat cag att atc tcg tgg ctt cgt ggt ttt gac gac cca gat 403  
 Gln Phe Asp Gln Ile Ile Ser Trp Leu Arg Gly Phe Asp Asp Pro Asp 100  
 90 95  
 cgc atc att gtg gtg gag ggc gct ggt ggc ctg ctg gtc aga tta ggg 451  
 Arg Ile Ile Val Val Glu Gly Ala Gly Gly Leu Leu Val Arg Leu Gly 115  
 105 110  
 gaa gat ttc acc ctg gca gat gtt gcc tcc gct ttg aat gca ccc tta 499

Glu Asp Phe Thr Leu Ala Asp Val Ala Ser Ala Leu Asn Ala Pro Leu  
 120 125 130  
 gtg att gtg aca agc acc gga ttg gga agc ctc aac gct gct gaa tta 547  
 Val Ile Val Thr Ser Thr Gly Leu Gly Ser Leu Asn Ala Ala Glu Leu  
 135 140 145  
 agc gtt gag gca gca aac cgc cga gga ctc aca gtg ttg gga gtc ctc 595  
 Ser Val Glu Ala Ala Asn Arg Arg Gly Leu Thr Val Leu Gly Val Leu  
 150 155 160 165  
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 Gly Gly Ser Ile Pro Gln Asn Pro Asp Leu Ala Thr Met Leu Asn Leu  
 170 175 180  
 gaa gaa ttt gag aga gtc acc ggc gtg ccc ttt tgg gga gct ttg ccg 691  
 Glu Glu Phe Glu Arg Val Thr Gly Val Pro Phe Trp Gly Ala Leu Pro  
 185 190 195  
 gaa ggg ttg tca cgg gtg gag ggg ttc gtc gaa aag caa tct ttt ccg 739  
 Glu Gly Leu Ser Arg Val Glu Gly Phe Val Glu Lys Gln Ser Phe Pro  
 200 205 210  
 gcc ctt gat gcc ttt aag aaa ccg ccg gca agg tgatcgtgaa caccgtgcct 792  
 Ala Leu Asp Ala Phe Lys Lys Pro Pro Ala Arg  
 215 220  
 tcg 795

&lt;210&gt; 642

&lt;211&gt; 224

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 642

Met Pro Phe Leu Phe Val Ser Gly Thr Gly Thr Gly Val Gly Lys Thr  
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 Phe Ser Thr Ala Val Leu Val Arg Tyr Leu Ala Asp Gln Gly His Asp  
 20 25 30  
 Val Leu Pro Val Lys Leu Val Gln Thr Gly Glu Leu Pro Gly Glu Gly  
 35 40 45  
 Asp Ile Phe Asn Ile Glu Arg Leu Thr Gly Ile Ala Gly Glu Glu Phe  
 50 55 60  
 Ala Arg Phe Lys Asp Pro Leu Ala Pro Asn Leu Ala Ala Arg Arg Glu  
 65 70 75 80  
 Gly Val Glu Pro Ile Gln Phe Asp Gln Ile Ile Ser Trp Leu Arg Gly  
 85 90 95  
 Phe Asp Asp Pro Asp Arg Ile Ile Val Val Glu Gly Ala Gly Gly Leu  
 100 105 110  
 Leu Val Arg Leu Gly Glu Asp Phe Thr Leu Ala Asp Val Ala Ser Ala  
 115 120 125  
 Leu Asn Ala Pro Leu Val Ile Val Thr Ser Thr Gly Leu Gly Ser Leu

130	135	140
Asn Ala Ala Glu Leu Ser Val Glu Ala Ala Asn Arg Arg Gly Leu Thr		
145	150	155 160
Val Leu Gly Val Leu Gly Gly Ser Ile Pro Gln Asn Pro Asp Leu Ala		
	165	170 175
Thr Met Leu Asn Leu Glu Glu Phe Glu Arg Val Thr Gly Val Pro Phe		
	180	185 190
Trp Gly Ala Leu Pro Glu Gly Leu Ser Arg Val Glu Gly Phe Val Glu		
	195	200 205
Lys Gln Ser Phe Pro Ala Leu Asp Ala Phe Lys Lys Pro Pro Ala Arg		
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 <213> Corynebacterium glutamicum

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 <223> RXA00295

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 Met Thr Ile Pro Gly  
 1 5  
 acc atc ctt gac acc gcc cgc acc caa gtt ctg gaa cag gga att ggc 163  
 Thr Ile Leu Asp Thr Ala Arg Thr Gln Val Leu Glu Gln Gly Ile Gly  
 10 15 20  
 ctt aat cag cag cag ttg atg gag gtt ctc acc ttg cct gaa gag caa 211  
 Leu Asn Gln Gln Gln Leu Met Glu Val Leu Thr Leu Pro Glu Glu Gln  
 25 30 35  
 atc cca gac ttg atg gaa tta gcc cac cag gtt cgg ttg aag tgg tgt 259  
 Ile Pro Asp Leu Met Glu Leu Ala His Gln Val Arg Leu Lys Trp Cys  
 40 45 50  
 ggg gaa gaa atc gag gtc gag ggc att att tcc ctc aaa act ggc ggt 307  
 Gly Glu Glu Ile Glu Val Glu Gly Ile Ile Ser Leu Lys Thr Gly Gly  
 55 60 65  
 tgc cct gaa gat tgt cat ttc tgc tca cag tct ggg ttg ttt gaa tcg 355  
 Cys Pro Glu Asp Cys His Phe Cys Ser Gln Ser Gly Leu Phe Glu Ser  
 70 75 80 85  
 ccg gtg cgt tcg gtg tgg ctg gat att ccg aat ctg gtt gaa gcc gct 403  
 Pro Val Arg Ser Val Trp Leu Asp Ile Pro Asn Leu Val Glu Ala Ala  
 90 95 100

aaa cag acc gca aaa act ggc gct acc gaa ttc tgt atc gtc gcc gca	451
Lys Gln Thr Ala Lys Thr Gly Ala Thr Glu Phe Cys Ile Val Ala Ala	
105 110 115	
gtc aag ggg cct gat gag agg ctc atg acc cag ctg gag gaa gca gtc	499
Val Lys Gly Pro Asp Glu Arg Leu Met Thr Gln Leu Glu Glu Ala Val	
120 125 130	
ctc gcg att cac tct gaa gtt gaa att gaa gtc gca gca tcg atc gga	547
Leu Ala Ile His Ser Glu Val Glu Ile Glu Val Ala Ala Ser Ile Gly	
135 140 145	
acg tta aat aag gaa cag gtg gat cgc ctc gct gct gcc ggc gtg cac	595
Thr Leu Asn Lys Glu Gln Val Asp Arg Leu Ala Ala Ala Gly Val His	
150 155 160 165	
cgc tac aac cat aat ttg gaa act gcg cgt tcc tat ttc cct gaa gtt	643
Arg Tyr Asn His Asn Leu Glu Thr Ala Arg Ser Tyr Phe Pro Glu Val	
170 175 180	
gtc acc act cat aca tgg gaa gag cgc cgc gaa act ttg cgc ctg gtg	691
Val Thr Thr His Thr Trp Glu Glu Arg Arg Glu Thr Leu Arg Leu Val	
185 190 195	
gca gaa gct gga atg gaa gtc tgt tcc ggc gga atc tta gga atg ggc	739
Ala Glu Ala Gly Met Glu Val Cys Ser Gly Gly Ile Leu Gly Met Gly	
200 205 210	
gaa act tta gag cag cgc gcc gag ttt gcc gtg cag ctg gcg gag ctt	787
Glu Thr Leu Glu Gln Arg Ala Glu Phe Ala Val Gln Leu Ala Glu Leu	
215 220 225	
gat ccg cac gaa gtc ccc atg aac ttc ctt gat cct cgc ccg ggc acc	835
Asp Pro His Glu Val Pro Met Asn Phe Leu Asp Pro Arg Pro Gly Thr	
230 235 240 245	
cca ttt gcc gat agg gaa ttg atg gac agc cgt gac gct ctg cgc tct	883
Pro Phe Ala Asp Arg Glu Leu Met Asp Ser Arg Asp Ala Leu Arg Ser	
250 255 260	
att ggt gcg ttc cgc ctt gcg atg cct cac acc atg ctt cgt ttt gct	931
Ile Gly Ala Phe Arg Leu Ala Met Pro His Thr Met Leu Arg Phe Ala	
265 270 275	
ggc ggt cgc gag ctg act ttg ggc gac aag ggt tcc gag caa gcc ctc	979
Gly Gly Arg Glu Leu Thr Leu Gly Asp Lys Gly Ser Glu Gln Ala Leu	
280 285 290	
ctg gga ggc atc aat gcg atg atc gtc gga aac tac ctg act acg ctc	
1027	
Leu Gly Gly Ile Asn Ala Met Ile Val Gly Asn Tyr Leu Thr Thr Leu	
295 300 305	
ggc cgc cca atg gaa gat gac ctc gac atg atg gat cgt ctc cag ctg	
1075	
Gly Arg Pro Met Glu Asp Asp Leu Asp Met Met Asp Arg Leu Gln Leu	
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1122	

Pro Ile Lys Val Leu Asn Lys Val Ile  
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gac  
1125

<210> 644

<211> 334

<212> PRT

<213> Corynebacterium glutamicum

<400> 644

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Leu Pro Glu Glu Gln Ile Pro Asp Leu Met Glu Leu Ala His Gln Val  
35 40 45

Arg Leu Lys Trp Cys Gly Glu Glu Ile Glu Val Glu Gly Ile Ile Ser  
50 55 60

Leu Lys Thr Gly Gly Cys Pro Glu Asp Cys His Phe Cys Ser Gln Ser  
65 70 75 80

Gly Leu Phe Glu Ser Pro Val Arg Ser Val Trp Leu Asp Ile Pro Asn  
85 90 95

Leu Val Glu Ala Ala Lys Gln Thr Ala Lys Thr Gly Ala Thr Glu Phe  
100 105 110

Cys Ile Val Ala Ala Val Lys Gly Pro Asp Glu Arg Leu Met Thr Gln  
115 120 125

Leu Glu Glu Ala Val Leu Ala Ile His Ser Glu Val Glu Ile Glu Val  
130 135 140

Ala Ala Ser Ile Gly Thr Leu Asn Lys Glu Gln Val Asp Arg Leu Ala  
145 150 155 160

Ala Ala Gly Val His Arg Tyr Asn His Asn Leu Glu Thr Ala Arg Ser  
165 170 175

Tyr Phe Pro Glu Val Val Thr Thr His Thr Trp Glu Glu Arg Arg Glu  
180 185 190

Thr Leu Arg Leu Val Ala Glu Ala Gly Met Glu Val Cys Ser Gly Gly  
195 200 205

Ile Leu Gly Met Gly Glu Thr Leu Glu Gln Arg Ala Glu Phe Ala Val  
210 215 220

Gln Leu Ala Glu Leu Asp Pro His Glu Val Pro Met Asn Phe Leu Asp  
225 230 235 240

Pro Arg Pro Gly Thr Pro Phe Ala Asp Arg Glu Leu Met Asp Ser Arg  
245 250 255



Asp Ala Leu Arg Ser Ile Gly Ala Phe Arg Leu Ala Met Pro His Thr  
 260 265 270  
 Met Leu Arg Phe Ala Gly Gly Arg Glu Leu Thr Leu Gly Asp Lys Gly  
 275 280 285  
 Ser Glu Gln Ala Leu Leu Gly Gly Ile Asn Ala Met Ile Val Gly Asn  
 290 295 300  
 Tyr Leu Thr Thr Leu Gly Arg Pro Met Glu Asp Asp Leu Asp Met Met  
 305 310 315 320  
 Asp Arg Leu Gln Leu Pro Ile Lys Val Leu Asn Lys Val Ile  
 325 330

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 <212> DNA  
 <213> Corynebacterium glutamicum

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 <222> (101)..(1189)  
 <223> RXA00223

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 Met Arg Glu Val Ala  
 1 5  
 gca gct gcg tgg atg gaa aac gcg cag gca ttg aat ccc gcg agt cag 163  
 Ala Ala Ala Trp Met Glu Asn Ala Gln Ala Leu Asn Pro Ala Ser Gln  
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 Tyr Gly Ser Gly Arg Lys Ala Arg Ser Val Ala Asp Ser Ala Arg Glu  
 25 30 35  
 gaa att gct tct ttg ctg ggc tgt gaa cct atc gag gtt gtg ttt acc 259  
 Glu Ile Ala Ser Leu Leu Gly Cys Glu Pro Ile Glu Val Val Phe Thr  
 40 45 50  
 gcg tcc ggc acg gag gca gat aac ctc gct gtg cag ggg tta ttc cac 307  
 Ala Ser Gly Thr Glu Ala Asp Asn Leu Ala Val Gln Gly Leu Phe His  
 55 60 65  
 gca tcg cct ctc aat cgg att att tct acg ccg atc gag cac ccc ggg 355  
 Ala Ser Pro Leu Asn Arg Ile Ile Ser Thr Pro Ile Glu His Pro Gly  
 70 75 80 85  
 att ctg gaa acc gtc aag gct cta gaa ctt ggc ggg gca gag gcg gag 403  
 Ile Leu Glu Thr Val Lys Ala Leu Glu Leu Gly Gly Ala Glu Ala Glu  
 90 95 100  
 ctc atg ccg atc ggt cca gat gga cga gtg tct tcc ttc gaa gcg ctg 451  
 Leu Met Pro Ile Gly Pro Asp Gly Arg Val Ser Ser Phe Glu Ala Leu  
 105 110 115

gac aag cct gcc gcg gtt gcc act atg atg tgg gcg aac aat gag acc	499
Asp Lys Pro Ala Ala Val Ala Thr Met Met Trp Ala Asn Asn Glu Thr	
120 125 130	
ggc gcg att cag ccg gtt tct gag ttc atc gcc gcc gcg cag gcg tcc	547
Gly Ala Ile Gln Pro Val Ser Glu Phe Ile Ala Ala Ala Gln Ala Ser	
135 140 145	
ggc acg cca aca cac atc gat gcg gtt cag gtc gtt ggc cat ctg ccg	595
Gly Thr Pro Thr His Ile Asp Ala Val Gln Val Val Gly His Leu Pro	
150 155 160 165	
gtc aat ttt gat gag ctc ggc gcc acc act ttg gct gcc tcc gcg cac	643
Val Asn Phe Asp Glu Leu Gly Ala Thr Thr Leu Ala Ala Ser Ala His	
170 175 180	
aaa ttc ggt gga cca cgt ggc gtc ggc ctg ctg ttg gtg agg cgc tca	691
Lys Phe Gly Gly Pro Arg Gly Val Gly Leu Leu Leu Val Arg Arg Ser	
185 190 195	
cca gca cct tca gcc gta ttg cac gga ggt ggt cag gag cgc ggc atc	739
Pro Ala Pro Ser Ala Val Leu His Gly Gly Gly Gln Glu Arg Gly Ile	
200 205 210	
cgt cca ggc acc ctt gat gtc gcc ggc gca gct gcc acc gca gcc gca	787
Arg Pro Gly Thr Leu Asp Val Ala Gly Ala Ala Ala Thr Ala Ala Ala	
215 220 225	
tta cgc gaa gca gtg gcc gag ctt gac ggc gaa gcc acc cgc ctg cgc	835
Leu Arg Glu Ala Val Ala Glu Leu Asp Gly Glu Ala Thr Arg Leu Arg	
230 235 240 245	
gga ctt aaa aag atg ctt ctc gac gcc atc ctc cac acc atc ccc aac	883
Gly Leu Lys Lys Met Leu Leu Asp Ala Ile Leu His Thr Ile Pro Asn	
250 255 260	
gta ctg gtc cac acc acc gaa cca tcc ctg cca gga cac ctg cat ctc	931
Val Leu Val His Thr Thr Glu Pro Ser Leu Pro Gly His Leu His Leu	
265 270 275	
tcc ttc cca gga gca gaa ggc gat agt ttg atc atg ctg ctc gac tcc	979
Ser Phe Pro Gly Ala Glu Gly Asp Ser Leu Ile Met Leu Leu Asp Ser	
280 285 290	
ttg cgg atc gaa gcc tcc aca ggt tcg gcc tgc tcc aac ggt gta aac	
1027	
Leu Arg Ile Glu Ala Ser Thr Gly Ser Ala Cys Ser Asn Gly Val Asn	
295 300 305	
cgt gcc agc cac gtc ctt ttg gcc atg gga att tcc gaa acc gac gcc	
1075	
Arg Ala Ser His Val Leu Leu Ala Met Gly Ile Ser Glu Thr Asp Ala	
310 315 320 325	
cgt ggt gcc atc cga ttc acc ctc gga aga acc acc act gaa gaa tcc	
1123	
Arg Gly Ala Ile Arg Phe Thr Leu Gly Arg Thr Thr Thr Glu Glu Ser	
330 335 340	
atc aag gca gtg atc gcc gtg atc gaa gac gta gtg acc agg gct cgt	
1171	

Ile Lys Ala Val Ile Ala Val Ile Glu Asp Val Val Thr Arg Ala Arg  
 345 350 355

act gcg gga atg gct ttt tagcgaccgt aaatcgcata gtg  
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 Thr Ala Gly Met Ala Phe  
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<210> 646

<211> 363

<212> PRT

<213> Corynebacterium glutamicum

<400> 646

Met Arg Glu Val Ala Ala Ala Ala Trp Met Glu Asn Ala Gln Ala Leu  
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Asn Pro Ala Ser Gln Tyr Gly Ser Gly Arg Lys Ala Arg Ser Val Ala  
 20 25 30

Asp Ser Ala Arg Glu Glu Ile Ala Ser Leu Leu Gly Cys Glu Pro Ile  
 35 40 45

Glu Val Val Phe Thr Ala Ser Gly Thr Glu Ala Asp Asn Leu Ala Val  
 50 55 60

Gln Gly Leu Phe His Ala Ser Pro Leu Asn Arg Ile Ile Ser Thr Pro  
 65 70 75 80

Ile Glu His Pro Gly Ile Leu Glu Thr Val Lys Ala Leu Glu Leu Gly  
 85 90 95

Gly Ala Glu Ala Glu Leu Met Pro Ile Gly Pro Asp Gly Arg Val Ser  
 100 105 110

Ser Phe Glu Ala Leu Asp Lys Pro Ala Ala Val Ala Thr Met Met Trp  
 115 120 125

Ala Asn Asn Glu Thr Gly Ala Ile Gln Pro Val Ser Glu Phe Ile Ala  
 130 135 140

Ala Ala Gln Ala Ser Gly Thr Pro Thr His Ile Asp Ala Val Gln Val  
 145 150 155 160

Val Gly His Leu Pro Val Asn Phe Asp Glu Leu Gly Ala Thr Thr Leu  
 165 170 175

Ala Ala Ser Ala His Lys Phe Gly Gly Pro Arg Gly Val Gly Leu Leu  
 180 185 190

Leu Val Arg Arg Ser Pro Ala Pro Ser Ala Val Leu His Gly Gly Gly  
 195 200 205

Gln Glu Arg Gly Ile Arg Pro Gly Thr Leu Asp Val Ala Gly Ala Ala  
 210 215 220

Ala Thr Ala Ala Ala Leu Arg Glu Ala Val Ala Glu Leu Asp Gly Glu  
 225 230 235 240

Ala Thr Arg Leu Arg Gly Leu Lys Lys Met Leu Leu Asp Ala Ile Leu

				245						250					255				
His	Thr	Ile	Pro	Asn	Val	Leu	Val	His	Thr	Thr	Glu	Pro	Ser	Leu	Pro				
			260					265					270						
Gly	His	Leu	His	Leu	Ser	Phe	Pro	Gly	Ala	Glu	Gly	Asp	Ser	Leu	Ile				
		275					280					285							
Met	Leu	Leu	Asp	Ser	Leu	Arg	Ile	Glu	Ala	Ser	Thr	Gly	Ser	Ala	Cys				
	290					295					300								
Ser	Asn	Gly	Val	Asn	Arg	Ala	Ser	His	Val	Leu	Leu	Ala	Met	Gly	Ile				
305					310					315					320				
Ser	Glu	Thr	Asp	Ala	Arg	Gly	Ala	Ile	Arg	Phe	Thr	Leu	Gly	Arg	Thr				
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Thr	Thr	Glu	Glu	Ser	Ile	Lys	Ala	Val	Ile	Ala	Val	Ile	Glu	Asp	Val				
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Val	Thr	Arg	Ala	Arg	Thr	Ala	Gly	Met	Ala	Phe									
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&lt;210&gt; 647

&lt;211&gt; 1197

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1174)

&lt;223&gt; RXN00262

&lt;400&gt; 647

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Met Leu Tyr Leu Asp
1 5

aat gca gcc acc acc agt gtg cgc aat gaa gca ctt gag gcc atg tgg 163
Asn Ala Ala Thr Thr Ser Val Arg Asn Glu Ala Leu Glu Ala Met Trp
10 15 20

cct tat ctc acc gga gcg ttt ggc aat ccg tca agt ccc cat gag gtg 211
Pro Tyr Leu Thr Gly Ala Phe Gly Asn Pro Ser Ser Pro His Glu Val
25 30 35

gga aga ctc gcc tct gcg ggg ctg gag gat gct cga act cgg gtg gcc 259
Gly Arg Leu Ala Ser Ala Gly Leu Glu Asp Ala Arg Thr Arg Val Ala
40 45 50

cgc att atc gga gga cgc ccc aca cag gtg acg ttt acg tcg ggt gga 307
Arg Ile Ile Gly Gly Arg Pro Thr Gln Val Thr Phe Thr Ser Gly Gly
55 60 65

tca gaa gcc aac aac ctc gct atc aaa gga gcg tgc tta gct aat cct 355
Ser Glu Ala Asn Asn Leu Ala Ile Lys Gly Ala Cys Leu Ala Asn Pro
70 75 80 85

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Arg Gly Arg His Leu Ile Thr Thr Pro Ile Glu His Asp Ser Val Leu	
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gaa act gct gct tat ctt gaa agg ttt cat gat ttc gag atc acc tac	451
Glu Thr Ala Ala Tyr Leu Glu Arg Phe His Asp Phe Glu Ile Thr Tyr	
105 110 115	
cta tcc ccc gat cac act ggg ctg atc tcc ccg gag ggt ctc cgc aaa	499
Leu Ser Pro Asp His Thr Gly Leu Ile Ser Pro Glu Gly Leu Arg Lys	
120 125 130	
gca gtc agg ccg gac acc aca ttg atc agc att ggt tat gcc aac aat	547
Ala Val Arg Pro Asp Thr Thr Leu Ile Ser Ile Gly Tyr Ala Asn Asn	
135 140 145	
gag gtg gga acc att cag ccg ata gct gag ttg gcg gcg gta agc agt	595
Glu Val Gly Thr Ile Gln Pro Ile Ala Glu Leu Ala Ala Val Ser Ser	
150 155 160 165	
acg cct ttt cac acc gat gca gtg caa gct gca cat tta acc ttt gac	643
Thr Pro Phe His Thr Asp Ala Val Gln Ala Ala His Leu Thr Phe Asp	
170 175 180	
ttg gga gtt gac gcg tta agt ttg tcg ggt cat aaa ttc ggt gcg cct	691
Leu Gly Val Asp Ala Leu Ser Leu Ser Gly His Lys Phe Gly Ala Pro	
185 190 195	
aaa ggg att gga gtg tta tgg tca aag ctt ccc ctg gag ccg gta atc	739
Lys Gly Ile Gly Val Leu Trp Ser Lys Leu Pro Leu Glu Pro Val Ile	
200 205 210	
cat ggc ggc ggc cag gaa aaa ggg ccg cgt agt ggc acg gaa aac gtt	787
His Gly Gly Gly Gln Glu Lys Gly Arg Arg Ser Gly Thr Glu Asn Val	
215 220 225	
gcg ggg gct atc gcc ttt gcc act gcc ttg gaa ttg gcc agg gcg gaa	835
Ala Gly Ala Ile Ala Phe Ala Thr Ala Leu Glu Leu Ala Arg Ala Glu	
230 235 240 245	
tcc tat cca gat ctt ggc gaa ttc atc gag gaa gtt ctc act atc ccg	883
Ser Tyr Pro Asp Leu Gly Glu Phe Ile Glu Glu Val Leu Thr Ile Pro	
250 255 260	
gga gca cac ctg act gga cat cct agg atg cgc att gat gga cac gca	931
Gly Ala His Leu Thr Gly His Pro Arg Met Arg Ile Asp Gly His Ala	
265 270 275	
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Ser Phe Leu Phe Asp Ser Ile Gly Ser Glu Thr Val Leu Leu Glu Leu	
280 285 290	
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Glu Arg Gln Gly Ile Val Cys Ser Pro Gly Ser Ala Cys Gly Ser Gly	
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Glu Val Ser His Val Leu Leu Ala Leu Gly Leu Glu Glu Asp Gln Ala	
310 315 320 325	

cga acg gct gtg cgc tgt act ttt agt aca aca cac agc cgt gaa gat  
1123

Arg Thr Ala Val Arg Cys Thr Phe Ser Thr Thr His Ser Arg Glu Asp  
330 335 340

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1197

Gly

<210> 648

<211> 358

<212> PRT

<213> Corynebacterium glutamicum

<400> 648

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Leu Glu Ala Met Trp Pro Tyr Leu Thr Gly Ala Phe Gly Asn Pro Ser  
20 25 30

Ser Pro His Glu Val Gly Arg Leu Ala Ser Ala Gly Leu Glu Asp Ala  
35 40 45

Arg Thr Arg Val Ala Arg Ile Ile Gly Gly Arg Pro Thr Gln Val Thr  
50 55 60

Phe Thr Ser Gly Gly Ser Glu Ala Asn Asn Leu Ala Ile Lys Gly Ala  
65 70 75 80

Cys Leu Ala Asn Pro Arg Gly Arg His Leu Ile Thr Thr Pro Ile Glu  
85 90 95

His Asp Ser Val Leu Glu Thr Ala Ala Tyr Leu Glu Arg Phe His Asp  
100 105 110

Phe Glu Ile Thr Tyr Leu Ser Pro Asp His Thr Gly Leu Ile Ser Pro  
115 120 125

Glu Gly Leu Arg Lys Ala Val Arg Pro Asp Thr Thr Leu Ile Ser Ile  
130 135 140

Gly Tyr Ala Asn Asn Glu Val Gly Thr Ile Gln Pro Ile Ala Glu Leu  
145 150 155 160

Ala Ala Val Ser Ser Thr Pro Phe His Thr Asp Ala Val Gln Ala Ala  
165 170 175

His Leu Thr Phe Asp Leu Gly Val Asp Ala Leu Ser Leu Ser Gly His  
180 185 190

Lys Phe Gly Ala Pro Lys Gly Ile Gly Val Leu Trp Ser Lys Leu Pro  
195 200 205

Leu Glu Pro Val Ile His Gly Gly Gly Gln Glu Lys Gly Arg Arg Ser  
 210 215 220  
 Gly Thr Glu Asn Val Ala Gly Ala Ile Ala Phe Ala Thr Ala Leu Glu  
 225 230 235 240  
 Leu Ala Arg Ala Glu Ser Tyr Pro Asp Leu Gly Glu Phe Ile Glu Glu  
 245 250 255  
 Val Leu Thr Ile Pro Gly Ala His Leu Thr Gly His Pro Arg Met Arg  
 260 265 270  
 Ile Asp Gly His Ala Ser Phe Leu Phe Asp Ser Ile Gly Ser Glu Thr  
 275 280 285  
 Val Leu Leu Glu Leu Glu Arg Gln Gly Ile Val Cys Ser Pro Gly Ser  
 290 295 300  
 Ala Cys Gly Ser Gly Glu Val Ser His Val Leu Leu Ala Leu Gly Leu  
 305 310 315 320  
 Glu Glu Asp Gln Ala Arg Thr Ala Val Arg Cys Thr Phe Ser Thr Thr  
 325 330 335  
 His Ser Arg Glu Asp Ala Leu Val Ala Ala Ser Ala Leu Lys Ser Ala  
 340 345 350  
 Val Ala Leu Ile Arg Gly  
 355

&lt;210&gt; 649

&lt;211&gt; 920

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (79)..(897)

&lt;223&gt; FRXA00262

&lt;400&gt; 649

cacacaggtg acgtttacgt cgggtggatc agaagccaac aacctcgctt atcaaaggag 60

cgtgcttagc taatcctagtg gcc ggg cac ctc atc acc acc ccg atc gag 111

Val Ala Gly His Leu Ile Thr Thr Pro Ile Glu  
 1 5 10

cat gac agt gtc cta gaa act gct gct tat ctt gaa agg ttt cat gat 159

His Asp Ser Val Leu Glu Thr Ala Ala Tyr Leu Glu Arg Phe His Asp  
 15 20 25

ttc gag atc acc tac cta tcc ccc gat cac act ggg ctg atc tcc ccg 207

Phe Glu Ile Thr Tyr Leu Ser Pro Asp His Thr Gly Leu Ile Ser Pro  
 30 35 40

gag ggt ctc cgc aaa gca gtc agg ccg gac acc aca ttg atc agc att 255

Glu Gly Leu Arg Lys Ala Val Arg Pro Asp Thr Thr Leu Ile Ser Ile  
 45 50 55

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ggt tat gcc aac aat gag gtg gga acc att cag ccg ata gct gag ttg 303
Gly Tyr Ala Asn Asn Glu Val Gly Thr Ile Gln Pro Ile Ala Glu Leu
60 65 70 75

gcg gcg gta agc agt acg cct ttt cac acc gat gca gtg caa gct gca 351
Ala Ala Val Ser Ser Thr Pro Phe His Thr Asp Ala Val Gln Ala Ala
80 85 90

cat tta acc ttt gac ttg gga gtt gac gcg tta agt ttg tcg ggt cat 399
His Leu Thr Phe Asp Leu Gly Val Asp Ala Leu Ser Leu Ser Gly His
95 100 105

aaa ttc ggt gcg cct aaa ggg att gga gtg tta tgg tca aag ctt ccc 447
Lys Phe Gly Ala Pro Lys Gly Ile Gly Val Leu Trp Ser Lys Leu Pro
110 115 120

ctg gag ccg gta atc cat ggc ggc ggc cag gaa aaa ggg cgg cgt agt 495
Leu Glu Pro Val Ile His Gly Gly Gly Gln Glu Lys Gly Arg Arg Ser
125 130 135

ggc acg gaa aac gtt gcg ggg gct atc gcc ttt gcc act gcc ttg gaa 543
Gly Thr Glu Asn Val Ala Gly Ala Ile Ala Phe Ala Thr Ala Leu Glu
140 145 150 155

ttg gcc agg gcg gaa tcc tat cca gat ctt ggc gaa ttc atc gag gaa 591
Leu Ala Arg Ala Glu Ser Tyr Pro Asp Leu Gly Glu Phe Ile Glu Glu
160 165 170

gtt ctc act atc ccg gga gca cac ctg act gga cat cct agg atg cgc 639
Val Leu Thr Ile Pro Gly Ala His Leu Thr Gly His Pro Arg Met Arg
175 180 185

att gat gga cac gca tct ttt ctc ttc gac agc ata gga tct gaa act 687
Ile Asp Gly His Ala Ser Phe Leu Phe Asp Ser Ile Gly Ser Glu Thr
190 195 200

gtt ctt ctg gaa ttg gaa cgc caa ggc att gtg tgc tcc cct ggt tct 735
Val Leu Leu Glu Leu Glu Arg Gln Gly Ile Val Cys Ser Pro Gly Ser
205 210 215

gcc tgt ggt tcc gga gag gta tcc cat gtg ttg ctg gcg ttg ggg ctt 783
Ala Cys Gly Ser Gly Glu Val Ser His Val Leu Leu Ala Leu Gly Leu
220 225 230 235

gag gag gat caa gca cga acg gct gtg cgc tgt act ttt agt aca aca 831
Glu Glu Asp Gln Ala Arg Thr Ala Val Arg Cys Thr Phe Ser Thr Thr
240 245 250

cac agc cgt gaa gat gcg ctc gtg gca gcc tct gct ctt aaa tcc gcg 879
His Ser Arg Glu Asp Ala Leu Val Ala Ala Ser Ala Leu Lys Ser Ala
255 260 265

gtc gcc tta atc aga ggg tgacgctagt cagaggttta cgg 920
Val Ala Leu Ile Arg Gly
270

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&lt;210&gt; 650

&lt;211&gt; 273

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum



&lt;400&gt; 650

Val Ala Gly His Leu Ile Thr Thr Pro Ile Glu His Asp Ser Val Leu  
 1 5 10 15  
 Glu Thr Ala Ala Tyr Leu Glu Arg Phe His Asp Phe Glu Ile Thr Tyr  
 20 25 30  
 Leu Ser Pro Asp His Thr Gly Leu Ile Ser Pro Glu Gly Leu Arg Lys  
 35 40 45  
 Ala Val Arg Pro Asp Thr Thr Leu Ile Ser Ile Gly Tyr Ala Asn Asn  
 50 55 60  
 Glu Val Gly Thr Ile Gln Pro Ile Ala Glu Leu Ala Ala Val Ser Ser  
 65 70 75 80  
 Thr Pro Phe His Thr Asp Ala Val Gln Ala Ala His Leu Thr Phe Asp  
 85 90 95  
 Leu Gly Val Asp Ala Leu Ser Leu Ser Gly His Lys Phe Gly Ala Pro  
 100 105 110  
 Lys Gly Ile Gly Val Leu Trp Ser Lys Leu Pro Leu Glu Pro Val Ile  
 115 120 125  
 His Gly Gly Gly Gln Glu Lys Gly Arg Arg Ser Gly Thr Glu Asn Val  
 130 135 140  
 Ala Gly Ala Ile Ala Phe Ala Thr Ala Leu Glu Leu Ala Arg Ala Glu  
 145 150 155 160  
 Ser Tyr Pro Asp Leu Gly Glu Phe Ile Glu Glu Val Leu Thr Ile Pro  
 165 170 175  
 Gly Ala His Leu Thr Gly His Pro Arg Met Arg Ile Asp Gly His Ala  
 180 185 190  
 Ser Phe Leu Phe Asp Ser Ile Gly Ser Glu Thr Val Leu Leu Glu Leu  
 195 200 205  
 Glu Arg Gln Gly Ile Val Cys Ser Pro Gly Ser Ala Cys Gly Ser Gly  
 210 215 220  
 Glu Val Ser His Val Leu Leu Ala Leu Gly Leu Glu Glu Asp Gln Ala  
 225 230 235 240  
 Arg Thr Ala Val Arg Cys Thr Phe Ser Thr Thr His Ser Arg Glu Asp  
 245 250 255  
 Ala Leu Val Ala Ala Ser Ala Leu Lys Ser Ala Val Ala Leu Ile Arg  
 260 265 270

Gly

&lt;210&gt; 651

&lt;211&gt; 1296

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1273)

&lt;223&gt; RXN00435

&lt;400&gt; 651

cgacaggtga attcatgcac gtttgagtgt cccgtgtgtg gggtaatggt gtccaagaga 60

gtggaaggaa atgctgtggc gggtgaaagg agtgcctttc gtg ggt ttt gat gtg 115  
 Val Gly Phe Asp Val  
 1 5

gcc agg gtt cgg ggg ctt tat acc tct ttg ggc gat ggc tgg acg tac 163  
 Ala Arg Val Arg Gly Leu Tyr Thr Ser Leu Gly Asp Gly Trp Thr Tyr  
 10 15 20

ctt aat tca cat caa att ccg cag gtt ccg gag cgg gtg gcg tcg gga 211  
 Leu Asn Ser His Gln Ile Pro Gln Val Pro Glu Arg Val Ala Ser Gly  
 25 30 35

gtt gcg gcg gct ttc cgc acg cat gcg cag att tct gag gtg acg tcg 259  
 Val Ala Ala Ala Phe Arg Thr His Ala Gln Ile Ser Glu Val Thr Ser  
 40 45 50

cag ccg att gcg gtg gat cag ttg gag gct gct cgc gag gca gtt gcg 307  
 Gln Pro Ile Ala Val Asp Gln Leu Glu Ala Ala Arg Glu Ala Val Ala  
 55 60 65

tcg ttg gcg ggt gtg gat ccg gac tgt gtt gtg ctg ggt ccc acg agg 355  
 Ser Leu Ala Gly Val Asp Pro Asp Cys Val Val Leu Gly Pro Thr Arg  
 70 75 80 85

cag ttt ttg gct cat aca ttg gcg cgc ggt ttg ggt ggg ttt gta cgt 403  
 Gln Phe Leu Ala His Thr Leu Ala Arg Gly Leu Gly Gly Phe Val Arg  
 90 95 100

cga aaa gcg ggc gtg gtg ttg tcg cgc gcg gac gcg gac tgg ctg acc 451  
 Arg Lys Ala Gly Val Val Leu Ser Arg Ala Asp Ala Asp Trp Leu Thr  
 105 110 115

gcg ccg ttc cgc tcc ctc gac ggc gtt ttt agc tgg gcc gag ccc gat 499  
 Ala Pro Phe Arg Ser Leu Asp Gly Val Phe Ser Trp Ala Glu Pro Asp  
 120 125 130

ttg ggc acc ggc atg ctg ccg gat tgg cag tac gag aag ctt gtt gac 547  
 Leu Gly Thr Gly Met Leu Pro Asp Trp Gln Tyr Glu Lys Leu Val Asp  
 135 140 145

ggc tcg acg cgc ctt gtc gtg ctc agc gcc gcg cac ccg ctg ctc ggc 595  
 Gly Ser Thr Arg Leu Val Val Leu Ser Ala Ala His Pro Leu Leu Gly  
 150 155 160 165

acg gtc gcc cca gtg ggc aag att gtg gat aaa gtg cgg gcg cgt tcg 643  
 Thr Val Ala Pro Val Gly Lys Ile Val Asp Lys Val Arg Ala Arg Ser  
 170 175 180

cgt gcc tgg gtg ctt gtc gac gcc acc acc tac gca gcc tac cgc ccc 691  
 Arg Ala Trp Val Leu Val Asp Ala Thr Thr Tyr Ala Ala Tyr Arg Pro  
 185 190 195

ctg cgc cta gac gag tgg gaa gcc gat atc gtc atg ctt gat ctc ggc 739  
 Leu Arg Leu Asp Glu Trp Glu Ala Asp Ile Val Met Leu Asp Leu Gly  
 200 205 210

gag ttg ggc ggc ccg cag att tcg gcg ttg att ttc cgt gat acc tcg 787  
 Glu Leu Gly Gly Pro Gln Ile Ser Ala Leu Ile Phe Arg Asp Thr Ser  
 215 220 225

atg ttc ccg cgc ctg gat cgc acc gtt cca ctc gaa ctg ccc gca agc 835  
 Met Phe Pro Arg Leu Asp Arg Thr Val Pro Leu Glu Leu Pro Ala Ser  
 230 235 240 245

tcc ctg ccg cat ggg ctg ctc ggc ggc gtg ccc aac ctg gtg cgg cac 883  
 Ser Leu Pro His Gly Leu Leu Gly Gly Val Pro Asn Leu Val Arg His  
 250 255 260

ctg gga aac ctg gat gaa aac gcc ccg tcc gtc gtt gag gcg atg ggc 931  
 Leu Gly Asn Leu Asp Glu Asn Ala Pro Ser Val Val Glu Ala Met Gly  
 265 270 275

gag atg gcg aaa ttc cac aag gga ctt ttt gag cat ctt gtg gaa tcg 979  
 Glu Met Ala Lys Phe His Lys Gly Leu Phe Glu His Leu Val Glu Ser  
 280 285 290

ctc gaa gga ctt cac gcg gtg cat atc gtg gga att tcc ggc gat gcc  
 1027  
 Leu Glu Gly Leu His Ala Val His Ile Val Gly Ile Ser Gly Asp Ala  
 295 300 305

gca ggt caa gac gcc ccg ttc ctg gat cga gtg ccc cgc ttg acc ttc  
 1075  
 Ala Gly Gln Asp Ala Pro Phe Leu Asp Arg Val Pro Arg Leu Thr Phe  
 310 315 320 325

acc atg gaa ggc gtg ccc gca gat atg gtg tac cgc cga ttg gtg gac  
 1123  
 Thr Met Glu Gly Val Pro Ala Asp Met Val Tyr Arg Arg Leu Val Asp  
 330 335 340

aat cgt ttg atc act acc gtc agc cct gct gac ccg ctg ctc gaa gca  
 1171  
 Asn Arg Leu Ile Thr Thr Val Ser Pro Ala Asp Pro Leu Leu Glu Ala  
 345 350 355

atg ggt gtg act gaa gct ggc gga tcg atc act atc gga cta agc ccg  
 1219  
 Met Gly Val Thr Glu Ala Gly Gly Ser Ile Thr Ile Gly Leu Ser Pro  
 360 365 370

ttt agc acc tac tat gaa gtg gat cag ctg acc agg gtg ctg gca tcg  
 1267  
 Phe Ser Thr Tyr Tyr Glu Val Asp Gln Leu Thr Arg Val Leu Ala Ser  
 375 380 385

ctt gcc taaaccgcaa gcacgagctt gcc  
 1296  
 Leu Ala  
 390

&lt;210&gt; 652

&lt;211&gt; 391

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 652

Val	Gly	Phe	Asp	Val	Ala	Arg	Val	Arg	Gly	Leu	Tyr	Thr	Ser	Leu	Gly	1	5	10	15
Asp	Gly	Trp	Thr	Tyr	Leu	Asn	Ser	His	Gln	Ile	Pro	Gln	Val	Pro	Glu	20	25	30	
Arg	Val	Ala	Ser	Gly	Val	Ala	Ala	Ala	Phe	Arg	Thr	His	Ala	Gln	Ile	35	40	45	
Ser	Glu	Val	Thr	Ser	Gln	Pro	Ile	Ala	Val	Asp	Gln	Leu	Glu	Ala	Ala	50	55	60	
Arg	Glu	Ala	Val	Ala	Ser	Leu	Ala	Gly	Val	Asp	Pro	Asp	Cys	Val	Val	65	70	75	80
Leu	Gly	Pro	Thr	Arg	Gln	Phe	Leu	Ala	His	Thr	Leu	Ala	Arg	Gly	Leu	85	90	95	
Gly	Gly	Phe	Val	Arg	Arg	Lys	Ala	Gly	Val	Val	Leu	Ser	Arg	Ala	Asp	100	105	110	
Ala	Asp	Trp	Leu	Thr	Ala	Pro	Phe	Arg	Ser	Leu	Asp	Gly	Val	Phe	Ser	115	120	125	
Trp	Ala	Glu	Pro	Asp	Leu	Gly	Thr	Gly	Met	Leu	Pro	Asp	Trp	Gln	Tyr	130	135	140	
Glu	Lys	Leu	Val	Asp	Gly	Ser	Thr	Arg	Leu	Val	Val	Leu	Ser	Ala	Ala	145	150	155	160
His	Pro	Leu	Leu	Gly	Thr	Val	Ala	Pro	Val	Gly	Lys	Ile	Val	Asp	Lys	165	170	175	
Val	Arg	Ala	Arg	Ser	Arg	Ala	Trp	Val	Leu	Val	Asp	Ala	Thr	Thr	Tyr	180	185	190	
Ala	Ala	Tyr	Arg	Pro	Leu	Arg	Leu	Asp	Glu	Trp	Glu	Ala	Asp	Ile	Val	195	200	205	
Met	Leu	Asp	Leu	Gly	Glu	Leu	Gly	Gly	Pro	Gln	Ile	Ser	Ala	Leu	Ile	210	215	220	
Phe	Arg	Asp	Thr	Ser	Met	Phe	Pro	Arg	Leu	Asp	Arg	Thr	Val	Pro	Leu	225	230	235	240
Glu	Leu	Pro	Ala	Ser	Ser	Leu	Pro	His	Gly	Leu	Leu	Gly	Gly	Val	Pro	245	250	255	
Asn	Leu	Val	Arg	His	Leu	Gly	Asn	Leu	Asp	Glu	Asn	Ala	Pro	Ser	Val	260	265	270	
Val	Glu	Ala	Met	Gly	Glu	Met	Ala	Lys	Phe	His	Lys	Gly	Leu	Phe	Glu	275	280	285	
His	Leu	Val	Glu	Ser	Leu	Glu	Gly	Leu	His	Ala	Val	His	Ile	Val	Gly	290	295	300	

Ile Ser Gly Asp Ala Ala Gly Gln Asp Ala Pro Phe Leu Asp Arg Val  
 305 310 315 320  
 Pro Arg Leu Thr Phe Thr Met Glu Gly Val Pro Ala Asp Met Val Tyr  
 325 330 335  
 Arg Arg Leu Val Asp Asn Arg Leu Ile Thr Thr Val Ser Pro Ala Asp  
 340 345 350  
 Pro Leu Leu Glu Ala Met Gly Val Thr Glu Ala Gly Gly Ser Ile Thr  
 355 360 365  
 Ile Gly Leu Ser Pro Phe Ser Thr Tyr Tyr Glu Val Asp Gln Leu Thr  
 370 375 380  
 Arg Val Leu Ala Ser Leu Ala  
 385 390

<210> 653  
 <211> 638  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(615)  
 <223> FRXA00435

<400> 653  
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 Val Asp Ala Thr Thr Tyr Ala Ala Tyr Arg Pro Leu Arg Leu Asp Glu  
 1 5 10 15  
 tgg gaa gcc gat atc gtc atg ctt gat ctc ggc gag ttg ggc ggc ccg 96  
 Trp Glu Ala Asp Ile Val Met Leu Asp Leu Gly Glu Leu Gly Gly Pro  
 20 25 30  
 cag att tcg gcg ttg att ttc cgt gat acc tcg atg ttc ccg cgc ctg 144  
 Gln Ile Ser Ala Leu Ile Phe Arg Asp Thr Ser Met Phe Pro Arg Leu  
 35 40 45  
 gat cgc acc gtt cca ctc gaa ctg ccc gca agc tcc ctg ccg cat ggg 192  
 Asp Arg Thr Val Pro Leu Glu Leu Pro Ala Ser Ser Leu Pro His Gly  
 50 55 60  
 ctg ctc ggc ggc gtg ccc aac ctg gtg cgg cac ctg gga aac ctg gat 240  
 Leu Leu Gly Gly Val Pro Asn Leu Val Arg His Leu Gly Asn Leu Asp  
 65 70 75 80  
 gaa aac gcc ccg tcc gtc gtt gag gcg atg ggg gag atg gcg aaa ttc 288  
 Glu Asn Ala Pro Ser Val Val Glu Ala Met Gly Glu Met Ala Lys Phe  
 85 90 95  
 cac aag gga ctt ttt gag cat ctt gtg gaa tcg ctc gaa gga ctt cac 336  
 His Lys Gly Leu Phe Glu His Leu Val Glu Ser Leu Glu Gly Leu His  
 100 105 110  
 gcg gtg cat atc gtg gga att tcc ggc gat gcc gca ggt caa gac gcc 384  
 Ala Val His Ile Val Gly Ile Ser Gly Asp Ala Ala Gly Gln Asp Ala

115	120	125	
ccg ttc ctg gat cga gtg	ccc cgc ttg acc ttc	acc atg gaa ggc gtg	432
Pro Phe Leu Asp Arg Val	Pro Arg Leu Thr Phe	Thr Met Glu Gly Val	
130	135	140	
ccc gca gat atg gtg tac	cgc cga ttg gtg gac	aat cgt ttg atc act	480
Pro Ala Asp Met Val Tyr	Arg Arg Leu Val Asp	Asn Arg Leu Ile Thr	
145	150	155	160
acc gtc agc cct gct gac	ccg ctg ctc gaa gca	atg ggt gtg act gaa	528
Thr Val Ser Pro Ala Asp	Pro Leu Leu Glu Ala	Met Gly Val Thr Glu	
165	170	175	
gct ggc gga tcg atc act	atc gga cta agc ccg	ttt agc acc tac tat	576
Ala Gly Gly Ser Ile Thr	Ile Gly Leu Ser Pro	Phe Ser Thr Tyr Tyr	
180	185	190	
gaa gtg gat cag ctg acc	agg gtg ctg gca tcg	ctt gcc taaaccgcaa	625
Glu Val Asp Gln Leu Thr	Arg Val Leu Ala Ser	Leu Ala	
195	200	205	
gcacgagctt gcc			638

&lt;210&gt; 654

&lt;211&gt; 205

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 654

Val	Asp	Ala	Thr	Thr	Tyr	Ala	Ala	Tyr	Arg	Pro	Leu	Arg	Leu	Asp	Glu
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Trp	Glu	Ala	Asp	Ile	Val	Met	Leu	Asp	Leu	Gly	Glu	Leu	Gly	Gly	Pro
			20					25					30		

Gln	Ile	Ser	Ala	Leu	Ile	Phe	Arg	Asp	Thr	Ser	Met	Phe	Pro	Arg	Leu
		35					40					45			

Asp	Arg	Thr	Val	Pro	Leu	Glu	Leu	Pro	Ala	Ser	Ser	Leu	Pro	His	Gly
	50					55					60				

Leu	Leu	Gly	Gly	Val	Pro	Asn	Leu	Val	Arg	His	Leu	Gly	Asn	Leu	Asp
65					70					75					80

Glu	Asn	Ala	Pro	Ser	Val	Val	Glu	Ala	Met	Gly	Glu	Met	Ala	Lys	Phe
				85					90					95	

His	Lys	Gly	Leu	Phe	Glu	His	Leu	Val	Glu	Ser	Leu	Glu	Gly	Leu	His
			100					105					110		

Ala	Val	His	Ile	Val	Gly	Ile	Ser	Gly	Asp	Ala	Ala	Gly	Gln	Asp	Ala
		115					120					125			

Pro	Phe	Leu	Asp	Arg	Val	Pro	Arg	Leu	Thr	Phe	Thr	Met	Glu	Gly	Val
	130					135					140				

Pro	Ala	Asp	Met	Val	Tyr	Arg	Arg	Leu	Val	Asp	Asn	Arg	Leu	Ile	Thr
145					150					155					160

Thr	Val	Ser	Pro	Ala	Asp	Pro	Leu	Leu	Glu	Ala	Met	Gly	Val	Thr	Glu
				165					170					175	
Ala	Gly	Gly	Ser	Ile	Thr	Ile	Gly	Leu	Ser	Pro	Phe	Ser	Thr	Tyr	Tyr
			180					185					190		
Glu	Val	Asp	Gln	Leu	Thr	Arg	Val	Leu	Ala	Ser	Leu	Ala			
		195					200					205			

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<210> 655
<211> 535
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(535)  
<223> FRXA02801
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<400> 655																	
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				Val	Gly	Phe	Asp	Val								5	
				1													
gcc	agg	gtt	cgg	ggg	ctt	tat	acc	tct	ttg	ggc	gat	ggc	tgg	acg	tac		163
Ala	Arg	Val	Arg	Gly	Leu	Tyr	Thr	Ser	Leu	Gly	Asp	Gly	Trp	Thr	Tyr		
				10					15					20			
ctt	aat	tca	cat	caa	att	ccg	cag	gtt	ccg	gag	cgg	gtg	gcg	tcg	gga		211
Leu	Asn	Ser	His	Gln	Ile	Pro	Gln	Val	Pro	Glu	Arg	Val	Ala	Ser	Gly		
			25					30					35				
gtt	gcg	gcg	gct	ttc	cgc	acg	cat	gcg	cag	att	tct	gag	gtg	acg	tcg		259
Val	Ala	Ala	Ala	Phe	Arg	Thr	His	Ala	Gln	Ile	Ser	Glu	Val	Thr	Ser		
			40				45					50					
cag	ccg	att	gcg	gtg	gat	cag	ttg	gag	gct	gct	cgc	gag	gca	gtt	gcg		307
Gln	Pro	Ile	Ala	Val	Asp	Gln	Leu	Glu	Ala	Ala	Arg	Glu	Ala	Val	Ala		
			55			60					65						
tcg	ttg	gcg	ggc	gtg	gat	ccg	gac	tgt	gtt	gtg	ctg	ggc	ccc	acg	agg		355
Ser	Leu	Ala	Gly	Val	Asp	Pro	Asp	Cys	Val	Val	Leu	Gly	Pro	Thr	Arg		
70					75					80					85		
cag	ttt	ttg	gct	cat	aca	ttg	gcg	cgc	ggc	ttg	ggc	ggg	ttt	gta	cgt		403
Gln	Phe	Leu	Ala	His	Thr	Leu	Ala	Arg	Gly	Leu	Gly	Gly	Phe	Val	Arg		
				90					95					100			
cga	aaa	gcg	ggc	gtg	gtg	ttg	tcg	cgc	gcg	gac	gcg	gac	tgg	ctg	acc		451
Arg	Lys	Ala	Gly	Val	Val	Leu	Ser	Arg	Ala	Asp	Ala	Asp	Trp	Leu	Thr		
			105					110					115				
gcg	ccg	ttc	cgc	tcc	ctc	gac	ggc	gtt	ttt	agc	tgg	gcc	gag	ccc	gat		499
Ala	Pro	Phe	Arg	Ser	Leu	Asp	Gly	Val	Phe	Ser	Trp	Ala	Glu	Pro	Asp		
			120				125					130					
ttg	ggc	acc	ggc	atg	ctg	ccg	gat	tgg	cag	tac	cag						535
Leu	Gly	Thr	Gly	Met	Leu	Pro	Asp	Trp	Gln	Tyr	Gln						

135

140

145

<210> 656  
 <211> 145  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 656  
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 Asp Gly Trp Thr Tyr Leu Asn Ser His Gln Ile Pro Gln Val Pro Glu  
                     20                    25                    30  
 Arg Val Ala Ser Gly Val Ala Ala Ala Phe Arg Thr His Ala Gln Ile  
                     35                    40                    45  
 Ser Glu Val Thr Ser Gln Pro Ile Ala Val Asp Gln Leu Glu Ala Ala  
                     50                    55                    60  
 Arg Glu Ala Val Ala Ser Leu Ala Gly Val Asp Pro Asp Cys Val Val  
                     65                    70                    75                    80  
 Leu Gly Pro Thr Arg Gln Phe Leu Ala His Thr Leu Ala Arg Gly Leu  
                     85                    90                    95  
 Gly Gly Phe Val Arg Arg Lys Ala Gly Val Val Leu Ser Arg Ala Asp  
                     100                    105                    110  
 Ala Asp Trp Leu Thr Ala Pro Phe Arg Ser Leu Asp Gly Val Phe Ser  
                     115                    120                    125  
 Trp Ala Glu Pro Asp Leu Gly Thr Gly Met Leu Pro Asp Trp Gln Tyr  
                     130                    135                    140

Gln  
 145

<210> 657  
 <211> 1386  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1363)  
 <223> RXA02516

<400> 657  
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   Met Ser Asp Phe Leu  
   1                    5  
 aat gca gat gga tcc ctc aat gtg gat aag gtg cgg gaa gaa ttc cca 163  
 Asn Ala Asp Gly Ser Leu Asn Val Asp Lys Val Arg Glu Glu Phe Pro  
                     10                    15                    20



atc ctg aag cgc act gtt agg gat ggg aaa ccg ctt gct tac ctg gac	211
Ile Leu Lys Arg Thr Val Arg Asp Gly Lys Pro Leu Ala Tyr Leu Asp	
25 30 35	
tca ggt gcg aca tcg cag cga ccc gag cgg gtg tgg cgt gca gag gag	259
Ser Gly Ala Thr Ser Gln Arg Pro Glu Arg Val Trp Arg Ala Glu Glu	
40 45 50	
cac ttt gtg ctg cac acc aac gcc ccc gtg cac cgc ggt gcc tac caa	307
His Phe Val Leu His Thr Asn Ala Pro Val His Arg Gly Ala Tyr Gln	
55 60 65	
ctg gct gag gaa gca acg gat gct tat gaa ggt gcc cgc gag aag atc	355
Leu Ala Glu Glu Ala Thr Asp Ala Tyr Glu Gly Ala Arg Glu Lys Ile	
70 75 80 85	
gct gcc ttt gtt ggt gcc gag cag cat gaa att gcg ttc act aag aat	403
Ala Ala Phe Val Gly Ala Glu Gln His Glu Ile Ala Phe Thr Lys Asn	
90 95 100	
gca act gaa gca ctc aat ctt gtt gcg tac acc ttg ggt gat gac cgt	451
Ala Thr Glu Ala Leu Asn Leu Val Ala Tyr Thr Leu Gly Asp Asp Arg	
105 110 115	
tcc ggt aag tat cgt gtc cag gcc ggg gat acc gtg gtc atc acg gag	499
Ser Gly Lys Tyr Arg Val Gln Ala Gly Asp Thr Val Val Ile Thr Glu	
120 125 130	
cta gag cac cac gca aac ttg gtg cca tgg cag gag ctg tgc cgt cga	547
Leu Glu His His Ala Asn Leu Val Pro Trp Gln Glu Leu Cys Arg Arg	
135 140 145	
acc ggt gcg aca ttg aag tgg tac aag gtg act gaa gat ggt cgc att	595
Thr Gly Ala Thr Leu Lys Trp Tyr Lys Val Thr Glu Asp Gly Arg Ile	
150 155 160 165	
gat ctc gat tca ctc gag ctt gat gaa act gtc aag gtc gtt gcc ttc	643
Asp Leu Asp Ser Leu Glu Leu Asp Glu Thr Val Lys Val Val Ala Phe	
170 175 180	
act cac cag tcc aat gtg acc ggt gct gtg gct gat gtt cca gag ttg	691
Thr His Gln Ser Asn Val Thr Gly Ala Val Ala Asp Val Pro Glu Leu	
185 190 195	
gtt cgt cgt gcc aag gct gtc ggc gct ctc acg gtg ctt gat gcg tgc	739
Val Arg Arg Ala Lys Ala Val Gly Ala Leu Thr Val Leu Asp Ala Cys	
200 205 210	
cag tct gtt cct cat atg cca gtg aat ttc cac gag ctg gat gta gat	787
Gln Ser Val Pro His Met Pro Val Asn Phe His Glu Leu Asp Val Asp	
215 220 225	
ttc tct gca ttc tct ggc cat aag atg ctg gga cct gca ggc gtg ggc	835
Phe Ser Ala Phe Ser Gly His Lys Met Leu Gly Pro Ala Gly Val Gly	
230 235 240 245	
gtt gtg tat gca aag tcc cca atc ttg gat gaa ctg cca cca ttt ttg	883
Val Val Tyr Ala Lys Ser Pro Ile Leu Asp Glu Leu Pro Pro Phe Leu	
250 255 260	
act ggt ggt tcc atg att gaa gtt gtc acc atg gag ggt tcc acc tac	931

Thr Gly Gly Ser Met Ile Glu Val Val Thr Met Glu Gly Ser Thr Tyr  
265 270 275

gct gcc gca cct caa cgt ttt gag gcc ggc acg cag atg acc agc cag 979  
Ala Ala Ala Pro Gln Arg Phe Glu Ala Gly Thr Gln Met Thr Ser Gln  
280 285 290

gtt gtg ggc ttg ggt gct gcc gtg gac atg ctg aat gaa atc ggt atg  
1027  
Val Val Gly Leu Gly Ala Ala Val Asp Met Leu Asn Glu Ile Gly Met  
295 300 305

gaa gca atc gca gcg cat gag cac gca ttg act gct tac gcg ttg gaa  
1075  
Glu Ala Ile Ala Ala His Glu His Ala Leu Thr Ala Tyr Ala Leu Glu  
310 315 320 325

aag ctc acg gca att aag gga cta acc att gct ggt cct ttg act gca  
1123  
Lys Leu Thr Ala Ile Lys Gly Leu Thr Ile Ala Gly Pro Leu Thr Ala  
330 335 340

gag cag cgc ggc ggt gca atc agc ttc ggt gtc gag ggc att cac cca  
1171  
Glu Gln Arg Gly Gly Ala Ile Ser Phe Gly Val Glu Gly Ile His Pro  
345 350 355

cac gat cta ggc caa gtg ctt gac gat cag ggc gtg aat atc cgc gtc  
1219  
His Asp Leu Gly Gln Val Leu Asp Asp Gln Gly Val Asn Ile Arg Val  
360 365 370

ggc cac cac tgc gcg tgg ccc gtg cac cgc agc atg aac gta caa tcg  
1267  
Gly His His Cys Ala Trp Pro Val His Arg Ser Met Asn Val Gln Ser  
375 380 385

aca gca aga gca tct ttc tat ctc tat aac acc ttc gaa gaa atc gac  
1315  
Thr Ala Arg Ala Ser Phe Tyr Leu Tyr Asn Thr Phe Glu Glu Ile Asp  
390 395 400 405

cgc ctc gcg gca gcg atc gag aag gcc aag caa ttc ttt gga gtt gag  
1363  
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1386

<210> 658

<211> 421

<212> PRT

<213> Corynebacterium glutamicum

<400> 658

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Arg Glu Glu Phe Pro Ile Leu Lys Arg Thr Val Arg Asp Gly Lys Pro

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Leu	Ala	Tyr	Leu	Asp	Ser	Gly	Ala	Thr	Ser	Gln	Arg	Pro	Glu	Arg	Val
		35					40					45			
Trp	Arg	Ala	Glu	Glu	His	Phe	Val	Leu	His	Thr	Asn	Ala	Pro	Val	His
	50					55					60				
Arg	Gly	Ala	Tyr	Gln	Leu	Ala	Glu	Glu	Ala	Thr	Asp	Ala	Tyr	Glu	Gly
65					70					75					80
Ala	Arg	Glu	Lys	Ile	Ala	Ala	Phe	Val	Gly	Ala	Glu	Gln	His	Glu	Ile
				85					90					95	
Ala	Phe	Thr	Lys	Asn	Ala	Thr	Glu	Ala	Leu	Asn	Leu	Val	Ala	Tyr	Thr
			100					105					110		
Leu	Gly	Asp	Asp	Arg	Ser	Gly	Lys	Tyr	Arg	Val	Gln	Ala	Gly	Asp	Thr
		115					120					125			
Val	Val	Ile	Thr	Glu	Leu	Glu	His	His	Ala	Asn	Leu	Val	Pro	Trp	Gln
	130					135					140				
Glu	Leu	Cys	Arg	Arg	Thr	Gly	Ala	Thr	Leu	Lys	Trp	Tyr	Lys	Val	Thr
145					150					155					160
Glu	Asp	Gly	Arg	Ile	Asp	Leu	Asp	Ser	Leu	Glu	Leu	Asp	Glu	Thr	Val
				165					170					175	
Lys	Val	Val	Ala	Phe	Thr	His	Gln	Ser	Asn	Val	Thr	Gly	Ala	Val	Ala
			180					185					190		
Asp	Val	Pro	Glu	Leu	Val	Arg	Arg	Ala	Lys	Ala	Val	Gly	Ala	Leu	Thr
		195					200					205			
Val	Leu	Asp	Ala	Cys	Gln	Ser	Val	Pro	His	Met	Pro	Val	Asn	Phe	His
	210					215					220				
Glu	Leu	Asp	Val	Asp	Phe	Ser	Ala	Phe	Ser	Gly	His	Lys	Met	Leu	Gly
225					230					235					240
Pro	Ala	Gly	Val	Gly	Val	Val	Tyr	Ala	Lys	Ser	Pro	Ile	Leu	Asp	Glu
				245					250					255	
Leu	Pro	Pro	Phe	Leu	Thr	Gly	Gly	Ser	Met	Ile	Glu	Val	Val	Thr	Met
			260					265					270		
Glu	Gly	Ser	Thr	Tyr	Ala	Ala	Ala	Pro	Gln	Arg	Phe	Glu	Ala	Gly	Thr
		275					280					285			
Gln	Met	Thr	Ser	Gln	Val	Val	Gly	Leu	Gly	Ala	Ala	Val	Asp	Met	Leu
	290					295					300				
Asn	Glu	Ile	Gly	Met	Glu	Ala	Ile	Ala	Ala	His	Glu	His	Ala	Leu	Thr
305					310					315					320
Ala	Tyr	Ala	Leu	Glu	Lys	Leu	Thr	Ala	Ile	Lys	Gly	Leu	Thr	Ile	Ala
				325					330					335	
Gly	Pro	Leu	Thr	Ala	Glu	Gln	Arg	Gly	Gly	Ala	Ile	Ser	Phe	Gly	Val
			340					345					350		

Glu Gly Ile His Pro His Asp Leu Gly Gln Val Leu Asp Asp Gln Gly  
 355 360 365  
 Val Asn Ile Arg Val Gly His His Cys Ala Trp Pro Val His Arg Ser  
 370 375 380  
 Met Asn Val Gln Ser Thr Ala Arg Ala Ser Phe Tyr Leu Tyr Asn Thr  
 385 390 395 400  
 Phe Glu Glu Ile Asp Arg Leu Ala Ala Ala Ile Glu Lys Ala Lys Gln  
 405 410 415  
 Phe Phe Gly Val Glu  
 420

&lt;210&gt; 659

&lt;211&gt; 570

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(547)

&lt;223&gt; RXA02517

&lt;400&gt; 659

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cagcgatcga gaaggccaag caattctttg gagttgagta atg aac ctt gag cag 115  
 Met Asn Leu Glu Gln  
 1 5

atg tac cag gag gtg atc ctg gac cac tac aaa aac cca cag cac aag 163  
 Met Tyr Gln Glu Val Ile Leu Asp His Tyr Lys Asn Pro Gln His Lys  
 10 15 20

ggc ctt cgg gat cct ttc gat gct gag gtt cac cac gtc aac cct tct 211  
 Gly Leu Arg Asp Pro Phe Asp Ala Glu Val His His Val Asn Pro Ser  
 25 30 35

tgt ggc gac gaa ttg act ctg cgc gtg aag ctg tct gag gac ggc tcc 259  
 Cys Gly Asp Glu Leu Thr Leu Arg Val Lys Leu Ser Glu Asp Gly Ser  
 40 45 50

acc gtg gag gac gtc tcc tac gaa gca gtt ggt tgc tca atc agc cag 307  
 Thr Val Glu Asp Val Ser Tyr Glu Ala Val Gly Cys Ser Ile Ser Gln  
 55 60 65

gcc tcc acg tcc gtt atg gcc gag gag atc gtg ggc caa ccc gtc gac 355  
 Ala Ser Thr Ser Val Met Ala Glu Glu Ile Val Gly Gln Pro Val Asp  
 70 75 80 85

aag gcg ctg gaa aag ctc aca gaa ttt gag aag atg atc gtt tcc cgc 403  
 Lys Ala Leu Glu Lys Leu Thr Glu Phe Glu Lys Met Ile Val Ser Arg  
 90 95 100

ggt cag ttt gtt ggc gat gaa gat ctc atc gga gat ggc gtt gct ttc 451  
 Gly Gln Phe Val Gly Asp Glu Asp Leu Ile Gly Asp Gly Val Ala Phe  
 105 110 115

tcc gga gtc gcc aag tac ccg gca cgc gtg aag tgc gcg ctg ctt ggg 499  
 Ser Gly Val Ala Lys Tyr Pro Ala Arg Val Lys Cys Ala Leu Leu Gly  
           120                          125                          130

tgg aag gct ttc cag gcg gca acc gct gac gct gtt gcg cac gca cat 547  
 Trp Lys Ala Phe Gln Ala Ala Thr Ala Asp Ala Val Ala His Ala His  
           135                          140                          145

tagcccgctg tattaattgg agg 570

<210> 660

<211> 149

<212> PRT

<213> Corynebacterium glutamicum

<400> 660

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Asn Pro Gln His Lys Gly Leu Arg Asp Pro Phe Asp Ala Glu Val His  
           20                          25                          30

His Val Asn Pro Ser Cys Gly Asp Glu Leu Thr Leu Arg Val Lys Leu  
           35                          40                          45

Ser Glu Asp Gly Ser Thr Val Glu Asp Val Ser Tyr Glu Ala Val Gly  
       50                          55                          60

Cys Ser Ile Ser Gln Ala Ser Thr Ser Val Met Ala Glu Glu Ile Val  
       65                          70                          75                          80

Gly Gln Pro Val Asp Lys Ala Leu Glu Lys Leu Thr Glu Phe Glu Lys  
           85                          90                          95

Met Ile Val Ser Arg Gly Gln Phe Val Gly Asp Glu Asp Leu Ile Gly  
           100                          105                          110

Asp Gly Val Ala Phe Ser Gly Val Ala Lys Tyr Pro Ala Arg Val Lys  
           115                          120                          125

Cys Ala Leu Leu Gly Trp Lys Ala Phe Gln Ala Ala Thr Ala Asp Ala  
       130                          135                          140

Val Ala His Ala His  
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<210> 661

<211> 1167

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1144)

<223> RXA01747

<400> 661

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ctaaaaatat cactaactcg aaagatgtaa ggttgcattt	gtg act atc gca cct	115
	Val Thr Ile Ala Pro	
	1 5	
gaa gga cga cga ctg cta cgc gtc gaa gct cga aac tca gaa acc ccg	163	
Glu Gly Arg Arg Leu Leu Arg Val Glu Ala Arg Asn Ser Glu Thr Pro		
	10 15 20	
att gag acg aag cct cga tgg att aga aac cag gtc aaa aac gga cct	211	
Ile Glu Thr Lys Pro Arg Trp Ile Arg Asn Gln Val Lys Asn Gly Pro		
	25 30 35	
gag tat cag gat atg aag gaa cgt gtc gct ggc gca tca cta cac act	259	
Glu Tyr Gln Asp Met Lys Glu Arg Val Ala Gly Ala Ser Leu His Thr		
	40 45 50	
gtg tgt cag gag gct ggc tgt cct aat atc cat gag tgt tgg gaa tcc	307	
Val Cys Gln Glu Ala Gly Cys Pro Asn Ile His Glu Cys Trp Glu Ser		
	55 60 65	
cgt gag gca acc ttc ctc att ggt ggc gcc aac tgc tct cgc cgc tgt	355	
Arg Glu Ala Thr Phe Leu Ile Gly Gly Ala Asn Cys Ser Arg Arg Cys		
	70 75 80 85	
gat ttc tgc atg atc aac tcg gct cgc cct gag cca ctc gac cgc ggt	403	
Asp Phe Cys Met Ile Asn Ser Ala Arg Pro Glu Pro Leu Asp Arg Gly		
	90 95 100	
gag cca ctg cgt gtc gct gag tct gtt cgt gag atg cag ctg aat tac	451	
Glu Pro Leu Arg Val Ala Glu Ser Val Arg Glu Met Gln Leu Asn Tyr		
	105 110 115	
tcc acc atc acc ggt gtt acc cgt gat gat ctg gat gat gaa ggc gca	499	
Ser Thr Ile Thr Gly Val Thr Arg Asp Asp Leu Asp Asp Glu Gly Ala		
	120 125 130	
tgg ctg tac tca gaa gtg gtt cgt aag atc cac gag ctg aac cca cac	547	
Trp Leu Tyr Ser Glu Val Val Arg Lys Ile His Glu Leu Asn Pro His		
	135 140 145	
acc ggt gtg gaa aac ctg gtg cct gat ttc tcc ggc aag aag gat ctg	595	
Thr Gly Val Glu Asn Leu Val Pro Asp Phe Ser Gly Lys Lys Asp Leu		
	150 155 160 165	
ctg cag gaa gtt ttt gaa tcc cgc cca gag gtt ttc gct cac aac gtg	643	
Leu Gln Glu Val Phe Glu Ser Arg Pro Glu Val Phe Ala His Asn Val		
	170 175 180	
gaa act gtg cca cgt att ttc aag cgc att cgc cca gca ttc cgc tac	691	
Glu Thr Val Pro Arg Ile Phe Lys Arg Ile Arg Pro Ala Phe Arg Tyr		
	185 190 195	
gag cgt tca ctt gat gtg atc cgt cag gct cgc gat ttc ggt ctg gtg	739	
Glu Arg Ser Leu Asp Val Ile Arg Gln Ala Arg Asp Phe Gly Leu Val		
	200 205 210	
acc aag tcc aac ctg att ttg ggc atg ggt gaa acc aag gaa gaa atc	787	
Thr Lys Ser Asn Leu Ile Leu Gly Met Gly Glu Thr Lys Glu Glu Ile		
	215 220 225	

acc gag gcg ctg cag gat ctg cac gac gct ggc tgt gac atc atc acc 835  
 Thr Glu Ala Leu Gln Asp Leu His Asp Ala Gly Cys Asp Ile Ile Thr  
 230 235 240 245

atc acc cag tac ctg cgt cct ggt cct ttg ttc cac ccc atc gag cgt 883  
 Ile Thr Gln Tyr Leu Arg Pro Gly Pro Leu Phe His Pro Ile Glu Arg  
 250 255 260

tgg gtg aag cct gag gag ttc ctc gag cac gct gat gct gca aag gaa 931  
 Trp Val Lys Pro Glu Glu Phe Leu Glu His Ala Asp Ala Lys Glu  
 265 270 275

atg ggc ttc gct gct gtt atg tcc ggc cca ttg gtt cgt tcc tct tac 979  
 Met Gly Phe Ala Ala Val Met Ser Gly Pro Leu Val Arg Ser Ser Tyr  
 280 285 290

cgt gca ggc cgt ctg tac gcg cag gcc atg gag ttc cgt ggc gag gaa  
 1027  
 Arg Ala Gly Arg Leu Tyr Ala Gln Ala Met Glu Phe Arg Gly Glu Glu  
 295 300 305

atc cca gca cac ctc gcg cac ctg aag gat act tcc gga gga tcc acc  
 1075  
 Ile Pro Ala His Leu Ala His Leu Lys Asp Thr Ser Gly Gly Ser Thr  
 310 315 320 325

gcc cag gaa gca tct aca ctt ctg gag cgt tac ggt gct tcc gaa gac  
 1123  
 Ala Gln Glu Ala Ser Thr Leu Leu Glu Arg Tyr Gly Ala Ser Glu Asp  
 330 335 340

acc cca gtg gtg tcc ttc aac taagcccgaa gttttttaac cgc  
 1167  
 Thr Pro Val Val Ser Phe Asn  
 345

<210> 662

<211> 348

<212> PRT

<213> Corynebacterium glutamicum

<400> 662

Val Thr Ile Ala Pro Glu Gly Arg Arg Leu Leu Arg Val Glu Ala Arg  
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Asn Ser Glu Thr Pro Ile Glu Thr Lys Pro Arg Trp Ile Arg Asn Gln  
 20 25 30

Val Lys Asn Gly Pro Glu Tyr Gln Asp Met Lys Glu Arg Val Ala Gly  
 35 40 45

Ala Ser Leu His Thr Val Cys Gln Glu Ala Gly Cys Pro Asn Ile His  
 50 55 60

Glu Cys Trp Glu Ser Arg Glu Ala Thr Phe Leu Ile Gly Gly Ala Asn  
 65 70 75 80

Cys Ser Arg Arg Cys Asp Phe Cys Met Ile Asn Ser Ala Arg Pro Glu  
 85 90 95

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Pro Leu Asp Arg Gly Glu Pro Leu Arg Val Ala Glu Ser Val Arg Glu
      100                      105                      110

Met Gln Leu Asn Tyr Ser Thr Ile Thr Gly Val Thr Arg Asp Asp Leu
      115                      120                      125

Asp Asp Glu Gly Ala Trp Leu Tyr Ser Glu Val Val Arg Lys Ile His
      130                      135                      140

Glu Leu Asn Pro His Thr Gly Val Glu Asn Leu Val Pro Asp Phe Ser
      145                      150                      155                      160

Gly Lys Lys Asp Leu Leu Gln Glu Val Phe Glu Ser Arg Pro Glu Val
      165                      170                      175

Phe Ala His Asn Val Glu Thr Val Pro Arg Ile Phe Lys Arg Ile Arg
      180                      185                      190

Pro Ala Phe Arg Tyr Glu Arg Ser Leu Asp Val Ile Arg Gln Ala Arg
      195                      200                      205

Asp Phe Gly Leu Val Thr Lys Ser Asn Leu Ile Leu Gly Met Gly Glu
      210                      215                      220

Thr Lys Glu Glu Ile Thr Glu Ala Leu Gln Asp Leu His Asp Ala Gly
      225                      230                      235                      240

Cys Asp Ile Ile Thr Ile Thr Gln Tyr Leu Arg Pro Gly Pro Leu Phe
      245                      250                      255

His Pro Ile Glu Arg Trp Val Lys Pro Glu Glu Phe Leu Glu His Ala
      260                      265                      270

Asp Ala Ala Lys Glu Met Gly Phe Ala Ala Val Met Ser Gly Pro Leu
      275                      280                      285

Val Arg Ser Ser Tyr Arg Ala Gly Arg Leu Tyr Ala Gln Ala Met Glu
      290                      295                      300

Phe Arg Gly Glu Glu Ile Pro Ala His Leu Ala His Leu Lys Asp Thr
      305                      310                      315                      320

Ser Gly Gly Ser Thr Ala Gln Glu Ala Ser Thr Leu Leu Glu Arg Tyr
      325                      330                      335

Gly Ala Ser Glu Asp Thr Pro Val Val Ser Phe Asn
      340                      345

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&lt;210&gt; 663

&lt;211&gt; 876

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(853)

&lt;223&gt; RXA01746

&lt;400&gt; 663

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				Met	Thr	Ala	Pro	Arg								
				1				5								
gat	cct	ttt	ttc	ccc	gca	gat	ctt	tct	atc	cgc	gcg	tct	gca	gag	ccc	163
Asp	Pro	Phe	Phe	Pro	Ala	Asp	Leu	Ser	Ile	Arg	Ala	Ser	Ala	Glu	Pro	
				10					15					20		
att	gaa	att	cag	cgg	ttg	ggt	ttg	atc	gat	tat	caa	gag	gcc	tgg	gat	211
Ile	Glu	Ile	Gln	Arg	Leu	Gly	Leu	Ile	Asp	Tyr	Gln	Glu	Ala	Trp	Asp	
			25					30					35			
tat	caa	gca	gag	ctt	gct	acc	cgt	agg	gct	aat	gat	gaa	atc	cct	gat	259
Tyr	Gln	Ala	Glu	Leu	Ala	Thr	Arg	Arg	Ala	Asn	Asp	Glu	Ile	Pro	Asp	
		40					45					50				
cag	ctg	ctt	att	ttg	gag	cac	ccg	tcg	gtg	tat	acc	gca	ggt	aag	cgc	307
Gln	Leu	Leu	Ile	Leu	Glu	His	Pro	Ser	Val	Tyr	Thr	Ala	Gly	Lys	Arg	
	55					60					65					
acc	cag	ccg	gaa	gat	ctt	ccc	acc	aac	gga	ctg	ccg	gtg	atc	aat	gct	355
Thr	Gln	Pro	Glu	Asp	Leu	Pro	Thr	Asn	Gly	Leu	Pro	Val	Ile	Asn	Ala	
	70				75				80						85	
gat	cgt	ggt	ggt	cgc	atc	acg	tgg	cat	ggt	cct	ggc	caa	ttg	gtg	atc	403
Asp	Arg	Gly	Gly	Arg	Ile	Thr	Trp	His	Gly	Pro	Gly	Gln	Leu	Val	Ile	
				90					95				100			
tat	ccg	atc	atc	aaa	tta	gcc	gat	ccg	atc	gat	gtg	gtt	gat	tac	gta	451
Tyr	Pro	Ile	Ile	Lys	Leu	Ala	Asp	Pro	Ile	Asp	Val	Val	Asp	Tyr	Val	
			105				110						115			
aga	cgc	ctc	gag	gaa	gcg	ctc	atc	caa	gtt	gtc	ggc	gat	atg	ggt	gtt	499
Arg	Arg	Leu	Glu	Glu	Ala	Leu	Ile	Gln	Val	Val	Gly	Asp	Met	Gly	Val	
		120					125					130				
gcc	ggc	gct	ggg	cgc	att	gat	ggg	cgt	tcg	ggt	gtg	tgg	gtg	cca	gct	547
Ala	Gly	Ala	Gly	Arg	Ile	Asp	Gly	Arg	Ser	Gly	Val	Trp	Val	Pro	Ala	
	135					140					145					
cat	gat	ggt	tgg	gtg	gac	agc	aag	gtt	gcg	gcc	atc	ggc	att	cga	ata	595
His	Asp	Gly	Trp	Val	Asp	Ser	Lys	Val	Ala	Ala	Ile	Gly	Ile	Arg	Ile	
	150				155					160					165	
act	cgt	ggt	gtt	gca	atg	cac	ggt	gtg	gcc	atc	aac	tgc	aac	aac	acg	643
Thr	Arg	Gly	Val	Ala	Met	His	Gly	Val	Ala	Ile	Asn	Cys	Asn	Asn	Thr	
				170					175					180		
ttg	gat	ttc	tat	gag	cac	atc	att	ccg	tgt	ggc	att	gct	gat	gca	ggc	691
Leu	Asp	Phe	Tyr	Glu	His	Ile	Ile	Pro	Cys	Gly	Ile	Ala	Asp	Ala	Gly	
			185					190					195			
ttg	agc	aca	ctc	tcg	agg	gaa	ctg	aaa	agg	gac	gtt	tca	gtt	gag	gaa	739
Leu	Ser	Thr	Leu	Ser	Arg	Glu	Leu	Lys	Arg	Asp	Val	Ser	Val	Glu	Glu	
		200					205					210				
tta	gtc	gag	cca	tcg	atc	cgc	gca	ttg	gat	gat	gct	ttg	gct	ggt	cgg	787
Leu	Val	Glu	Pro	Ser	Ile	Arg	Ala	Leu	Asp	Asp	Ala	Leu	Ala	Gly	Arg	
	215					220					225					

ctg gtt gtt tct gat cat tct ttc ggc agc gcg ccc gac cca act aag 835  
 Leu Val Val Ser Asp His Ser Phe Gly Ser Ala Pro Asp Pro Thr Lys  
 230 235 240 245

aat ctc cct aaa cgg ggg tagtacgagg aattttgtcg gtg 876  
 Asn Leu Pro Lys Arg Gly  
 250

<210> 664

<211> 251

<212> PRT

<213> Corynebacterium glutamicum

<400> 664

Met Thr Ala Pro Arg Asp Pro Phe Phe Pro Ala Asp Leu Ser Ile Arg  
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Ala Ser Ala Glu Pro Ile Glu Ile Gln Arg Leu Gly Leu Ile Asp Tyr  
 20 25 30

Gln Glu Ala Trp Asp Tyr Gln Ala Glu Leu Ala Thr Arg Arg Ala Asn  
 35 40 45

Asp Glu Ile Pro Asp Gln Leu Leu Ile Leu Glu His Pro Ser Val Tyr  
 50 55 60

Thr Ala Gly Lys Arg Thr Gln Pro Glu Asp Leu Pro Thr Asn Gly Leu  
 65 70 75 80

Pro Val Ile Asn Ala Asp Arg Gly Gly Arg Ile Thr Trp His Gly Pro  
 85 90 95

Gly Gln Leu Val Ile Tyr Pro Ile Ile Lys Leu Ala Asp Pro Ile Asp  
 100 105 110

Val Val Asp Tyr Val Arg Arg Leu Glu Glu Ala Leu Ile Gln Val Val  
 115 120 125

Gly Asp Met Gly Val Ala Gly Ala Gly Arg Ile Asp Gly Arg Ser Gly  
 130 135 140

Val Trp Val Pro Ala His Asp Gly Trp Val Asp Ser Lys Val Ala Ala  
 145 150 155 160

Ile Gly Ile Arg Ile Thr Arg Gly Val Ala Met His Gly Val Ala Ile  
 165 170 175

Asn Cys Asn Asn Thr Leu Asp Phe Tyr Glu His Ile Ile Pro Cys Gly  
 180 185 190

Ile Ala Asp Ala Gly Leu Ser Thr Leu Ser Arg Glu Leu Lys Arg Asp  
 195 200 205

Val Ser Val Glu Glu Leu Val Glu Pro Ser Ile Arg Ala Leu Asp Asp  
 210 215 220

Ala Leu Ala Gly Arg Leu Val Val Ser Asp His Ser Phe Gly Ser Ala  
 225 230 235 240

Pro Asp Pro Thr Lys Asn Leu Pro Lys Arg Gly

245

250

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<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1156)
<223> RXA02106
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aagcaaaatc tctttagcaa attcgggttac tgtggggcgc																
										atg	aat	aac	cat	ttt		115
										Met	Asn	Asn	His	Phe		
										1				5		
gag ctc aaa gta cct ggt gga aag ctt gtc gtc gtt gat gtg acc acc																163
Glu	Leu	Lys	Val	Pro	Gly	Gly	Lys	Leu	Val	Val	Val	Asp	Val	Thr	Thr	
				10					15					20		
gat ctg gat tcc att gct gac gtg aag att tcc ggc gat ttc ttc ctc																211
Asp	Leu	Asp	Ser	Ile	Ala	Asp	Val	Lys	Ile	Ser	Gly	Asp	Phe	Phe	Leu	
			25					30					35			
gaa ccc gat gag gca ttc ttc gcc ctt ggc cgg gcg ctg cag ggg gcg																259
Glu	Pro	Asp	Glu	Ala	Phe	Phe	Ala	Leu	Gly	Arg	Ala	Leu	Gln	Gly	Ala	
			40				45					50				
tcg gtg ggt gat aac act gat cgt ttg cag gca aag ttg gat gga gcg																307
Ser	Val	Gly	Asp	Asn	Thr	Asp	Arg	Leu	Gln	Ala	Lys	Leu	Asp	Ala	Ala	
	55					60					65					
ttg gcg gaa tat gat gac gtt gag cta cac ggc ttt agc act gcg gat																355
Leu	Ala	Glu	Tyr	Asp	Asp	Val	Glu	Leu	His	Gly	Phe	Ser	Thr	Ala	Asp	
70					75					80					85	
att gct tta gct gtg cgt cgg gca gtc acc ggc gcg caa gat ttc acc																403
Ile	Ala	Leu	Ala	Val	Arg	Arg	Ala	Val	Thr	Gly	Ala	Gln	Asp	Phe	Thr	
				90					95					100		
gat tat gaa tgg gaa atc ctg cac cca ggg gtg ctt cct acc cca ctt																451
Asp	Tyr	Glu	Trp	Glu	Ile	Leu	His	Pro	Gly	Val	Leu	Pro	Thr	Pro	Leu	
			105					110					115			
aac gtt gcg ttg gat gag ctc ctt ttg gac caa gtt gcc agt ggt cag																499
Asn	Val	Ala	Leu	Asp	Glu	Leu	Leu	Leu	Asp	Gln	Val	Ala	Ser	Gly	Gln	
		120					125					130				
cgt ggc ccg acg atg cgc att tgg gat tgg gat gat cgc gcc aca gtg																547
Arg	Gly	Pro	Thr	Met	Arg	Ile	Trp	Asp	Trp	Asp	Asp	Arg	Ala	Thr	Val	
	135					140					145					
atc ggt agt ttc cag tca tat gtc aat gaa atc aac caa gaa ggc gtt																595
Ile	Gly	Ser	Phe	Gln	Ser	Tyr	Val	Asn	Glu	Ile	Asn	Gln	Glu	Gly	Val	
150					155					160					165	
aat gaa cat ggt gtg acc gtg gta cga cgc atg tct ggt ggc ggt gca																643

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      Asn Glu His Gly Val Thr Val Val Arg Arg Met Ser Gly Gly Gly Ala
      170                               175                               180

atg ttt atg gag ggc ggc aac tgc atc acc tat tcc ctg tat gca ccg      691
Met Phe Met Glu Gly Gly Asn Cys Ile Thr Tyr Ser Leu Tyr Ala Pro
      185                               190                               195

gaa tct ctc gtt gct ggt ttg agc tat gag cag tcc tat gaa tat ttg      739
Glu Ser Leu Val Ala Gly Leu Ser Tyr Glu Gln Ser Tyr Glu Tyr Leu
      200                               205                               210

gat cgt tgg gtg att gct gcg ctg aag aca cac gat gtt gac gct tgg      787
Asp Arg Trp Val Ile Ala Ala Leu Lys Thr His Asp Val Asp Ala Trp
      215                               220                               225

tac gtg cct atc aat gac atc acc tcc acc ggc gga aaa atc ggt ggc      835
Tyr Val Pro Ile Asn Asp Ile Thr Ser Thr Gly Gly Lys Ile Gly Gly
      230                               235                               240                               245

gct gca cag aaa cgt cgc agt ggc gca gtc ctc cac cac gtg acc atg      883
Ala Ala Gln Lys Arg Arg Ser Gly Ala Val Leu His His Val Thr Met
      250                               255                               260

tcc tat gac atc gat gcg gac atg atg acc cag gtg ttg cgc att gga      931
Ser Tyr Asp Ile Asp Ala Asp Met Met Thr Gln Val Leu Arg Ile Gly
      265                               270                               275

aag gtg aag att tcc gac aag ggt ctt cgc agc gca aag aag cgc gtt      979
Lys Val Lys Ile Ser Asp Lys Gly Leu Arg Ser Ala Lys Lys Arg Val
      280                               285                               290

gat cct ctg cgc cgc caa aca ggt gca tca cgt gag caa atc atc gac
1027
Asp Pro Leu Arg Arg Gln Thr Gly Ala Ser Arg Glu Gln Ile Ile Asp
      295                               300                               305

acc cta aag tcc aca ttc agt gct agg tac ggc gcg caa gaa gta gag
1075
Thr Leu Lys Ser Thr Phe Ser Ala Arg Tyr Gly Ala Gln Glu Val Glu
      310                               315                               320                               325

ctc agc gat gaa gat ttc gcg gca ggc cac gac cta gta aaa acc aaa
1123
Leu Ser Asp Glu Asp Phe Ala Ala Gly His Asp Leu Val Lys Thr Lys
      330                               335                               340

tac gcc acc gag gag tgg act aag cga gtt caa tagtttctat ggatctgcac
1176
Tyr Ala Thr Glu Glu Trp Thr Lys Arg Val Gln
      345                               350

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aag  
1179

<210> 666

<211> 352

<212> PRT

<213> Corynebacterium glutamicum

<400> 666

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 Gly Asp Phe Phe Leu Glu Pro Asp Glu Ala Phe Phe Ala Leu Gly Arg  
 35 40 45  
 Ala Leu Gln Gly Ala Ser Val Gly Asp Asn Thr Asp Arg Leu Gln Ala  
 50 55 60  
 Lys Leu Asp Ala Ala Leu Ala Glu Tyr Asp Asp Val Glu Leu His Gly  
 65 70 75 80  
 Phe Ser Thr Ala Asp Ile Ala Leu Ala Val Arg Arg Ala Val Thr Gly  
 85 90 95  
 Ala Gln Asp Phe Thr Asp Tyr Glu Trp Glu Ile Leu His Pro Gly Val  
 100 105 110  
 Leu Pro Thr Pro Leu Asn Val Ala Leu Asp Glu Leu Leu Leu Asp Gln  
 115 120 125  
 Val Ala Ser Gly Gln Arg Gly Pro Thr Met Arg Ile Trp Asp Trp Asp  
 130 135 140  
 Asp Arg Ala Thr Val Ile Gly Ser Phe Gln Ser Tyr Val Asn Glu Ile  
 145 150 155 160  
 Asn Gln Glu Gly Val Asn Glu His Gly Val Thr Val Val Arg Arg Met  
 165 170 175  
 Ser Gly Gly Gly Ala Met Phe Met Glu Gly Gly Asn Cys Ile Thr Tyr  
 180 185 190  
 Ser Leu Tyr Ala Pro Glu Ser Leu Val Ala Gly Leu Ser Tyr Glu Gln  
 195 200 205  
 Ser Tyr Glu Tyr Leu Asp Arg Trp Val Ile Ala Ala Leu Lys Thr His  
 210 215 220  
 Asp Val Asp Ala Trp Tyr Val Pro Ile Asn Asp Ile Thr Ser Thr Gly  
 225 230 235 240  
 Gly Lys Ile Gly Gly Ala Ala Gln Lys Arg Arg Ser Gly Ala Val Leu  
 245 250 255  
 His His Val Thr Met Ser Tyr Asp Ile Asp Ala Asp Met Met Thr Gln  
 260 265 270  
 Val Leu Arg Ile Gly Lys Val Lys Ile Ser Asp Lys Gly Leu Arg Ser  
 275 280 285  
 Ala Lys Lys Arg Val Asp Pro Leu Arg Arg Gln Thr Gly Ala Ser Arg  
 290 295 300  
 Glu Gln Ile Ile Asp Thr Leu Lys Ser Thr Phe Ser Ala Arg Tyr Gly  
 305 310 315 320  
 Ala Gln Glu Val Glu Leu Ser Asp Glu Asp Phe Ala Ala Gly His Asp

				325					330					335		
Leu	Val	Lys	Thr	Lys	Tyr	Ala	Thr	Glu	Glu	Trp	Thr	Lys	Arg	Val	Gln	
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<210> 667
<211> 403
<212> DNA
<213> Corynebacterium glutamicum
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<220>
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<222> (101) .. (403)
<223> RXS01183
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ttccggtttta acgacacgac ttgcgaggag tcttaaaata atg gcg ttc tcc gta 115															
Met Ala Phe Ser Val 5															
gag atg ccc gag ctg ggc gaa tca gta acc gaa ggc acg atc acc cag 163															
Glu Met Pro Glu Leu Gly Glu Ser Val Thr Glu Gly Thr Ile Thr Gln 20															
tgg ttg aag tct gtt ggt gac act gtt gag gta gat gag ccg ttg ctc 211															
Trp Leu Lys Ser Val Gly Asp Thr Val Glu Val Asp Glu Pro Leu Leu 35															
gag gtc tca act gac aag gtc gac acc gag att ccc tct cct gtc gcc 259															
Glu Val Ser Thr Asp Lys Val Asp Thr Glu Ile Pro Ser Pro Val Ala 50															
ggt gtc atc cta gag att aag gct gaa gag gat gac acc gtc gac gtc 307															
Gly Val Ile Leu Glu Ile Lys Ala Glu Glu Asp Asp Thr Val Asp Val 65															
ggc ggt gtc att gca ata atc ggc gat gct gat gag act cct gcc aac 355															
Gly Gly Val Ile Ala Ile Ile Gly Asp Ala Asp Glu Thr Pro Ala Asn 85															
gaa gct cct gcc gac gag gca cca gct cct gcc gaa gag gaa gaa cca 403															
Glu Ala Pro Ala Asp Glu Ala Pro Ala Pro Ala Glu Glu Glu Glu Pro 100															

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<210> 668
<211> 101
<212> PRT
<213> Corynebacterium glutamicum
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<400> 668
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Gly Thr Ile Thr Gln Trp Leu Lys Ser Val Gly Asp Thr Val Glu Val
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Asp	Glu	Pro	Leu	Leu	Glu	Val	Ser	Thr	Asp	Lys	Val	Asp	Thr	Glu	Ile
		35					40					45			
Pro	Ser	Pro	Val	Ala	Gly	Val	Ile	Leu	Glu	Ile	Lys	Ala	Glu	Glu	Asp
	50					55					60				
Asp	Thr	Val	Asp	Val	Gly	Gly	Val	Ile	Ala	Ile	Ile	Gly	Asp	Ala	Asp
65					70					75					80
Glu	Thr	Pro	Ala	Asn	Glu	Ala	Pro	Ala	Asp	Glu	Ala	Pro	Ala	Pro	Ala
				85					90					95	
Glu	Glu	Glu	Glu	Pro											
				100											

&lt;210&gt; 669

&lt;211&gt; 1305

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1282)

&lt;223&gt; RXS01260

&lt;400&gt; 669

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ctttacccat gagaagaaga ccttcggcat caatggcgaa gtg acc ttc aac tat 115  
 Val Thr Phe Asn Tyr 5

gag gat gct cac aag cgt tcc cgt ggc gtt tcc gac aag atc gtt gga 163  
 Glu Asp Ala His Lys Arg Ser Arg Gly Val Ser Asp Lys Ile Val Gly 20

ggc gtt cat tac ttg atg aag aag aac aag atc atc gaa att cat ggt 211  
 Gly Val His Tyr Leu Met Lys Lys Asn Lys Ile Ile Glu Ile His Gly 35

ctt gga aac ttc aag gat gct aag act ctt gag gtc acc gac ggt aag 259  
 Leu Gly Asn Phe Lys Asp Ala Lys Thr Leu Glu Val Thr Asp Gly Lys 50

gat gct ggc aag acc atc acc ttt gat gac tgc atc atc gca acc ggt 307  
 Asp Ala Gly Lys Thr Ile Thr Phe Asp Asp Cys Ile Ile Ala Thr Gly 65

tcg gta gtc aac acc ctc cgt ggc gtt gac ttc tca gag aac gtt gtg 355  
 Ser Val Val Asn Thr Leu Arg Gly Val Asp Phe Ser Glu Asn Val Val 85

tct ttt gaa gag cag att ctt aac cct gtt gcg cca aag aag atg gtc 403  
 Ser Phe Glu Glu Gln Ile Leu Asn Pro Val Ala Pro Lys Lys Met Val 100

att gtt ggt gca ggc gca att gga atg gaa ttc gcc tac gtt ctt ggt 451  
 Ile Val Gly Ala Gly Ala Ile Gly Met Glu Phe Ala Tyr Val Leu Gly

105				110				115								
aac	tac	ggt	gta	gat	gta	acc	gtc	atc	gag	ttc	atg	gat	cgt	gtg	ctt	499
Asn	Tyr	Gly	Val	Asp	Val	Thr	Val	Ile	Glu	Phe	Met	Asp	Arg	Val	Leu	
		120					125					130				
cca	aat	gaa	gat	gct	gaa	gtc	tcc	aag	gtt	att	gca	aag	gcc	tac	aag	547
Pro	Asn	Glu	Asp	Ala	Glu	Val	Ser	Lys	Val	Ile	Ala	Lys	Ala	Tyr	Lys	
		135				140					145					
aag	atg	ggc	gtt	aag	ctt	ctt	cct	ggc	cat	gca	acc	act	gct	gtt	cgg	595
Lys	Met	Gly	Val	Lys	Leu	Leu	Pro	Gly	His	Ala	Thr	Thr	Ala	Val	Arg	
150					155					160					165	
gac	aac	ggt	gac	ttt	gtc	gag	gtt	gat	tac	cag	aag	aag	ggc	tct	gac	643
Asp	Asn	Gly	Asp	Phe	Val	Glu	Val	Asp	Tyr	Gln	Lys	Lys	Gly	Ser	Asp	
				170					175					180		
aag	aca	gag	act	ctt	act	gtt	gat	cga	gtc	atg	gtt	tcc	gtt	ggt	ttc	691
Lys	Thr	Glu	Thr	Leu	Thr	Val	Asp	Arg	Val	Met	Val	Ser	Val	Gly	Phe	
			185					190					195			
cgt	cca	cgc	gtt	gag	gga	ttt	ggt	ctt	gaa	aac	act	ggc	gtt	aag	ctc	739
Arg	Pro	Arg	Val	Glu	Gly	Phe	Gly	Leu	Glu	Asn	Thr	Gly	Val	Lys	Leu	
		200					205					210				
acc	gag	cgt	ggc	gca	atc	gag	atc	gat	gat	tac	atg	cgt	acc	aac	gtc	787
Thr	Glu	Arg	Gly	Ala	Ile	Glu	Ile	Asp	Asp	Tyr	Met	Arg	Thr	Asn	Val	
	215					220					225					
gat	ggc	att	tac	gcc	atc	ggt	gac	gtg	acc	gcc	aag	ctt	cag	ctt	gct	835
Asp	Gly	Ile	Tyr	Ala	Ile	Gly	Asp	Val	Thr	Ala	Lys	Leu	Gln	Leu	Ala	
230					235					240					245	
cac	gtc	gca	gaa	gca	cag	ggc	att	gtt	gcc	gca	gag	act	att	gct	ggt	883
His	Val	Ala	Glu	Ala	Gln	Gly	Ile	Val	Ala	Ala	Glu	Thr	Ile	Ala	Gly	
				250					255					260		
gca	gaa	act	cag	act	ctt	ggt	gat	tac	atg	atg	atg	cca	cgt	gca	acc	931
Ala	Glu	Thr	Gln	Thr	Leu	Gly	Asp	Tyr	Met	Met	Met	Pro	Arg	Ala	Thr	
			265					270					275			
ttc	tgc	aac	cca	cag	gtt	tct	tcc	ttt	ggt	tac	acc	gaa	gag	cag	gcc	979
Phe	Cys	Asn	Pro	Gln	Val	Ser	Ser	Phe	Gly	Tyr	Thr	Glu	Glu	Gln	Ala	
		280					285					290				
aag	gag	aag	tgg	cca	gat	cgt	gag	atc	aag	gtt	gct	tcc	ttc	cca	ttc	
1027																
Lys	Glu	Lys	Trp	Pro	Asp	Arg	Glu	Ile	Lys	Val	Ala	Ser	Phe	Pro	Phe	
	295					300					305					
tct	gca	aac	ggt	aaa	gca	gtt	ggc	ctg	gca	gaa	act	gat	ggt	ttc	gca	
1075																
Ser	Ala	Asn	Gly	Lys	Ala	Val	Gly	Leu	Ala	Glu	Thr	Asp	Gly	Phe	Ala	
310					315					320					325	
aag	atc	gtt	gct	gat	gca	gaa	ttc	ggt	gag	ctg	ctc	ggt	gca	cac	ctg	
1123																
Lys	Ile	Val	Ala	Asp	Ala	Glu	Phe	Gly	Glu	Leu	Leu	Gly	Ala	His	Leu	
				330					335					340		



gtt gga gca aat gca tca gag ctc atc aat gaa ttg gtg ctt gct cag  
 1171  
 Val Gly Ala Asn Ala Ser Glu Leu Ile Asn Glu Leu Val Leu Ala Gln  
                   345                  350                  355

aac tgg gat ctc acc act gaa gag atc tct cgt agc gtc cat att cac  
 1219  
 Asn Trp Asp Leu Thr Thr Glu Glu Ile Ser Arg Ser Val His Ile His  
                   360                  365                  370

cca acg cta tct gag gca gtt aag gaa gct gca cac ggt atc tct gga  
 1267  
 Pro Thr Leu Ser Glu Ala Val Lys Glu Ala Ala His Gly Ile Ser Gly  
                   375                  380                  385

cac atg atc aac ttc tagaatccac ctcgttggcc ctg  
 1305  
 His Met Ile Asn Phe  
 390

<210> 670

<211> 394

<212> PRT

<213> Corynebacterium glutamicum

<400> 670

Val Thr Phe Asn Tyr Glu Asp Ala His Lys Arg Ser Arg Gly Val Ser  
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Asp Lys Ile Val Gly Gly Val His Tyr Leu Met Lys Lys Asn Lys Ile  
                   20                  25                  30

Ile Glu Ile His Gly Leu Gly Asn Phe Lys Asp Ala Lys Thr Leu Glu  
                   35                  40                  45

Val Thr Asp Gly Lys Asp Ala Gly Lys Thr Ile Thr Phe Asp Asp Cys  
                   50                  55                  60

Ile Ile Ala Thr Gly Ser Val Val Asn Thr Leu Arg Gly Val Asp Phe  
   65                  70                  75                  80

Ser Glu Asn Val Val Ser Phe Glu Glu Gln Ile Leu Asn Pro Val Ala  
                   85                  90                  95

Pro Lys Lys Met Val Ile Val Gly Ala Gly Ala Ile Gly Met Glu Phe  
                   100                  105                  110

Ala Tyr Val Leu Gly Asn Tyr Gly Val Asp Val Thr Val Ile Glu Phe  
                   115                  120                  125

Met Asp Arg Val Leu Pro Asn Glu Asp Ala Glu Val Ser Lys Val Ile  
                   130                  135                  140

Ala Lys Ala Tyr Lys Lys Met Gly Val Lys Leu Leu Pro Gly His Ala  
   145                  150                  155                  160

Thr Thr Ala Val Arg Asp Asn Gly Asp Phe Val Glu Val Asp Tyr Gln  
                   165                  170                  175

Lys Lys Gly Ser Asp Lys Thr Glu Thr Leu Thr Val Asp Arg Val Met

180						185						190					
Val	Ser	Val	Gly	Phe	Arg	Pro	Arg	Val	Glu	Gly	Phe	Gly	Leu	Glu	Asn		
		195					200					205					
Thr	Gly	Val	Lys	Leu	Thr	Glu	Arg	Gly	Ala	Ile	Glu	Ile	Asp	Asp	Tyr		
	210					215					220						
Met	Arg	Thr	Asn	Val	Asp	Gly	Ile	Tyr	Ala	Ile	Gly	Asp	Val	Thr	Ala		
225					230					235					240		
Lys	Leu	Gln	Leu	Ala	His	Val	Ala	Glu	Ala	Gln	Gly	Ile	Val	Ala	Ala		
				245					250					255			
Glu	Thr	Ile	Ala	Gly	Ala	Glu	Thr	Gln	Thr	Leu	Gly	Asp	Tyr	Met	Met		
			260					265					270				
Met	Pro	Arg	Ala	Thr	Phe	Cys	Asn	Pro	Gln	Val	Ser	Ser	Phe	Gly	Tyr		
		275					280					285					
Thr	Glu	Glu	Gln	Ala	Lys	Glu	Lys	Trp	Pro	Asp	Arg	Glu	Ile	Lys	Val		
	290					295					300						
Ala	Ser	Phe	Pro	Phe	Ser	Ala	Asn	Gly	Lys	Ala	Val	Gly	Leu	Ala	Glu		
305					310					315					320		
Thr	Asp	Gly	Phe	Ala	Lys	Ile	Val	Ala	Asp	Ala	Glu	Phe	Gly	Glu	Leu		
				325					330					335			
Leu	Gly	Ala	His	Leu	Val	Gly	Ala	Asn	Ala	Ser	Glu	Leu	Ile	Asn	Glu		
			340					345					350				
Leu	Val	Leu	Ala	Gln	Asn	Trp	Asp	Leu	Thr	Thr	Glu	Glu	Ile	Ser	Arg		
		355					360					365					
Ser	Val	His	Ile	His	Pro	Thr	Leu	Ser	Glu	Ala	Val	Lys	Glu	Ala	Ala		
	370					375					380						
His	Gly	Ile	Ser	Gly	His	Met	Ile	Asn	Phe								
385					390												

&lt;210&gt; 671

&lt;211&gt; 294

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(271)

&lt;223&gt; RXS01261

&lt;400&gt; 671

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atgcacgaca	atgacccact	aaacacgtat	ccttgaatgc	gtg	act	gaa	cat	tat	115
				Val	Thr	Glu	His	Tyr	
				1				5	

gac	gta	gta	gta	ctc	gga	gcc	ggc	ccc	ggg	ggc	tat	gtc	tcc	gcc	atc	163
Asp	Val	Val	Val	Leu	Gly	Ala	Gly	Pro	Gly	Gly	Tyr	Val	Ser	Ala	Ile	

	10	15	20	
cgt gca gcg cag ctt ggc aag aag gtt gct gta att gag aag cag tac				211
Arg Ala Ala Gln Leu Gly Lys Lys Val Ala Val Ile Glu Lys Gln Tyr				
	25	30	35	
tgg ggt ggt gtt tgc cta aac gtg ggc tgc att cct tcc aaa gtc tct				259
Trp Gly Gly Val Cys Leu Asn Val Gly Cys Ile Pro Ser Lys Val Ser				
	40	45	50	
gat caa aaa cgc tgaagttgcc cataccttta ccc				294
Asp Gln Lys Arg				
55				

<210> 672  
 <211> 57  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 672  
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 Tyr Val Ser Ala Ile Arg Ala Ala Gln Leu Gly Lys Lys Val Ala Val  
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 Ile Glu Lys Gln Tyr Trp Gly Gly Val Cys Leu Asn Val Gly Cys Ile  
 35 40 45  
 Pro Ser Lys Val Ser Asp Gln Lys Arg  
 50 55

<210> 673  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(982)  
 <223> RXA02717

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 gcgtccttca cccggccgag taccttttttc tgctcgagttt atg cca ccc cgc gac 115  
 Met Pro Pro Arg Asp  
 1 5  
 gat gca gct gaa gag cgt ctt tac cgc gca gca gag gtc ttc cat gac 163  
 Asp Ala Ala Glu Glu Arg Leu Tyr Arg Ala Ala Glu Val Phe His Asp  
 10 15 20  
 ctc ggt gca tcg ttt gtc tcc gtg act tat ggt gct ggc gga tca acc 211  
 Leu Gly Ala Ser Phe Val Ser Val Thr Tyr Gly Ala Gly Gly Ser Thr  
 25 30 35  
 cgt gag aga acc tca cgt att gct cga cga tta gcg aaa caa ccg ttg 259  
 Arg Glu Arg Thr Ser Arg Ile Ala Arg Arg Leu Ala Lys Gln Pro Leu

40						45						50						
acc	act	ctg	gtg	cac	ctg	acc	ctg	gtt	aac	cac	act	cgc	gaa	gag	atg			307
Thr	Thr	Leu	Val	His	Leu	Thr	Leu	Val	Asn	His	Thr	Arg	Glu	Glu	Met			
	55						60				65							
aag	gca	att	ctt	cgg	gaa	tac	cta	gag	ctg	gga	tta	aca	aac	ctg	ttg			355
Lys	Ala	Ile	Leu	Arg	Glu	Tyr	Leu	Glu	Leu	Gly	Leu	Thr	Asn	Leu	Leu			
	70				75					80					85			
gcg	ctt	cga	gga	gat	ccg	cct	gga	gac	cca	tta	ggc	gat	tgg	gtg	agc			403
Ala	Leu	Arg	Gly	Asp	Pro	Pro	Gly	Asp	Pro	Leu	Gly	Asp	Trp	Val	Ser			
				90					95					100				
acc	gat	gga	gga	ctg	aac	tat	gcc	tct	gag	ctc	atc	gat	ctt	att	aag			451
Thr	Asp	Gly	Gly	Leu	Asn	Tyr	Ala	Ser	Glu	Leu	Ile	Asp	Leu	Ile	Lys			
			105					110					115					
tcc	act	cct	gag	ttc	cgg	gaa	ttc	gac	ctc	ggc	atc	gcc	tcc	ttc	ccc			499
Ser	Thr	Pro	Glu	Phe	Arg	Glu	Phe	Asp	Leu	Gly	Ile	Ala	Ser	Phe	Pro			
		120					125					130						
gaa	ggg	cat	ttc	cgg	gcg	aaa	act	cta	gaa	gaa	gac	acc	aaa	tac	act			547
Glu	Gly	His	Phe	Arg	Ala	Lys	Thr	Leu	Glu	Glu	Asp	Thr	Lys	Tyr	Thr			
	135					140					145							
ctg	gcg	aag	ctg	cgt	gga	ggg	gca	gag	tac	tcc	atc	acg	cag	atg	ttc			595
Leu	Ala	Lys	Leu	Arg	Gly	Gly	Ala	Glu	Tyr	Ser	Ile	Thr	Gln	Met	Phe			
	150				155					160					165			
ttt	gat	gtg	gaa	gac	tac	ctg	cga	ctt	cgt	gat	cgc	ctt	gtc	gct	gca			643
Phe	Asp	Val	Glu	Asp	Tyr	Leu	Arg	Leu	Arg	Asp	Arg	Leu	Val	Ala	Ala			
				170					175					180				
gac	ccc	att	cat	ggc	gcg	aag	cca	atc	att	cct	ggc	atc	atg	ccc	att			691
Asp	Pro	Ile	His	Gly	Ala	Lys	Pro	Ile	Ile	Pro	Gly	Ile	Met	Pro	Ile			
			185					190					195					
acg	agc	ctg	cgg	tct	gtg	cgt	cga	cag	gtc	gaa	ctc	tct	ggc	gct	caa			739
Thr	Ser	Leu	Arg	Ser	Val	Arg	Arg	Gln	Val	Glu	Leu	Ser	Gly	Ala	Gln			
		200					205					210						
ttg	ccg	agc	caa	cta	gaa	gaa	tca	ctt	gtt	cga	gct	gca	aac	ggc	aat			787
Leu	Pro	Ser	Gln	Leu	Glu	Glu	Ser	Leu	Val	Arg	Ala	Ala	Asn	Gly	Asn			
	215					220					225							
gaa	gaa	gcg	aac	aaa	gac	gag	atc	cgc	aag	gtg	ggc	att	gaa	tat	tcc			835
Glu	Glu	Ala	Asn	Lys	Asp	Glu	Ile	Arg	Lys	Val	Gly	Ile	Glu	Tyr	Ser			
	230				235					240					245			
acc	aat	atg	gca	gag	cga	ctc	att	gcc	gaa	ggc	gcg	gaa	gat	ctg	cac			883
Thr	Asn	Met	Ala	Glu	Arg	Leu	Ile	Ala	Glu	Gly	Ala	Glu	Asp	Leu	His			
				250					255					260				
ttc	atg	acg	ctt	aac	ttc	acc	cgt	gca	acc	caa	gaa	gtg	ttg	tac	aac			931
Phe	Met	Thr	Leu	Asn	Phe	Thr	Arg	Ala	Thr	Gln	Glu	Val	Leu	Tyr	Asn			
			265					270					275					
ctt	ggc	atg	gcg	cct	gct	tgg	gga	gca	gag	cac	ggc	caa	gac	gcg	gtg			979
Leu	Gly	Met	Ala	Pro	Ala	Trp	Gly	Ala	Glu	His	Gly	Gln	Asp	Ala	Val			
		280					285					290						